



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification <sup>6</sup> : <b>A01N 37/18, 43/04, C12Q 1/00, 1/02, 1/68, C12N 5/00, 5/06, 15/00, 15/06, 15/09, 15/10, 15/11, G01N 33/53</b></p>	<p><b>A2</b></p>	<p>(11) International Publication Number: <b>WO 98/54963</b></p> <p>(43) International Publication Date: 10 December 1998 (10.12.98)</p>
<p>(21) International Application Number: PCT/US98/11422</p> <p>(22) International Filing Date: 4 June 1998 (04.06.98)</p> <p>(30) Priority Data:  60/048,915                      6 June 1997 (06.06.97)                      US  60/048,882                      6 June 1997 (06.06.97)                      US  (Continued on the following page)</p> <p>(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).</p> <p>(72) Inventors; and</p> <p>(75) Inventors/Applicants (for US only): YOUNG, Paul [US/US]; 122 Beckwith Street, Gaithersburg, MD 20878 (US). GREENE, John, M. [US/US]; 872 Diamond Drive, Gaithersburg, MD 20878 (US). FERRIE, Ann, M. [US/US]; 13203 L Astoria Hill Court, Germantown, MD 20874 (US). RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Olney, MD 20832 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). HU, Jing-Shan [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). EBNER, Reinhard [DE/US]; 9906 Shelburne Terrace #316,</p>		<p>Gaithersburg, MD 20878 (US). BREWER, Laurie, A. [US/US]; 14920 Mt. Nebo Road, Poolesville, MD 20837 (US). MOORE, Paul, A. [GB/US]; Apartment 104, 1908 Holly Ridge Drive, McLean, VA 22102 (US). SHI, Yanggu [CN/US]; 437 West Side Drive, Gaithersburg, MD 20878 (US). FLORENCE, Charles [US/US]; (US). FLORENCE, Kimberly [US/US]; 12805 Atlantic Avenue, Rockville, MD 20851 (US). LAFLEUR, David, W. [US/US]; 1615 Q Street, N.W. #807, Washington, DC 20009 (US). NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US). FAN, Ping [CN/US]; Apartment 302, 335 West Side Drive, Gaithersburg, MD 20878 (US). WEI, Ying-Fei [CN/US]; 13524 Straw Bale Lane, Darnestown, MD 20878 (US). FISCHER, Carrie, L. [US/US]; 5810 Hall Street, Burke, VA 22015 (US). SOPPET, Daniel, R. [US/US]; 15050 Stillfield Place, Centreville, VA 22020 (US). LI, Yi [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). ZENG, Zhizhen [CN/US]; 13950 Saddleview Drive, Gaithersburg, MD 20878 (US). KYAW, Hla [MM/US]; 520 Sugarbush Circle, Frederick, MD 21703 (US). YU, Guo-Liang [CN/US]; 13524 Straw Bale Lane, Darnestown, MD 20878 (US). FENG, Ping [CN/US]; 4 Relda Court, Gaithersburg, MD 20878 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). ENDRESS, Gregory, A. [US/US]; 9729 Clagett Farm Drive, Potomac, MD 20854 (US). CARTER, Kenneth, C. [US/US]; 11601 Brandy Hall Lane, North Potomac, MD 20878 (US).</p> <p>(74) Agents: HOOVER, Kenley, K. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 10850 (US).</p> <p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p><b>Published</b>  With declaration under Article 17(2)(a); without abstract;  title not checked by the International Searching Authority.</p>
<p>(54) Title: 207 HUMAN SECRETED PROTEINS</p>		

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Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

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## 207 Human Secreted Proteins

### *Field of the Invention*

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and their production.

### *Background of the Invention*

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using secreted proteins or the genes that encode them.

### *Summary of the Invention*

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

### *Detailed Description*

#### **Definitions**

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig



analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard,  
5 Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained  
10 in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42°C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the  
15 filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages  
20 of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH<sub>2</sub>PO<sub>4</sub>; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even  
25 lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include  
30 Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such  
35 as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5       The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

20       The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS -  
5 STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990);  
10 Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting  
15 activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present  
20 invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

## 25 Polynucleotides and Polypeptides of the Invention

### FEATURES OF PROTEIN ENCODED BY GENE NO: 1

This gene is expressed primarily in melanocytes and, to a lesser extent, in testes, ovary, kidney and other tissues.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer, disorders of neural crest derived cells including pigmentation defects, melanoma, reproductive organ defects, and defects of the kidney. Similarly,  
35 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skin,

reproductive, and renal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating disorders that arise from alterations in the number or fate of neural crest derived cells including cancers such as melanoma and defects of the developing reproductive system.

### **FEATURES OF PROTEIN ENCODED BY GENE NO: 2**

This gene is expressed primarily in infant brain and fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental disorders of the brain or lung. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and pulmonary systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating or diagnosing disorders associated with abnormal proliferation of cells in the Central nervous system and developing lung.

### **FEATURES OF PROTEIN ENCODED BY GENE NO: 3**

This gene is expressed primarily in breast lymph node and to a lesser extent in ovarian cancer and chondrosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune responses such as inflammation or immune surveillance for

tumors. This gene may be important for inflammatory responses associated with tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 236 as residues: Lys-45 to Val-50, Lys-69 to Arg-76.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of immune responses including those associated with tumor-induced inflammation.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 4**

This gene is expressed primarily in T-cells and T-cell lymphomas.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological diseases involving T-cells such as inflammation, autoimmunity, and cancers including T-cell lymphomas. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of T-cells and other cells of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosing and treating T-cell based disorders such as inflammatory diseases, autoimmune disease and tumors including T-cell lymphomas.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 5**

This gene is expressed primarily in activated monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation, autoimmunity, infection, or disorders involving activation of monocytes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 238 as residues: Asp-19 to Arg-31.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosing or treating diseases that result in activation of monocytes including infections, inflammatory responses or autoimmune diseases.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 6**

The translation product of this gene shares sequence homology with terminal deoxynucleotidyltransferase which is thought to be important in catalyzing the elongation of oligo- or polydeoxynucleotide chains.

This gene is expressed primarily in activated human neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer, particularly those of the blood such as leukemia and deficiencies in neutrophils such as neutropenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having

such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to terminal deoxynucleotidyltransferase indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and differential diagnosis of acute leukemia's. Alternatively, this gene may function in the proliferation of neutrophils and be useful as a treatment for neutropenia, for example, following neutropenia as a result of chemotherapy.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 7**

The contig exhibits a reasonable homology to the human chorionic gonadotropic (HCG) analogue-GT beta-subunit as disclosed in U.S. Patent No. 5,508,261 and PCT Publication No. WO 92/22568. There is a high degree of conservation of the structurally important cysteine residues in these identities.

This gene is expressed primarily in IL-1 and LPS induced neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system, including inflammatory diseases and allergies. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of diseases of the immune system since expression is primarily in neutrophils, and may be useful as a growth factor for the differentiation or proliferation of neutrophils for the treatment of neutropenia following chemotherapy.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 8**

This gene is expressed primarily in IL-1- and LPS-induced neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system, including inflammatory diseases and allergies. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 241 as residues: Ser-14 to Pro-22, Leu-43 to Val-53.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases of the immune system since expression is primarily in neutrophils, and may be useful as a growth factor for the differentiation or proliferation of neutrophils for the treatment of neutropenia following chemotherapy.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 9**

This gene is expressed primarily in IL-1 and LPS induced neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system, including inflammatory diseases and allergies. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 242 as residues: Tyr-22 to His-35.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of diseases of the immune system since expression is primarily in neutrophils, and may be useful as a growth



factor for the differentiation or proliferation of neutrophils for the treatment of neutropenia following chemotherapy.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 10**

5        This gene is expressed primarily in activated T-cells and to a lesser extent in endothelial cells.

         Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are  
10   not limited to, immune dysfunctions including cancer of the T lymphocytes and autoimmune disorders and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at  
15   significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20        The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of immune disorders particularly of T-cell origin and may act as a growth factor for particular subsets of T-cells such as CD4 positive cells which would make this a useful therapeutic for the treatment of HIV and other immune compromising illnesses.

25

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 11**

         This gene is expressed primarily in fetal tissue.

         Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
30   biological sample and for diagnosis of many developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the developing fetus, expression of this gene at significantly higher or lower levels may be routinely detected  
35   in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful as a growth factor or differentiation factor for particular cell types in the developing fetus and may be useful in replacement or other types of therapy in cases where the gene is expressed aberrantly.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 12**

This gene is expressed primarily in T-cells and to a lesser extent in tumor tissue including glioblastoma, meningioma, and Wilm's tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system including autoimmune conditions such as rheumatoid arthritis, inflammatory disorders and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 245 as residues: Thr-9 to Ser-14.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis/ modulation of immune function disorders, including rheumatoid arthritis and inflammatory responses.

#### **30 FEATURES OF PROTEIN ENCODED BY GENE NO: 13**

This gene is expressed primarily in placenta and to a lesser extent in fetal liver and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of hematological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of

disorders of the above tissues or cells, particularly of the hematological and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample  
 5 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful as a growth factor for hematopoietic stem cells or  
 10 progenitor cells in the treatment of chemotherapy patients or kidney disease.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 14**

This gene is expressed primarily in stromal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as  
 15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of hematopoietic disorders including cancer, neutropenia, anemia, and thrombocytopenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of  
 20 the above tissues or cells, particularly of the hematopoietic and immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,  
 25 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful as a growth factor for hematopoietic stem cells or  
 30 progenitor cells, in particular following chemotherapy treatment.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 15**

The translation product of this gene shares sequence homology with epsilon-COP from *Bos taurus* which is thought to be important as a component of coatamer, a complex of seven proteins, that is the major component of the non-clathrin membrane coat. Preferred polypeptides encoded by this gene comprise the following amino acid  
 35 sequences:

MAPPAPGPASGGSGEVDELFDVKNAFYIGSYQQCINEAXXVKLSSPERDVERD

VFLYRAYLAQRKFGVVLDEIKPSSAPELQAVRMFADYLAHESRRDSIVAELDRE  
 MSRSXDVTNTTFLDMAASIYLHDQNPDAALRALHQGDSLECTAMTVQILLKLD  
 RLDLARKELKRMQDLDEDATLTQLATAWVSLATGGEKLQDAYYIFQEMADKCS  
 PTLNLLNGQAACHMAQGRWEAAEGLLQEALDKDSGYPETLVNLIVLSQHLGKP  
 5 PEVTNRYLSQLKDAHRSHPIKEYQAKENDFDRLVLQYAPSAEAGPELSGP  
 (SEQ ID NO:458); or RDVERDVFLYRAYLAQRKFGVVLDEIKPSSAPELQAVRMF  
 ADYLAHESRRDSIVAELDREMSRSXDVTNTTFLDMAASIYLHDQNPDAALRALH  
 QGDSLECTAMTVQILLKLDRLDLARKELKRMQDLDEDATLTQLATAWVSLATG  
 GEKLQDAYYIFQEMADKCSPTLNLNGQAACHMAQGRWEAAEGLLQEALDKD  
 10 SGYPETLVNLIVLSQHLGKPPEVTNRYLSQLKDAHRSHPIKEYQAKENDFDRL  
 VLQYAPSA (SEQ ID NO:459).

This gene is expressed primarily in activated monocytes and T-cells, and to a lesser extent in multiple other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as  
 15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunomodulation, specifically relating to transport problems in these cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell  
 20 type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene  
 25 expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to epsilon-COP indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating  
 /diagnosing problems with the cellular transport of proteins that may result in  
 30 immunologic dysfunction.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 16

The translation product of this gene shares sequence homology with an RNA  
 helicase which is thought to be important in polynucleotide metabolism. The translation  
 35 product of this contig exhibits good homology to the LbeIF4A antigen of *Leishmania braziliensis*. The LbeIF4A antigen, or immunogenic portions of it, can be used to induce protective immunity against leishmaniasis, specifically *L. donovani*, *L. chagasi*,

L. infantum, L. major, L. braziliensis, L. panamensis, L. tropica and L. guyanensis. It can also be used diagnostically to detect Leishmania infection or to stimulate a cellular and/or humoral immune response or to stimulate the production of interleukin-12.

This gene is expressed primarily in colon cancer and to a lesser extent in  
5 pituitary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of cancers particularly of the colon. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing  
10 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the gastrointestinal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample  
15 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 249 as residues: Glu-93 to Ala-98, Gln-150 to Leu-156, Leu-220 to Leu-231, Leu-268 to Arg-273, Val-324 to Pro-341, Arg-372 to Asn-  
20 380, Ser-405 to Gly-410, Phe-426 to Ala-433, Glu-458 to Asp-470, Arg-506 to Ser-547.

The tissue distribution and homology to RNA helicase indicates that polynucleotides and polypeptides corresponding to this gene are useful for development of diagnostic tests for colon cancer.

## 25 FEATURES OF PROTEIN ENCODED BY GENE NO: 17

The translation product of this contig has sequence homology to a cytoplasmic protein that binds specifically to JNK designated the JNK interacting protein-1 or JIP-1 in mice. JIP-1 caused cytoplasmic retention of JNK and inhibition of JNK-regulated  
30 gene expression.

This gene is expressed primarily in brain including pituitary cerebellum frontal cortex, fetal brain and to a lesser extent in the kidney cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
35 biological sample and for diagnosis of the central nervous system disorders including ischemia, epilepsy, Parkinson's disease, and schizophrenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological

probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Furthermore, the translation product of this contig may suppress the effects of the JNK signaling pathway on cellular proliferation, including transformation by the Bcr-Abl oncogene. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 250 as residues: Pro-6 to Ser-26, Ala-30 to Asp-41, Gly-55 to Ser-61, Gly-74 to Thr-80, Tyr-117 to Ala-123, Tyr-167 to Asp-172, Ala-212 to Cys-223, Pro-239 to Tyr-244.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for enhanced survival and/or differentiation of neurons as a treatment for neurodegenerative disease.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 18**

The translation product of this gene shares sequence homology with a liver stage antigen from a protozoan parasite.

This gene is expressed primarily in fetal tissue and to a lesser extent in activated T-cells and other immune cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental abnormalities and diseases of immune function. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to a protozoan antigen indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/immune modulation of parasitic infections.

## 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 19

Preferred polypeptide encoded by this gene comprise the following polypeptide sequences:

MKAIGIEPSLATYHHIIRLFDQPGDPLKRSSFIIYDIMNELMGKRFSPKD  
 PDDDKFFQSAMSSICSSLRDLELAYQVHGLLKTGDNWKFIPDQHRNFYYSKFF  
 10 DLICLMEQIDVTLKWYEDLIPSA YFPHSQTMHLLQALDVANRLEVIPKIWER  
 (SEQ ID NO:460); and/or KDSKEYGHTFRSDLREEILMLMARDKHPPELQVAF  
 ADCAADIKSAYESQPIRQTAQDWPATSLNCIALFLRAGRTQEAWKMLGLFRKH  
 NKIPRSELLNELMDSAKVSNSPSQAIEVVELASAFSLPICEGLTQRVMSDFAINQ  
 EQKEALSNLTALTSDSDTSSSDSDSDTSEGK (SEQ ID NO:461). Polynucleotides

15 encoding such polypeptides are also provided.

This gene is expressed primarily in stromal and CD34 depleted bone marrow cells and to a lesser extent in tissues of embryonic origin.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
 20 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of hematologic origin including cancers and immune dysfunction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of  
 25 the hematopoietic and immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily  
 30 fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 252 as residues: Ser-28 to Gln-34.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful as a growth factor for hematopoietic stem cells or progenitor cells which may be useful in the treatment of chemotherapy patients  
 35 suffering from neutropenia.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 20**

Preferred polypeptide fragments can be found in an alternative open reading frame. These preferred polypeptides comprise the amino acid sequence:

MSSDNESDIEDEDLKLELRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVPPAVI  
 5 IPPAAPLSGRRRRPTKSKGSKSSRSSSLGNKSPQLSGNLSGQSAASVLHPQQT  
 HPPGNIPESGQNQLLQPLKPSRSSDNL YSAFTSDGAISVPSLSAPGQGTSSSTNTV  
 GATVNSQAAQAQPPAMTSSRKGTFTDDLHLVDNWARDAMNLSGRRGSKGH  
 MNYEGPGMARKFSAPGQLCISMTSNLGGAPISAASATSLGHFTKSMCPPQQY  
 GFPATPFGAQWSGTGGPAPQLGQFQPVGTASLQNFNISNLQKSISNPPGSNL  
 10 RTT (SEQ ID NO:462); IQDLQSRQKHEIESLYTKLGKVPPAVIIPPAAPLSGRRRR  
 PTKSKGSKSSRSSSLGNKSPQLSGNLSGQSAASVLHPQQT  
 HPPGNIPESGQNQLLQPLKPSRSSDNL YSAFTSDGAISVPSLSAPGQGTSSST (SEQ ID NO:463);  
 TSDGAISVPSLSAPGQGTSSSTNTVGATVNSQAAQAQPPAMTSSRKGTFTDDLH  
 (SEQ ID NO:464); KGHMNYEGPGMARKFSAPGQLCISMTSNLGGAPISAAS  
 15 ATSLGHFTK (SEQ ID NO:465); QPLKPSRSSDNL YSAFTSDGAISVPSLSAPG  
 (SEQ ID NO:466). Also preferred are polynucleotide fragments encoding these  
 polypeptide fragments.

This gene is expressed in fetal liver and tissues associated with the CNS.

Therefore, polynucleotides and polypeptides of the invention are useful as  
 20 reagents for differential identification of the tissue(s) or cell type(s) present in a  
 biological sample and for diagnosis of diseases and conditions, which include, but are  
 not limited to, liver and CNS diseases. Similarly, polypeptides and antibodies directed  
 to these polypeptides are useful in providing immunological probes for differential  
 identification of the tissue(s) or cell type(s). For a number of disorders of the above  
 25 tissues or cells, particularly of the liver and CNS, expression of this gene at  
 significantly higher or lower levels may be routinely detected in certain tissues (e.g.,  
 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial  
 fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
 such a disorder, relative to the standard gene expression level, i.e., the expression level  
 30 in healthy tissue or bodily fluid from an individual not having the disorder. Preferred  
 epitopes include those comprising a sequence shown in SEQ ID NO: 253 as residues:  
 Gln-26 to Lys-34.

The tissue distribution indicates that polynucleotides and polypeptides  
 corresponding to this gene are useful for diagnosis and treatment for liver diseases such  
 35 as hepatocellular carcinomas and diseases of the CNS.



**FEATURES OF PROTEIN ENCODED BY GENE NO: 21**

In an alternative reading frame, this gene shows sequence homology to two recently cloned genes, karyopherin beta 3 and Ran\_GTP binding protein 5. (See Accession Nos. gil2102696 and gnlIPIDle328731.) The Ran\_GTP binding protein is related to importin-beta, the key mediator of nuclear localization signal (NLS)-dependent nuclear transport. Based on homology, it is likely that this gene may activity similar to the RAN\_GTP binding protein. Preferred polypeptide fragments comprise the amino acid sequence: VRVAAAESMXLLLECAAXVRGPEYLTQMWHFMCDALIKA IGTEPDSVDLSEIMHSFAK (SEQ ID NO:467). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed in thymus tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment for immune disorders.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 22**

This gene is expressed primarily in prostate and osteoclastoma tissues. Preferred polypeptide fragments also comprise the amino acid sequence: MEINNQNCFIVIDLVRTVMENGVEGLLIFGAFLPESWLIGVRCSSSEPPKALLLIL AHSQKRRLDGWSFIRHLRVHYCVSLTIHFS (SEQ ID NO:468). Also preferred are polynucleotide sequences encoding this polypeptide fragment.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, bone and prostate diseases, and cancers, particularly of the bone and prostate. Similarly, polypeptides and antibodies directed to these polypeptides are

useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone and prostate systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded  
5 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 255 as residues: Met-1 to Ser-11.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment for bone and prostate disorders, especially cancers of those systems.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 23**

15 This gene shares sequence homology with the FK506-binding protein (FKBP-13) family, a known cytosolic receptor for the immunosuppressants. Recently, another group has cloned a very similar gene, recognizing the homology to FK506-binding protein family, calling their gene FKBP23. (See Accession No. 2827255.)

This gene is expressed primarily in lymphoid tissues.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample, especially for those susceptible to immune suppressant therapies and for diagnosis of diseases and conditions, which include, but are not limited to, immune suppressant disorders. Similarly, polypeptides and antibodies directed to these  
25 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or  
30 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 256 as residues: Ala-19 to Val-31, Arg-38 to Gly-49, Ala-61 to Lys-66, Tyr-68 to Pro-78, Gly-116 to Ala-121, Asp-154 to  
35 Ser-162, Glu-173 to Gln-186, Phe-194 to Gly-203, Pro-207 to Val-212.

The tissue distribution and homology to FKBP-12 and -13 indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment for immune suppressant disorders.

## 5    **FEATURES OF PROTEIN ENCODED BY GENE NO: 24**

This gene is expressed primarily in the brain and in the retina. This gene maps to chromosome 8, and therefore can be used in linkage analysis as a marker for chromosome 8.

Therefore, polynucleotides and polypeptides of the invention are useful as  
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological and ocular associated disease states. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of  
15 disorders of the above tissues or cells, particularly of the disorders of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard  
20 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 257 as residues: Cys-34 to Asp-40.

The tissue distribution in retina indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and/or detection of eye disorders  
25 including blindness, color blindness, impaired vision, short and long sightedness, retinitis pigmentosa, retinitis proliferans, and retinoblastoma. Expression in the brain indicates a role in the is useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive  
30 disorder and panic disorder.

## **FEATURES OF PROTEIN ENCODED BY GENE NO: 25**

This gene shows sequence homology to a newly identified class of proteins expressed in the nervous system, called stathmin family. (See Accession No. 2585991;  
35 see also Eur. J. Biochem. 248 (3), 794-806 (1997).) The stathmin family appears to be an ubiquitous phosphoprotein involved as a relay integrating various intracellular signaling pathways. These pathways affect cell proliferation and differentiation.

Preferred polypeptide fragments comprise the amino acid sequence:

QDKHAEVRKNKELKEEASR (SEQ ID NO:469); QQDLSPWAAPVGCPLXXASX  
TCHXLPLSGCLRRQSXSLPVVAXLCFWFSCPLASLFVPGQPCVTCFPFSLPFQD  
KHAEVRKNKELKEEASR (SEQ ID NO:470). Also preferred are the

5 polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are  
10 not limited to, neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,  
15 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides  
20 corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder.

## 25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 26**

The polynucleotide sequence of this gene contains a domain similar to a Flt3 ligand peptide. Preferred polypeptide fragments comprise the amino acid sequence:  
PTRCCTTQPCRSSARRPCWVPMVPSPEGREXQPTCPS (SEQ ID NO:471). Thus,  
30 this gene may have activity as binding to Flt3 receptors, a process known to promote angiogenesis and/or lymphangiogenesis.

This gene is expressed in human tonsil, and to a lesser extent in teratocarcinoma, placenta, colon carcinoma, and fetal kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample  
35 and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the tonsil, as well as cancers, such as colon, reproductive, and kidney cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful

in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the tonsils, colon, reproductive organs, and kidneys, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 259 as residues: Pro-22 to Glu-33.

The tissue distribution in tonsil and several cancers and fetal tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the tonsil or colon, such as tonsillitis, inflammatory diseases involving nose and paranasal sinuses, especially during the infection of influenza, adenoviruses, parainfluenza, rhinoviruses. The gene may also be useful in the diagnosis and treatment of neoplasms of nasopharynx or colon origins.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 27

In an alternative reading frame exists a large open reading frame that encodes a preferred polypeptide. Preferred polypeptide fragments comprise the amino acid sequence:

MKRSLNENSARSTAGCLPVPLFNQKKRNRQPLTSNPLKDDSGISTPSDNYDFP  
PLPTDWAVEAVNPEXAPVMKTVDTGQIPHVSRSRPLRSQDSVFNSIQSNTGRSQ  
GGWSYRDGNKNTSLKTWXXKNDFKPQCKRTNLVANDGKNSCPMSSGAQQQK  
QLRTPEPPNLSRNKETELLRQTHSSKISGCTMRGLDKNSALQTLKPNFQQNQY  
KXQMLDDIPEDNTLKETSLEYQLQFKEKASSLRISAVIESMKYWREHAQKTVLL  
FEVLAVLDSAVTPGPYYSKTFLMRDGKNTLPCVFYEIDRELPRIRGRVHRCVG  
NYDQKKNIFQCVSVRPASVSEQKTFQAFVKIADVEMQYYINVMNET (SEQ ID  
NO:472); SQDSVFNSIQSNTGRSQGGWSYRDGNKNTSLKTWXXKNDFKPQCKR  
(SEQ ID NO:473); NKETELLRQTHSSKISGCTMRGLDKNSALQTLKPNF (SEQ ID  
NO:474); SSLRISAVIESMKYWREHAQKTVLLFEVLAVLDSAVTPGPYYSKTFLM  
(SEQ ID NO:475); and PRLIRGRVHRCVGNYDQKKNIFQCVSVRPASVSEQK  
TFQAFV (SEQ ID NO:476).

This gene is expressed primarily in human testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, male reproductive disorders, including cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful as a hormone with reproductive or other systemic functions; contraceptive development; male infertility of testicular causes, such as Klinefelter's syndrome, varicocele, orchitis; male sexual dysfunctions; testicular neoplasms; and inflammatory disorders such as epididymitis.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 28**

This gene is expressed primarily in apoptotic T-cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases relating to T cells, as well as cancer in general. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the disorders of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for immune disorders. Moreover, since the gene was isolated from an apoptotic cell and based on the understanding of the relationship of apoptosis and cancer, it is likely that this gene may play a role in the genesis of cancer.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 29**

This gene is expressed primarily in human tonsils.

- Therefore, polynucleotides and polypeptides of the invention are useful as
- 5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, gastrointestinal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
- 10 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the gastrointestinal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
- 15 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of gastrointestinal diseases.

**20 FEATURES OF PROTEIN ENCODED BY GENE NO: 30**

The translation product of this gene shares sequence homology with C44C1.2 gene product of *Caenorhabditis elegans* with unknown function. Preferred polypeptide fragments comprise the amino acid sequence:

- GVFRPCVCGRPASLTCSPLDPEVGPYCDTPTMRTLFLNLLWLALACSPVHTTLSK
- 25 SDAKKAASKTLLEKSQFSDKPVQDRGLVVTDLKAESVVLEHRSYCSAKARDRH  
FAGDVLGYVTPWNSHGYDVTKVFGSKFTQISPVWLQLKRRGREMF EVTGLHD  
VDQGWMRAVRKHAKGLHIVPRLLFEDWTYDDFRNVLDSEDEIEELS KTVVQVA  
KNQHFDGFVVEVWNQLLSQKRVG LIHMLTHLAEALHQARLLALLVIPPAITPGT  
DQLGMFTHKEFEQLAPVLDGFS LMTYDYSTAHQPGPNAPLSWVRACVQVLDP
- 30 KXKWRTKSSWGSTSMXWTXRXPDARXPVVGXRXIQXLKDHXPRMVLD SK  
PQ (SEQ ID NO:477); TCSPLDPEVGPYCDTPTMRTLFLNLLWLALACSPVHTTLS  
(SEQ ID NO:478); LVVTDLKAESVVLEHRSYCSAKARDRH FAGDVLGYVTPW  
NSHGYDVTKVFGSKF (SEQ ID NO:479); REMFEVTGLHDVDQGWMRAVRK  
HAKGLHIVPRLLFEDWTYDDFRNVLDSEDE (SEQ ID NO:480); HFDGFVVEVW
- 35 NQLLSQKRVG LIHMLTHLAEALHQARLLALLVIPPAITPGTDQLGM (SEQ ID  
NO:481); DGFSLMTYDYSTAHQPGPNAPLSWVRACVQVLDPKXKWRTKSSW  
GST (SEQ ID NO:482). Also preferred are polynucleotide fragments encoding these

polypeptide fragments. This gene maps to human chromosome 11, and therefore is useful in linkage analysis as a marker for chromosome 11.

This gene is expressed primarily in human T cells and to a lesser extent in human colon carcinoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and gastrointestinal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 263 as residues: Leu-21 to Ala-30, Ser-38 to Asp-47, Pro-87 to Asp-94, Leu-197 to Thr-204, Pro-256 to Ser-262, Thr-277 to Arg-282, Thr-293 to Trp-303.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders and gastrointestinal diseases.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 31**

The translation product of this gene shares sequence homology with Ribosomal protein L11 of *Caenorhabditis elegans*. (See Accession No. 156201.) Preferred polypeptide fragments comprise the amino acid sequence:

ERGVSINQFCKEFNERTKDIKEGIPLPTKILVKPDRTFEIKIGQPTVSYFLKAAAG  
IEKGARQTGKEVAGLVTLKHVYEIARIKAQDEAFALQDVPLSSVVRISIIGSARSL  
GIRVVKDLSSSEELAAFQKERAIFLAAQKEADLAAQEEAAKK (SEQ ID NO:483).

Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed in human embryo tissue and to a lesser extent in human epithelioid sarcoma and other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, development disorders and epithelial cell cancer. Similarly, polypeptides and antibodies



directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the embryonic and epithelial cell systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 264 as residues: Lys-34 to Gly-40.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of developmental disorders and epithelial cancer.

#### 15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 32**

This gene is expressed primarily in resting T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammatory and general immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of disorders of immune system.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 33**

This gene is believed to reside on chromosome 1. Accordingly, polynucleotides derived from this gene are useful in linkage analysis as chromosome 1 markers.

This gene is expressed primarily in prostate and to a lesser extent in soares adult brain, human umbilical vein endothelial cells, and amniotic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, prostate-related disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the urinary system and nervous system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for the diagnosis and treatment of disorders of the urinary and nervous systems.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 34

This gene shares sequence homology with R05G6.4 gene product. (See Accession No. gil1326338.) This gene also shares sequence homology with the cyclophilin-like protein CyP-60. (See Accession No. 1199598, see also Biochem. J. 314 (1), 313-319 (1996).) Preferred polypeptide fragments comprise the amino acid sequence:  
 AVYTYHEKKKDTAASGYGTQNIRLSRDAVKDFDCCCLSLQPCHDPVVTPDGYL  
 YERE AILEYILHQKKEIARQMKA YEKQRGTRREEQKELQRAASQDHVRGFLEKE  
 SAIVSRP LNPFTAKALSGTSPDDVQPGPSVGPPSKDKDKVLPSFWIPSLTPEAK  
 ATKLEKPSRTVTCMSGKPLRMSDLTPVHFTPLDSSVDRVGLITRSEYVCAVT  
 RDSLSNATPCAVLRPSGAVVTLECVKELIRKDMVDPVTGDKLTDRDIIVLQRG  
 T (SEQ ID NO:484); YLYERE AILEYILHQKKEIARQMKA YEKQRGTRREEQKELQ  
 RAASQDHVRGFLE (SEQ ID NO:485); and FTAALSGTSPDDVQPGPSVGPP  
 SKDKDKVLPSFWIPSLTPEAKATKLEKPSRTVTCMSGKPL (SEQ ID NO:486).  
 Also preferred are polynucleotide fragments that encode these polypeptide fragments.

This gene is expressed primarily in human testis and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male reproductive disorders and in particular testicular cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system. Expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders of the male reproductive system and in particular of testicular cancer.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 35**

The translation product of this gene shares sequence homology with Lpe5p of *Saccharomyces cerevisiae* which is thought to be important in the metabolism of phospholipids.

This gene is expressed primarily in liver and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic and nervous systems expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 268 as residues: Pro-14 to Leu-20, Lys-28 to Asn-38, Arg-109 to Arg-114, Lys-119 to Asn-124, Glu-152 to Leu-157, Pro-172 to Val-180.

The tissue distribution and homology to Lpe5p of *Saccharomyces cerevisiae* indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of metabolic and nervous disorders.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 36**

This gene shares sequence homology with the nuclear ribonucleoprotein U (HNRNP U), encoded by *C. elegans* (See Accession gil1703576.) Preferred polypeptide fragments comprise the amino acid sequence:

- 5 MDTSENRPENDVPEPPMPIADQVSNDDEEGSVEDEEKKESLPPKSFKRKISVV  
SATKGVPAAGNSDTEGGQPGRKRRWGASTATTQKKPSISITTESLKS LIPDIKPL  
AGQEA VVDLHADDSRISEDETERNGDDGTHDKGLKICRTVTQV VPAEGQENGQ  
REEEEEEKEPEAEPPVPPQVSVEVALPPPAEHEVKKVTLGDTLTRRSISQQKSGV  
SITIDDPVRTAQVPSPPRGKISNIVHISNLVRPFTLGQLKELLGRTGTLVEEAFWI  
10 DKIKSHCFVTYSTVEEAVATRTALHGVKWPQSNPKFLCADYAEQDELDYHRGL  
LVDRPSETKTEEQGIPRPLHPPPPPPVQPPQHPRAEQREQERAVREQWAERERE  
MERRERTRSEREWRDKVREGPRSRSRSRXRRRKERAKSKEKKSEKKEKAQE  
EPPAKLLDDLFRKTKAAPCIYWLPLTDSQIVQKEAERAERAKEREKRRKEQEEE  
EQKEREKEAERERNRQLEREKRREHSRERDRERERERERDRGDRDRDRERDRE  
15 RGRERDRRDTKRHSRSRSTPVRDRGGR (SEQ ID NO:488). Also preferred are  
the polynucleotide fragments encoding this polypeptide fragments.

This gene is expressed primarily in epididymus.

- Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
20 biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, diseases of the male reproductive system. Similarly, polypeptides and  
antibodies directed to these polypeptides are useful in providing immunological probes  
for differential identification of the tissue(s) or cell type(s). For a number of disorders  
of the above tissues or cells, particularly of the male reproductive system, expression of  
25 this gene at significantly higher or lower levels may be routinely detected in certain  
tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,  
urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an  
individual having such a disorder, relative to the standard gene expression level, i.e.,  
the expression level in healthy tissue or bodily fluid from an individual not having the  
30 disorder.

The tissue distribution indicates that polynucleotides and polypeptides  
corresponding to this gene are useful for the diagnosis and treatment of male  
reproductive disorders.

**35 FEATURES OF PROTEIN ENCODED BY GENE NO: 37**

This gene is expressed primarily in amygdala.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammatory diseases and reproductive disorders. Similarly,

5 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the amygdala, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,

10 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides

15 corresponding to this gene are useful for diagnosis and treatment of inflammatory diseases and reproductive disorders.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 38**

This gene shares sequence homology with human opsonin protein P35

20 fragment. (See Accession No. R94181.) The opsonin protein activates the phagocytosis of pathogenic microbes by phagocytic cells. Preferred polypeptide fragments comprise the amino acid sequence: GCDSCPPHLPREAFAQDTQAECESSRAERADMCPDAP PSQEVPEGPGAAP (SEQ ID NO:489). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

25 This gene is expressed in immune-related tissues such as thymus, macrophage, T cells and to a lesser extent in many other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

30 not limited to, immune disorders and infectious disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and infectious disease, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,

35 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 271 as residues: Lys-9 to Arg-14, Met-38 to Asp-51.

- 5 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders, as well as the treatment and/or diagnosis of infectious disease.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 39**

- 10 The translation product of this gene shares sequence homology with alpha-2 type I collagen which is thought to be important in tissue repair. (See, e.g., 211607.) Preferred polypeptide fragments comprise the amino acid sequence: PQLPSCGRPWP GTASVFQSHTQGPREDPDP CRAQGSAGTHCPISLSPPRQ (SEQ ID NO:490). Also preferred are the polynucleotide sequences encoding these polypeptide sequences.

- 15 This gene is expressed primarily in the brain and to a lesser extent in the kidney and thymus

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, brain, kidney, and immune disorders. Similarly, polypeptides and  
20 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, kidney, and immune disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,  
25 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 30 The tissue distribution and homology to alpha-2 type I collagen indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tissue repair, and brain, kidney, immune disorders.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 40**

- 35 The translation product of this gene shares sequence homology with mini-collagen which is thought to be important in tissue repair tumor metastasis. (See Accession No. gnllPIDld1006976.) Preferred polypeptide fragments comprise the amino acid sequence: PGFRGPSGLGCSFFPRSLGRVLPPGCQRPGAHAD

SSPPPTP (SEQ ID NO:491). Also preferred are polynucleotides encoding this polypeptide fragment.

This gene is expressed in ovarian cancer and to a lesser extent in dendritic cells and smooth muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumor metastasis and tissue repair. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the tumor metastasis and tissue repair, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 273 as residues: Asn-2 to His-11.

The tissue distribution and homology to mini-collagen gene indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tumor metastasis and tissue repair.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene shares sequence homology with the HIV TAT protein. (See Accession No. 328416.) Preferred polypeptide fragments comprise the amino acid sequence: EDLKKPDPA SLRAASCGEGKKRKACKNCTCGLAE ELEKEK SREQMSSQPKSACGNCYLGD AFRASC PYLGMPAFKPGEKVLLS (SEQ ID NO:492); EDLKKPDPA SLRAASCGEGKKRKACKNCTCGLAE ELEKEK SREQMSSQPKSACGNCYLGD AFRASC PYLGMPAFKPGEKVLLSDSNLHD (SEQ ID NO:493); CGNCYLGD AFRASC PYLGMPAFKPGEKVLLSDS (SEQ ID NO:494); SCGEGKKRKACKNCTCGLAE ELEKE (SEQ ID NO:495); SQPKSAC GNCYLGD AFRASC (SEQ ID NO:496); and REAGQNSERQYVS LSRD (SEQ ID NO:497). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in the infant brain and to a lesser extent in the breast and testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, brain, testes and breast disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, testes and breast disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 274 as residues: Pro-7 to Val-15.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of brain, testes and breast, and other related disorders.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 42**

This gene is expressed primarily in the infant brain, human cerebellum, and to a lesser extent in medulloblastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, brain related disorders and medulloblastoma and other brain cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain related disorders and brain cancers, including medulloblastoma, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 275 as residues: Thr-41 to Glu-47.



The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of human brain related disorders, brain cancers, and medulloblastoma.

## 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 43

The translation product of this gene shares sequence homology with a phosphotyrosine-independent ligand for the lck SH2 domain which is thought to be important in signal transduction related to phosphotyrosine-independent ligand for the lck SH2 domain. (See Accession No. gi1184951.) Preferred polypeptide fragments  
 10 comprise the amino acid sequence: ESSGQARTLADPGPGWPRQQGMCFGSLT  
 GLSTTPHGFLTVSAEADPRLIESLSQMLSMGFSDEGGWLTRLLQTKNYDIGAAL  
 DTIQYSKH (SEQ ID NO:498). Also preferred are polynucleotide fragments encoding this polypeptide fragment. It is likely that this gene is a new member of a family of  
 phosphotyrosine-independent ligands for the lck SH2 domains.

15 This gene is expressed primarily in the placenta and to a lesser extent in endothelial cells and neutrophil.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are  
 20 not limited to, reproductive, cardiovascular, immune, and infectious diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular, reproductive, and immune system, and infectious diseases, expression  
 25 of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the  
 30 disorder.

The tissue distribution and homology to a phosphotyrosine-independent ligand for the lck SH2 domain indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cardiovascular, reproductive, and immune system diseases, as well as infectious diseases.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 44**

This gene is expressed primarily in the fetal brain, cerebellum and to a lesser extent in the placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neuronal cell related disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuronal cell related disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 277 as residues: Thr-20 to Gly-28.

The tissue distribution and homology to proline-rich protein genes indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal cell related disorders.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 45**

The translation product of this gene shares sequence homology with precerebellin of human, which is thought to be important in synaptic physiology. (See Accession No. gil180251.) It has been observed that cerebellin-like immunoreactivity is associated with Purkinje cell postsynaptic structures. Thus, it is likely that this gene also have synaptic activity. Preferred polypeptide fragments comprise the amino acid sequence: QEGSEPVLLEGECLVVCEPGRAAAGGPGGAALGEAPPGRVAFXAV RSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVYSFRFH VVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLR LRRGXSTGW (SEQ ID NO:499). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in cerebellum and infant brain. By Northern analysis, a single transcript of 2.4 kb was observed in brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, neuronal cell signal transduction and synaptic physiology. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuronal cell  
5 signal transduction and synaptic physiology expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue  
10 or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to gene or gene family indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal cell related disorders.

#### 15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 46**

This gene is expressed in fetal liver and spleen, and to a lesser extent in bone marrow, umbilical vein, and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
20 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the immune system, particularly hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoiesis  
25 and immune disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily  
30 fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 279 as residues: Asp-30 to Glu-57.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hematopoietic and immune disorders.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 47**

The translation product of this gene shares sequence homology with a 12 kD nucleic acid binding protein of Feline calicivirus which is thought to be important in viral replication. (See Accession No. 59264)

5 This gene is expressed primarily in human cardiomyopathy and to a lesser extent in T helper cells, fetal brain and synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiomyopathy as well as viral infection. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 280 as residues: Trp-20 to Cys-26.

The tissue distribution in cardiomyopathy and homology to viral 12 kD nucleic acid binding protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of cardiomyopathy, including those caused by ischemic, hypertensive, congenital, valvular, or pericardial abnormalities.

25 The gene expression pattern may be the consequence or the cause for these conditions.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 48**

The translation product of this gene shares sequence homology with tumor necrosis factor related gene product which is thought to be important in tumor necrosis, bacterial and viral infection, immune diseases and immunoreactions.

This gene is expressed primarily in colon and to a lesser extent in ovarian and breast cancers.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumors of colon, ovary or breast origins. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the colon, ovary and breast, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, 5 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution and homology to Tumor necrosis factors indicates that polynucleotides and polypeptides corresponding to this gene are useful for intervention of cancers of colon, ovary and breast origins, because TNF family members are known to be involved in the tumor development.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 49

15 The translation product of this gene shares sequence homology with mucins, such as epithelial mucin, which is thought to be important in extracellular matrix functions such as protection, lubrication and cell adhesion (See for example Accession No. R68002). Preferred polypeptide fragments comprise the following amino acid sequence: PRSRPALRPGRQRPPSHSATSGVLRPRKKPDP (SEQ ID NO:500).  
20 Also preferred are polynucleotide fragments encoding these polypeptide fragments. Moreover, this gene maps to chromosome 22q11.2-qter, and therefore, can be used as a marker in linkage analysis for chromosome 22.

This gene is expressed primarily in corpus colosum.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumors, especially of corpus colosum, as well as metastatic lesions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell  
30 type(s). For a number of disorders of the above tissues or cells, particularly of the corpus colosum and other solid tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,  
35 relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to mucins indicates that polynucleotides and polypeptides corresponding to this gene are useful for serum tumor markers or immunotherapy targets because tumor cells have greatly elevated level of mucin expression and shed the molecules into the epithelial tissues.

5

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 50**

This gene is expressed primarily in CD34 depleted buffy coat cord blood and primary dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic disorders and immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in CD34 depleted buffy coat cord blood and primary dendritic cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hematopoietic and immune disorders. Secreted or cell surface proteins in the above tissue distribution often are involved in cell activation (e.g. cytokines) or molecules involved in cell surface activation.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 51**

The translation product of this gene shares sequence homology with Interferon induced 1-8 gene encoded polypeptide which is thought to be important in binding to retroviral rev responsive element. Preferred polypeptide fragment comprise the following amino acid sequences: MTLITPSXKLTFXKGNKSWSRACSSSTLVDP (SEQ ID NO:501). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in CD34 positive cells and neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, retroviral infection, such as AIDS, and other immune disorders.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 284 as residues: Gln-51 to Trp-62.

The tissue distribution and homology to interferon induced gene 1-8 indicates that polynucleotides and polypeptides corresponding to this gene are useful for intervention of retroviral infection including HIV. The factor may be involved in viral stability or viral entry into the cells. Alternatively, the virus/factor complex may elicit the cellular immune reaction.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 52**

This gene shares sequence homology to immunoglobulin lambda chain (See Accession No. 2865484). Therefore it is likely that this gene has activity similar to an immunoglobulin lambda chain. Preferred polypeptide fragments comprise the following amino acid sequence: GHPSPALSIAPSDGSQLPCDEVYPYGEAHVTRYCKKPLTNS HLETEAQSSSL (SEQ ID NO:502). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in Hodgkin's lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, Hodgkin's lymphoma and other immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 285 as residues: Pro-27 to Thr-32.

5 The tissue distribution in Hodgkin's lymphoma and the sequence homology indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of Hodgkin's lymphoma, since the elevated expression and secretion by the tumor mass may be indicative of tumors of this type. Additionally the gene product may be used as a target in the immunotherapy of the cancer. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune  
10 functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

### FEATURES OF PROTEIN ENCODED BY GENE NO: 53

15 This gene has extensive homology to cDNA for Homo sapiens mRNA for the ISLR gene(See Accession No. AB003184). This protein is considered to be a new member of the Ig superfamily and contains a leucine-rich repeat (LRR) with conserved flanking sequences and a C2-type immunoglobulin (Ig)-like domain. These domains are important for protein-protein interaction or cell adhesion, and therefore it is possible that the novel protein ISLR may also interact with other proteins or cells. The ISLR gene  
20 was mapped on human chromosome 15q23-q24 by fluorescence in situ hybridization (See Medline Article No. 97468140). Homology to the ISLR gene has been confirmed by another independent group as well (See Accession No. Hs.102171)

This gene is expressed in a number of tissues including human retina, heart, skeletal muscle, prostate, ovary, small intestine, thyroid, adrenal cortex, testis,  
25 stomach, spinal cord, fetal lung and fetal kidney tissues, colon, tonsil and stomach cancer, and to a lesser extent in endometrial stromal cells treated with estradiol, breast tissue, synovium, lymphoma, and number of other tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
30 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumors of colon, ovary and breast origins. However, due to the wide range of expression in various tissues, protein may play a vital role in the development of cancer in other tissues as well, not just those mentioned above. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing  
35 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the colon, ovary and breast, expression of this gene at significantly higher or lower levels may be routinely



detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Additionally, this gene maps to chromosome 15q23-q24, and therefore, can be used as a marker in linkage analysis for chromosome 15.

The tissue distribution in tumors of colon, ovary, and breast origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 54**

Gene has homology to multidrug resistance gene 1 (See Accession No. P06795). Preferred polynucleotide fragments comprise the following sequence:  
 GCTTCGTGTCCAACCTCTTGCCCTTCGCCTGTGTGCCTGGAGCCAGTCCCA  
 CCACGCTCGCGTTTCCTCCTGTAGTGCTCACAGGTCCCAGCACCGATGGCA  
 TTCCCTTTGCCCTGAGTCTGCAGCGGGTCCCTTTTGTGCTTCCTTCCCCTCA  
 GG TAGCCTCTCTCCCCCTGGGCCACTCCCGGGGGTGAGGGGGTTACCCCTT  
 CCCAGTGT TTTTATTCCTGTGGGGCTCACCCCAAAGTATTAAAAGTAGCTTT  
 GTAA (SEQ ID NO:503). Also preferred are polypeptide fragments encoded by these polynucleotide fragments.

This gene is expressed primarily in lung, esophagus, leukemia (Jurkat cells) and breast cancers and to a lesser extent in macrophages treated with GM-CSF fetal tissues and wide range of tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer of wide range of origins. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the solid tumors, lung and leukemia, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Furthermore, due to the high expression level in lung tissue and the proposed function of the multidrug resistance protein 1 gene as the efflux pump responsible for low-drug accumulation in multidrug-resistant cells, protein as well mutants thereof, may also be beneficial as a target for gene therapy, particularly for the chronic patient. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 287 as residues: Met-1 to Lys-16.

The tissue distribution in wide range of cancers and fetal tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection of cells in active proliferation, such as cancers. The gene products may be used for cancer markers or immunotherapy target.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 55**

This gene maps to the X chromosome.

This gene is expressed primarily in the brain and to a lesser extent in the developing embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative disease states and developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders, including sex-linked disorders, of the above tissues or cells, particularly of the neurological, developmental systems, and cardiovascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Moreover, this gene maps to the X chromosome, and therefore, may be used as a marker in linkage analysis for this chromosome.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, Klinefelter's, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental

disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 56

- 5       The translation product of this gene shares sequence homology with paxillin which is thought to be important in mediating signal transduction from growth factor receptors to the cytoskeleton. Preferred polynucleotide fragments comprise the following sequence: TGGCTCACTGTCTTACAATCACTGCTGTGGAATCATGA TACCACTTTTAGCTCTTTGCATCTTCCTTCAGTGTATTTTTGTTTTTCAAGAGG
- 10   AAGTAGATTTTAACTGGACAACCTTGAGTACTGACATCATTGATAAATAAACT GGCTTGTGGTTTCAA (SEQ ID NO:506). Also preferred are polypeptide fragments encoded by these polynucleotide fragments. More preferably, polypeptide fragments comprise the amino acid sequence: LDELM AHLTEMQAKVAVRAD
- 15   AGKKHL PDKQDHKASLDSMLGGLEQELQDLGIATVPKGHCASCQKPIAGKVI HALGQSWHPEHFVCTHCKEEIGSSPFFERSGLXYCPNDYHQLFSPRCAYCAAP
- 20   ILDKVLTAMNQTWHPHFCSHCGEVFGAEGFHEKDKKPYCRKDFLAMFSPK CGGCNRPVLENYLSAMDTVWHPECFVCGDCFTSFSTGSFFELDGRPFCE LH YH HRRGTLCHGCGQPITGRCISAMGYKFHPEHFVCAFCLTQLSKGIFREQNDKTY
- 25   CQPCFNKLF (SEQ ID NO:507); KASLDSMLGGLEQELQDLGIATVPKGHC ASCQKPIAGKVIHAL (SEQ ID NO:508); CPNDYHQLFSPRCAYCAAPILDKVL TAMNQTWHPHFCSHCGEVFGAEG (SEQ ID NO:509); DKKPYCRKDFLAM FSPKCGGCNRPVLENYLSAMDTVWHPECFVCGDCFTSFSTGSFFELDGRPFCE L (SEQ ID NO:510); CGQPITGRCISAMGYKFHPEHFVCAFCLTQLSKGIFRE QNDKTYCQ (SEQ ID NO:511). Polynucleotide fragments encoding these preferred polypeptide fragments are also contemplated.

This gene is expressed primarily in brain, and to a lesser extent in the developing embryo.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
- 30   biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disease states and developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and
- 35   nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or

cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Moreover, since this gene shares homology with a gene that maps to chromosome 11, (See Accession No.T87404), gene as well as its translated product may be used for linkage analysis on chromosome 11.

The tissue distribution and homology to paxillin indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and or detection of disease states associated with abnormal signal transduction in brain and/or the developing embryo. This would include treatment or detection of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder and also in the treatment and or detection of embryonic development defects.

#### 15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 57**

This gene is expressed primarily in fetal spleen, brain, and to a lesser extent in six week old embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders, neurological disorders, and developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and developmental systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 290 as residues: Arg-28 to Gly-34.

The expression of this gene in fetal spleen indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/detection of immune disorders such as arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia. In addition the expression of this gene in the early embryo, indicates a key role in embryo development and hence the gene or gene product could be used in the treatment and or detection of embryonic development defects. This would include

treatment or detection of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntintons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder and also in the treatment and or detection of embryonic development defects.

5

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 58

The translation product of this gene shares sequence homology with the gene disrupted in the neurodegenerative disease dentatorubal-pallidoluyian atrophy. Moreover a long open reading fame exists in an alternative frame. Preferred polypeptide fragments

10 comprise the following:

MGSSQSVEIPGGGTEGYHVLRVQENSPGHRAGLEPFFDFIVSINGSRLNKDND  
 TLKDLLKXNVEKPKVKMLIYSSKTLELRETSVTPSNLWGGQGLLGVSIRFCSFD  
 GANENVWHVLEVESNSPAALAGLRPHSDYIIGADTMNESEDLFSLIETHEAKP  
 LKLYVYNTDTDNCREVIITPNSAWGGEGSLGCGIGYGYLHRIPTRPFEEGKKIS  
 15 LPGQMAGTPITPLKDGFTVQLSSVNPPSLSPGTTGIEQSLTGLSISSTPPAVSS  
 VLSTGVPTVPLLPPQVNQSLTSVPPMNPATTLPGLMPLPAGLPNLPNLPNLP  
 PHIMPGVGLPELVNPGLPPLPSMPPRNLPGIAPLPSEFLPSFPLVPESSSAASS  
 GELLSSLPPTSNA PSDPATTTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPV  
 SEKPVSAAVDANASESP (SEQ ID NO:512); SVEIPGGGTEGYHVLRVQENSPGH  
 20 RAGLEPFFDFIVSINGSRLNKDNDTLKDLLKXNVEKPKVKMLIYSSKTLELRETS  
 VTPSNLWGGQGLLGVSIRFCSFDGANENVWH (SEQ ID NO:513); ESNSPA  
 LAGLRPHSDYIIGADTMNESEDLFSLIETHEAKPLKLYVYNTDTDNCREVIITP  
 NAWGGEGSLGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTV  
 QLSSVNPPSLSPGTTGIEQSLTG LSISS (SEQ ID NO:514); RIPTRPFEEGKKI  
 25 SLPGQMAGTPITPLKDGFTVQLSSVNPPSLSPGTTGIEQSLTGLSISSTPPAVS  
 SVLSTGVPTVPLLPPQVNQSLTSVPPMNPATTLPGLMPLPAGLPNLPNLPNLP  
 APHIMPGVGLPELVNPGLPPLPSMPPRN (SEQ ID NO:516); PGLPPLPSMPPRN  
 LPGIAPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNA PSDPATTTAKADAA  
 SSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAAVDAN (SEQ ID NO:517).

30 This gene is expressed primarily in prostate cancer, and to a lesser extent in the pineal glands and in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are  
 35 not limited to, neurological conditions and pulmonary disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For

a number of disorders of the above tissues or cells, particularly of the nervous, pulmonary, and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or  
5 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 291 as residues: Asn-9 to Leu-14.

The abundance of this gene in the pineal gland and its homology to a gene  
10 disrupted in the neurodegenerative disease state Dentatorubral-pallidoluysian atrophy indicates that this gene may be useful in the treatment and/or detection of other neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. The abundance of this gene in fetal  
15 lung would suggest that misregulation of the expression of this protein product in the adult could lead to lymphoma or sarcoma formation, particularly in the lung; that it may also be involved in predisposition to certain pulmonary defects such as pulmonary edema and embolism, bronchitis and cystic fibrosis; and thus the gen or the gene protein encoded by the gene could be used in the detection and/or treatment of these  
20 pulmonary disorders.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 59**

This gene is expressed primarily in the developing embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as  
25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of  
30 the above tissues or cells, particularly of the developmental system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the  
35 expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene primarily in the embryo, indicates the gene plays a key role in embryo development and that the gene or the protein encoded by the gene could be used in the treatment and or detection of developmental defects in the embryo or in infants.

5

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 60**

This gene displays homology to nestin, an intermediate filament protein, the expression of which correlates with the proliferation of Central Nervous System progenitor cells and that is useful in the identification of brain tumors. This gene maps to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1 (See Accession No. AA527348).

This gene is expressed primarily in kidney and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, renal disorders and neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the excretory and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 293 as residues: Thr-128 to Asn-135.

The tissue distribution and homology to nestin indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection and/or treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, its abundance in kidney indicates that it is useful in the treatment and detection of acute renal failure and other disease states associated with the kidney.

#### **35 FEATURES OF PROTEIN ENCODED BY GENE NO: 61**

Gene shares homology with the latrophilin-related protein 1 precursor as well as the calcium-independent alpha-latrotoxin receptor. Preferred polypeptide fragments

comprise the following amino acid sequence:

IYKVRHTAGLKPEVSCFENIRSCARXXXXXXXXXXXXXWIFGVLHVHVSVV  
TAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNPCC (SEQ ID NO:518);  
WIFGVLHVHVSVV TAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNPVC

- 5 C (SEQ ID NO:519). Also preferred are polynucleotide fragments encoding these polypeptide fragments. (See Accession No. 2213659) The translation product of this gene shares sequence homology with CD 97, a seven transmembrane bound receptor.

This gene is expressed primarily in infant brain and in endothelial cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as  
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disorders and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For  
15 a number of disorders of the above tissues or cells, particularly of the neurological and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another  
20 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 294 as residues: Lys-13 to Leu-21.

- The tissue distribution of this gene suggest that it may be useful in the detection and/or treatment of neurodegenerative disease states and behavioral disorders such as  
25 Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder, while its expression in hematopoietic cell types indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma and immunodeficiency diseases.

30

## **FEATURES OF PROTEIN ENCODED BY GENE NO: 62**

This gene is expressed primarily in fetal liver and fetal spleen.

- Therefore, polynucleotides and polypeptides of the invention are useful as  
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematological and immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes



for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 295 as residues: Ser-91 to Lys-98.

The tissue distribution of this gene fetal liver and spleen indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, leukemia, asthma and immunodeficiency diseases.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 63**

Gene shares homology with human serum amyloid protein. Preferred polypeptide fragments comprise the following amino acid sequence:

ALTRIPPGDWVINVTAVSFAGKTTARFFHSSPPSLGDQARTDPGHQRRD (SEQ ID NO:520) (See Accession No. W13671). Also preferred are polynucleotide fragments encoding these polypeptide fragments This gene maps to chromosome 9, and therefore, may be used as a marker in linkage analysis for chromosome 9 (See Accession No. AA004342).

This gene is expressed primarily in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene in fetal liver-spleen indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, leukemia, asthma, and immunodeficiency diseases.

#### 5    **FEATURES OF PROTEIN ENCODED BY GENE NO: 64**

This gene maps to chromosome 3, and therefore, may be used as a marker in linkage analysis for chromosome 3 (See Accession No. AA219669).

This gene is expressed specifically in the brain.

Therefore, polynucleotides and polypeptides of the invention are useful as  
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative disease states. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of  
15 the above tissues or cells, particularly of the neurological systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the  
20 expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's  
25 Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 65**

Gene shares homology with a yeast protein. Preferred polypeptide fragments  
30 comprise the following amino acid sequence: LQEVNITLPENSVWYERYKFDIP VFHL (SEQ ID NO:521). Also preferred are polynucleotide fragments encoding these polypeptide fragments. (See Accession No. 1332638)

This gene is expressed primarily in fetal tissue (fetus and fetal liver).

Therefore, polynucleotides and polypeptides of the invention are useful as  
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, liver disorders and cancers (e.g. hepatoblastoma). Similarly,

polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected

5 in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID

10 NO: 298 as residues: Asn-59 to Glu-64.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). In

15 addition the expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various wound-healing models and/or tissue trauma.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 66**

20 Gene has homology with a B-cell surface antigen which may indicate gene plays a role in the immune response, including, but not limited to disorders and infections of the immune system. Preferred polynucleotide fragments comprise the following sequence: TAGCATGTAGCCAGTCTGAATAACNTATAAGGACAAAGTGGAGTCCACGCGTGCGGCCGTCTAGACTAGTGGATCCCCGGCTGCAGGATTTCGGC

25 ACGAG (SEQ ID NO:523). Also preferred are polypeptide fragments encoded by these polynucleotide fragments (See Accession No.T94535). Additionally, this gene shares homology with an interferon-gamma receptor. Preferred polypeptide fragments also comprise the following amino acid sequence: MQGSGSQFRACLLCLCFSCPCSPGGPRWNSRQGGRRFPKTCRAISQNLVFKYKTFCPVRYMQPHRSSLCLHFTSYVFILSTWGLR

30 TYSTD LKKKKKNSRGGPVPIRPKS (SEQ ID NO:522); MQGSGSQFRACLLCLCFSCPCSPGGPRWNSRQGGRRFPKTCRAISQNLVFK (SEQ ID NO:524); PVRYMQPHRSSLCLHFTSYVFILSTWGLR

35 TYSTD LKKKKKNSRGGPVPIRPKS (SEQ ID NO:525); and GEEQRDCSLGWRGVGMRATHCQAA RMFVLFSLPKYAGL (SEQ ID NO:526). Also preferred are polynucleotide fragments encoding these polypeptide fragments

This gene is expressed primarily in T-cells and gall bladder.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological disorders and conditions (immunodeficiencies, cancer, leukemia, hematopoeisis). Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and digestive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 299 as residues: Thr-41 to Gly-52.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune disorders, immunosuppressive (transplantation) and immunodeficiencies (e.g. AIDS), inflammation and hematopoeitic disorders. The expression of this gene in gall bladder would suggest a possible role for this gene product in digestive disorders, particularly of the pancreas.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 67**

This gene maps to chromosome 11, and therefore, may be used as a marker in linkage analysis for chromosome 11 (See Accession No. AA011622).

This gene is expressed primarily in a variety of fetal and developmental tissues (e.g. fetal spleen, infant brain).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental, immune or neurological abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the developing immune and central nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 300 as residues: Ser-38 to Ser-43.

- 5       The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for developmental abnormalities or fetal deficiencies. The detection in infant brain would suggest a role in neurological disorders (both developmental and neurodegenerative conditions of the brain and nervous system, behavioral disorders, depression, schizophrenia, Alzheimer's disease, Parkinson's
- 10       disease, Huntington's disease, mania, dementia). In addition, the detection in spleen would similarly suggest a role in detection and treatment of immunologically mediated disorders (e.g. immunodeficiency, inflammation, cancer, wound healing, tissue repair, hematopoiesis).

15       **FEATURES OF PROTEIN ENCODED BY GENE NO: 68**

          This gene is expressed primarily in spleen, T-cells, and fetal heart.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
- 20       not limited to, immunological deficiencies, including AIDS and cardiovascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and cardiovascular systems, expression of this gene at significantly higher
- 25       or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 30       The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders including: leukemias, lymphomas, autoimmune disorders, immunodeficiencies (e.g. AIDS), immuno-suppressive conditions (transplantation) and hematopoietic disorders. The expression in fetal heart indicates that polynucleotides and
- 35       polypeptides corresponding to this gene are useful for the treatment and diagnosis of cardiovascular disorders (e.g. heart disease, restenosis, atherosclerosis, stroke, angina, thrombosis).

**FEATURES OF PROTEIN ENCODED BY GENE NO: 69**

Gene shares homology with a human collagen protein. Preferred polypeptide fragments comprise the following amino acid sequence:

- 5 MPRKTSKCRQLLCGASRNADTAARQSTCSSHRPPGKIPSLGPRRXPGCXSV  
 SSRGEQSTGSPAAPRCGRRDAHRGLPGGAAMTPGDTWASFNPRAGHSKSQGE  
 GQESSGASRQDRHPVSHWVERQREAWGAPRSSSAGGVKVAATTEREPEFKIK  
 TGKA (SEQ ID NO:527); CSGASRNADTAARQSTCSSHRPPGKIPSLGPRRXPG  
 CXSVPSRGEQSTGSPAAPRCGRRDAHRGLPGGAAMTPGDTWASFNPRAGHS  
 10 (SEQ ID NO:528); QGEGQESSGASRQDRHPVSHWVERQREAWGAPRSSSAGG  
 VKVAATTEREPEFKIKTGKA (SEQ ID NO:529) (See Accession No. 124886). Also  
 preferred are polynucleotide fragments encoding these polypeptide fragments

This gene is expressed primarily in fetal heart.

- Therefore, polynucleotides and polypeptides of the invention are useful as  
 15 reagents for differential identification of the tissue(s) or cell type(s) present in a  
 biological sample and for diagnosis of diseases and conditions, which include, but are  
 not limited to, cardiovascular disorders. Similarly, polypeptides and antibodies directed  
 to these polypeptides are useful in providing immunological probes for differential  
 identification of the tissue(s) or cell type(s). For a number of disorders of the above  
 20 tissues or cells, particularly of the cardiovascular system, expression of this gene at  
 significantly higher or lower levels may be routinely detected in certain tissues (e.g.,  
 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial  
 fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
 such a disorder, relative to the standard gene expression level, i.e., the expression level  
 25 in healthy tissue or bodily fluid from an individual not having the disorder. Preferred  
 epitopes include those comprising a sequence shown in SEQ ID NO: 302 as residues:  
 Pro-32 to Ser-39.

- The tissue distribution indicates that polynucleotides and polypeptides  
 corresponding to this gene are useful for the treatment and diagnosis of cardiovascular  
 30 disorders (e.g. heart disease, restenosis, atherosclerosis, stroke, angina, thrombosis).

**FEATURES OF PROTEIN ENCODED BY GENE NO: 70**

- The translation product of this gene shares sequence homology with a chicken  
 single-strand DNA-binding protein. Preferred polypeptide fragments comprise the  
 35 following amino acid sequence:  
 MSPRYPGGPRPPLRIPNQALGGVPGSQPLLPSGMDPTRQQGHPNMGGPMQRM  
 TPRGMVPLGPQNYGGAMRPPLNALGGPGMPGMNMGPGGGRPWPNTNAN

SIPYSSASPGNYVGPPGGGGPPGTPIMPSPADSTNSGDNMYTLMNAVPPGPNR  
 PNFPMPGSDGPMGGLGGMESHMHMNGSLGSGDMDMSISKNSPNNMSLSNQ  
 GTPRDDGEMGGNFLNPFQSESYSPSMTMSV (SEQ ID NO:530); MSPRYPGG  
 PRPPLRIPNQALGGVPGSQPLLPSGMDPTRQQGHPNMGGPMQRMTPPRGMVP  
 5 LGPQNYGGAMRPLNALGGPGMPGMNMGPGGGRPWPNTNANSIPYSSASP  
 GNY (SEQ ID. NO:531); LNALGGPGMPGMNMGPGGGRPWPNTNANSIPYSS  
 ASPGNYVGPPGGGGPPGTPIMPSPADSTNSGDNMYTLMNAVPPGPN (SEQ ID  
 NO:532); GPMGGLGGMESHMHMNGSLGSGDMDMSISKNSPNNMSLSNQPGTPR  
 DDGEMGGNFLNPFQSESYSPSMTMSV (SEQ ID NO:533); TCEHSSEAKAFHDY  
 10 (SEQ ID NO:534). Also preferred are polynucleotide fragments encoding these  
 polypeptide fragments. (See Accession No. 1562534)

This gene is expressed primarily in placenta and to a lesser extent in the fetal heart and a variety of other tissues and cell types.

Therefore, polynucleotides and polypeptides of the invention are useful as  
 15 reagents for differential identification of the tissue(s) or cell type(s) present in a  
 biological sample and for diagnosis of diseases and conditions, which include, but are  
 not limited to, developmental abnormalities, fetal deficiencies, and particularly of the  
 cardiovascular system. Similarly, polypeptides and antibodies directed to these  
 polypeptides are useful in providing immunological probes for differential identification  
 20 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,  
 particularly of the reproductive system, expression of this gene at significantly higher or  
 lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded  
 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or  
 another tissue or cell sample taken from an individual having such a disorder, relative to  
 25 the standard gene expression level, i.e., the expression level in healthy tissue or bodily  
 fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides  
 corresponding to this gene are useful for the detection and treatment of developmental  
 abnormalities or fetal deficiencies, ovarian and other endometrial cancers, reproductive  
 30 dysfunction, cardiovascular disorders, and pre-natal disorders.

## FEATURES OF PROTEIN ENCODED BY GENE NO: 71

This gene is expressed primarily in fetal liver and to a lesser extent in the breast and testes.

35 Therefore, polynucleotides and polypeptides of the invention are useful as  
 reagents for differential identification of the tissue(s) or cell type(s) present in a  
 biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, liver disorders (including hepatoblastomas) and reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). The expression in testes and breast indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of endocrine and reproductive disorders (e.g. sperm maturation, milk production, testicular and breast cancers).

## 20 **FEATURES OF PROTEIN ENCODED BY GENE NO: 72**

This gene maps to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1 (See Accession No. W93595).

This gene is expressed primarily in smooth muscle and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiovascular and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular and central nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.



The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of restenosis, atherosclerosis, stroke, angina, thrombosis, wound healing and other conditions of heart disease. In addition, the expression in brain would suggest that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of developmental, degenerative and behavioral conditions of the brain and nervous system (e.g. schizophrenia, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, mania, dementia, paranoia, addictive behavior and sleep disorders).

### FEATURES OF PROTEIN ENCODED BY GENE NO: 73

Gene shares homology with human stromalin-2. Preferred polypeptide fragments comprise the following amino acid sequence:

QAFVLLSLLLLIFSPQMIVGGRDFLRPLVFFPEATLQSELASFLMDHVFQPGDL  
GSGA (SEQ ID NO:535); ACSYLLCNPEFTFFSRADFARSQLVDLLTDRFQQE  
LEELLQVG (SEQ ID NO:536), QKQLSSLRDRMVAFCCLCQSCLSDVDTEIQEQV  
ST (SEQ ID NO:537); QVILPALTLVYFSILWTLTHISKSDAS (SEQ ID NO:538);  
STHDLTRWELYECCQLLQKAVDTGXVPHQV (SEQ ID NO:539). Also preferred  
are polynucleotide fragments encoding these polypeptide fragments (See Accession  
No.R65208 ) This gene maps to chromosome 7, and therefore, may be used as a  
marker in linkage analysis for chromosome 7 (See Accession No. D52585).

This gene is expressed primarily in the brain (infant brain, adult brain, pituitary, cerebellum, hippocampus, schizophrenic hypothalamus, amygdala).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental and neurodegenerative diseases of the brain and nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those

comprising a sequence shown in SEQ ID NO: 306 as residues: Thr-25 to Lys-36, Lys-55 to Ser-63.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection and treatment of developmental, degenerative and behavioral conditions of the brain and nervous system (e.g. schizophrenia, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, mania, dementia, paranoia, addictive behavior and sleep disorders).

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 74**

This gene is expressed primarily in the hypothalamus of a human suffering from schizophrenia.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the CNS particularly schizophrenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the CNS, such as schizophrenia expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 307 as residues: Gly-38 to Ala-44.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of schizophrenia and other disorders involving the CNS.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 75**

Preferred polypeptides of the invention comprise the following amino acid sequence encoded by this gene:

LAVSTSFICCADISTALPLGSSRPAPAPRHREHEHGHQARPPRLXSTLMPLSTP  
AAAQLLWTQLTPMGGRPGGRHSPPTLHTGPRALPPGPPHPSLHVAALSLLR

(SEQ ID NO:540). Polynucleotides encoding such polypeptides are also provided.

This gene is expressed primarily in endometrial tumor and to a lesser extent in amniotic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, reproductive and immune disorders particularly cancers of those systems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 308 as residues: Ser-3 to Arg-9.

The tissue distribution indicates that the protein products of this gene are useful for study and treatment of immune and reproductive disorders particularly cancers of those systems.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 76**

This gene is expressed primarily in kidney cortex and to a lesser extent in early stage human brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, renal disorders such as renal cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the kidney expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 309 as residues: Gly-38 to Gly-45, Gly-47 to Gly-52, Pro-92 to Lys-110.

The tissue distribution indicates that the protein products of this gene are useful for study, treatment and diagnosis of renal diseases such as cancer of the kidney.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 77**

This gene is expressed primarily in kidney medulla.

Therefore, polynucleotides and polypeptides of the invention are useful as  
5 reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, metabolic and renal disorders. Similarly, polypeptides and antibodies  
directed to these polypeptides are useful in providing immunological probes for  
differential identification of the tissue(s) or cell type(s). For a number of disorders of  
10 the above tissues or cells, particularly of the metabolic and renal systems, expression of  
this gene at significantly higher or lower levels may be routinely detected in certain  
tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,  
urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an  
individual having such a disorder, relative to the standard gene expression level, i.e.,  
15 the expression level in healthy tissue or bodily fluid from an individual not having the  
disorder.

The tissue distribution indicates that the protein products of this gene are useful  
for study, treatment and diagnosis of metabolic and renal diseases and disorders.

**20 FEATURES OF PROTEIN ENCODED BY GENE NO: 78**

This gene is expressed in chronic synovitis and microvascular endothelium.

Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
25 not limited to, arthritis and atherosclerosis. Similarly, polypeptides and antibodies  
directed to these polypeptides are useful in providing immunological probes for  
differential identification of the tissue(s) or cell type(s). For a number of disorders of  
the above tissues or cells, particularly of the vascular and skeletal systems, expression  
of this gene at significantly higher or lower levels may be routinely detected in certain  
30 tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,  
urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an  
individual having such a disorder, relative to the standard gene expression level, i.e.,  
the expression level in healthy tissue or bodily fluid from an individual not having the  
disorder.

35 The tissue distribution indicates that the protein products of this gene are useful  
for study, diagnosis and treatment of arthritic and other inflammatory diseases as well  
as cardiovascular diseases.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 79**

This gene is expressed in resting T-cells and activated monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as  
5 reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, immune disorders. Similarly, polypeptides and antibodies directed to  
these polypeptides are useful in providing immunological probes for differential  
10 identification of the tissue(s) or cell type(s). For a number of disorders of the above  
tissues or cells, particularly of the immune system, expression of this gene at  
significantly higher or lower levels may be routinely detected in certain tissues (e.g.,  
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial  
fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
15 such a disorder, relative to the standard gene expression level, i.e., the expression level  
in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful  
for the study and treatment of immune diseases such as inflammatory conditions.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 80**

20 This gene is expressed in a variety of immune system tissues, e.g., neutrophils,  
T-cells, and TNF induced epithelial and endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
25 not limited to, infectious and immune disorders. Similarly, polypeptides and antibodies  
directed to these polypeptides are useful in providing immunological probes for  
differential identification of the tissue(s) or cell type(s). For a number of disorders of  
the above tissues or cells, particularly of the immune and vascular systems, expression  
of this gene at significantly higher or lower levels may be routinely detected in certain  
30 tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,  
urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an  
individual having such a disorder, relative to the standard gene expression level, i.e.,  
the expression level in healthy tissue or bodily fluid from an individual not having the  
disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID  
35 NO: 313 as residues: Met-1 to Trp-6.

The tissue distribution indicates that the protein products of this gene are useful  
for study and treatment of infectious diseases, immune and vascular disorders.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 81**

This gene is expressed in activated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as  
5 reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, inflammation and other immune conditions. Similarly, polypeptides and  
antibodies directed to these polypeptides are useful in providing immunological probes  
10 for differential identification of the tissue(s) or cell type(s). For a number of disorders  
of the above tissues or cells, particularly of the immune system, expression of this gene  
at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,  
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial  
fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
15 such a disorder, relative to the standard gene expression level, i.e., the expression level  
in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful  
for study and treatment of immune disorders.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 82**

20 This gene is expressed in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, inflammatory and other immune conditions. Similarly, polypeptides and  
25 antibodies directed to these polypeptides are useful in providing immunological probes  
for differential identification of the tissue(s) or cell type(s). For a number of disorders  
of the above tissues or cells, particularly of the immune system, expression of this gene  
at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,  
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial  
30 fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
such a disorder, relative to the standard gene expression level, i.e., the expression level  
in healthy tissue or bodily fluid from an individual not having the disorder. Preferred  
epitopes include those comprising a sequence shown in SEQ ID NO: 315 as residues:  
Ala-83 to Thr-91.

35 The tissue distribution indicates that the protein products of this gene are useful  
for study and treatment of immune disorders.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 83**

This gene is expressed in human neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as  
5 reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, inflammation and immune disorders. Similarly, polypeptides and  
antibodies directed to these polypeptides are useful in providing immunological probes  
for differential identification of the tissue(s) or cell type(s). For a number of disorders  
10 of the above tissues or cells, particularly of the immune and inflammatory system,  
expression of this gene, at significantly higher or lower levels may be routinely detected  
in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,  
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from  
an individual having such a disorder, relative to the standard gene expression level, i.e.,  
15 the expression level in healthy tissue or bodily fluid from an individual not having the  
disorder.

The tissue distribution indicates that the protein products of this gene are useful  
for diagnosis and treatment of disorders of the inflammatory and immune systems.

**20 FEATURES OF PROTEIN ENCODED BY GENE NO: 84**

This gene is expressed in human neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
25 not limited to, disorders of the inflammatory and immune systems. Similarly,  
polypeptides and antibodies directed to these polypeptides are useful in providing  
immunological probes for differential identification of the tissue(s) or cell type(s). For  
a number of disorders of the above tissues or cells, particularly of the inflammatory and  
immune systems, expression of this gene at significantly higher or lower levels may be  
30 routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily  
fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or  
cell sample taken from an individual having such a disorder, relative to the standard  
gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an  
individual not having the disorder.

35 The tissue distribution indicates that the protein products of this gene are useful  
for diagnosis and treatment of disorders of the immune and inflammatory systems.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 85**

This gene is expressed in activated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as  
5 reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, inflammation and immune system diseases. Similarly, polypeptides and  
antibodies directed to these polypeptides are useful in providing immunological probes  
for differential identification of the tissue(s) or cell type(s). For a number of disorders  
10 of the above tissues or cells, particularly of the immune system and inflammatory  
system, expression of this gene at significantly higher or lower levels may be routinely  
detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g.,  
serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample  
taken from an individual having such a disorder, relative to the standard gene  
15 expression level, i.e., the expression level in healthy tissue or bodily fluid from an  
individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful  
for diagnosis and treatment of diseases of the inflammatory and immune systems.

**20 FEATURES OF PROTEIN ENCODED BY GENE NO: 86**

This gene is expressed in activated neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
25 not limited to, inflammation and immune system disorders. Similarly, polypeptides and  
antibodies directed to these polypeptides are useful in providing immunological probes  
for differential identification of the tissue(s) or cell type(s). For a number of disorders  
of the above tissues or cells, particularly of the inflammatory and immune system,  
expression of this gene at significantly higher or lower levels may be routinely detected  
30 in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,  
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from  
an individual having such a disorder, relative to the standard gene expression level, i.e.,  
the expression level in healthy tissue or bodily fluid from an individual not having the  
disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID  
35 NO: 319 as residues: Met-1 to Gly-6, Gly-32 to Pro-43, Leu-55 to Gln-60.

The tissue distribution indicates that the protein products of this gene are useful  
for diagnosis and treatment of disorders of the immune and inflammatory system.



**FEATURES OF PROTEIN ENCODED BY GENE NO: 87**

In specific embodiments, polypeptides of the invention comprise the sequence:  
 EQVLALLWPRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALVSIN  
 5 QTIPNERTMQLLGQLQVEVENFVLRVAAEFSSRKEQLVFLINNYDMMLGVLME  
 RAADDKEVESFQQLLNARTQEFIEELLSPFGLVAFVKEAEALIERGQAERLR  
 GEEARVTQLIRGFGSSWKSSVESLSQDVMRSFTNFRNGTSIIQG (SEQ ID  
 NO:541), ALLKYRFFYQFLGNERATAKEIRDEYVETLSKIYLSYYRSYLGRMLK  
 VQYEEVAEKDDLGMVEDTAKKGFXSKPSRSRNTIFTLGTRGSVISPTELEAPILV  
 10 PHTAQR (SEQ ID NO: 542); EQRYPFALFRSQHYXLLDNSCREYLFICEFFVVS  
 GPXAHDLFHAVMGRTLSMTLKHLD SYLADCYDAIAVFLCIHIVLRFRNIAAKRD  
 VPALDRYW (SEQ ID NO:543), GGLDTRPHYITRRYAEFSSALVSINQ (SEQ ID  
 NO:544); SRKEQLVFLINNYDMMLGVL (SEQ ID NO: 545) and/or ALLKYRFFY  
 QFLGNERATAKEIRDEYVETLSKIYLSYYRSYLGRMLKVQYEEVAEKDDLGM  
 15 VEDTAKKGFXSKPSLSRNTIFTLGTRGSVISPTELEAPILVPHTAQRXEQRYPF  
 EALFRSQHYXLLDNSCREYLFICEFFVVS GPXAHDLFHAVMGRTLSMTLKHLD  
 SYLADCYDAIAVFLCIHIVLRFRNIAAKRDVPALDRYWEQVLALLWPRFELILEM  
 NVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALVSINQTIPNERTMQLLGQLQV  
 EVENFVLRVAAEFSSRKEQLVFLINNYDMMLGVL MERAADDKEVESFQQLLN  
 20 ARTQEFIEELLSPFGLVAFVKEAEALIERGQAERLRGEEARVTQLIRGFGSSW  
 KSSVESLSQDVMRSFTNFRNGTS (SEQ ID NO:546). Polynucleotides encoding  
 these polypeptides are also encompassed by the invention. The translation product of  
 this gene shares sequence homology with suppressor of actin mutation which is thought  
 to be important in mutation suppression.

25 This gene is expressed primarily in fetal liver and to a lesser extent in a variety  
 of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as  
 reagents for differential identification of the tissue(s) or cell type(s) present in a  
 biological sample and for diagnosis of diseases and conditions, which include, but are  
 30 not limited to, liver and mutations. Similarly, polypeptides and antibodies directed to  
 these polypeptides are useful in providing immunological probes for differential  
 identification of the tissue(s) or cell type(s). For a number of disorders of the above  
 tissues or cells, particularly of the liver or cancer, expression of this gene at  
 significantly higher or lower levels may be routinely detected in certain tissues (e.g.,  
 35 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial  
 fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
 such a disorder, relative to the standard gene expression level, i.e., the expression level

in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 320 as residues: Val-53 to Arg-60, Thr-88 to Thr-94, Ala-142 to Ser-150, Gly-188 to Glu-196, Gly-208 to Ser-214, Thr-227 to Gly-232, Lys-279 to Phe-285.

- 5       The tissue distribution and homology to suppressor of actin mutation suggest that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and of liver disorder or cancer.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 88**

- 10       This gene maps to chromosome 9, and therefore can be used in linkage analysis as a marker for chromosome 9. In specific embodiments, polypeptides of the invention comprise the sequence:
- YEGKEFDYVFSIDVNEGGPSYKLPYNTSDDPWLTAYNFLQKNDLNPMFLDQVA  
KFIIDNTKGQMLGLGNPSFSDPFTGGGRYVPGSSGSSNTLPTADPFTGAGRYV  
15   PGSASMGTTMAGVDPFTGNSAYRSAASKTMNIYFPKKEAVTFDQANPTQILGK  
LKELNGTAPEEKKLTEDDLILLEKILSLICNSSSEKPTVQQLQILWKAINCPEDIV  
FPALDILRLSIKHPSVNENFCNEKEGAQFSSHLLNLLNPKGKPANQLLALRTFC  
NCFVGQAGQKLMMSQRESLSHAIELKSGSNKNI (SEQ ID NO: 547);  
HIALATLALNYSVCFHKD (SEQ ID NO: 548); HNIEGKAQCLSLISTILEVVQ  
20   DLEATFRLLVALGTLISDDSNVQLAKS (SEQ ID NO:549); LGVDSQIKKYSS  
VSEPAKVSECCRFILNLL (SEQ ID NO:550); and/or YEGKEFDYVFSIDVNEGGPS  
YKLPYNTSDDPWLTAYNFLQKNDLNPMFLDQVAKFIIDNTKGQMLGLGNPSFS  
DPFTGGGRYVPGSSGSSNTLPTADPFTGAGRYVPGSASMGTTMAGVDPFTGN  
SAYRSAASKTMNIYFPKKEAVTFDQANPTQILGKLKELNGTAPEEKKLTEDDLI  
25   LLEKILSLICNSSSEKPTVQQLQILWKAINCPEDIVFPALDILRLSIKHPSVNENFC  
NEKEGAQFSSHLLNLLNPKGKPANQLLALRTFCNCFVGQAGQKLMMSQRESL  
MSHAIELKSGSNKNIHIALATLALNYSVCFHKDHNIEGKAQCLSLISTILEVVQD  
LEATFRLLVALGTLISDDSNVQLAKSLGVDSQIKKYSSVSEPAKVSECCRFILN  
30   LL (SEQ ID NO:551). Polynucleotides encoding these polypeptides are also  
encompassed by the invention. These polypeptides share significant homology with  
phospholipase A2 activating protein which is thought to be important in signal  
transduction (see, e.g., Wang et al., Gene 161(2):237-241 (1995)).

- 35       This gene is expressed primarily in endothelial cells, to a less extent in placenta, endometrial stromal cells, osteosarcoma, testis tumor, muscle, and infant brain that are likely to be rich in blood vessels.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders in vascular system, aberrant angiogenesis, tumor angiogenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system or tumors, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene in endothelial cells and several potential highly vascularized tissues and its homology to phospholipase A2 activating protein suggest that this gene may be involved in transducing signals for endothelial cells in angiogenesis or vasculogenesis.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 89

In specific embodiments, polypeptides of the invention comprise the sequence: YPNQDGDILRDQVLHEHIQRLSKVVTANHRALQIPEVYLREAPWPSAQSEIRTIS AYKTPRDKVQCILRMCSTIMNLLSLANEDSVPGADDFVPVLVFLIKANPPCLL STVQYISSFYASCLSGEESYWWMQFTA AVE (SEQ ID NO:552); YPNQDGDILR DQVLHEHIQRLSKVVTANHRALQIPEVYLREAPWPSAQSEIRTIS AYKTPRDKVQ CILRMCSTIMNLLSLANEDSVPGADDFVPVLVFLIKANPPCLLSTVQYISSFYA SCLSGEESYWWMQFTA AVEFIKTI (SEQ ID NO:553); YPNQDGDILRDQVL (SEQ ID NO:554); EAPWPSAQSEI (SEQ ID NO:555); PVLVFLIKANP (SEQ ID NO:560); SGEESYWWMQFTA AVEFIKTI (SEQ ID NO:556); ADDFPVLVFLIKANPP (SEQ ID NO:557); YKTPRDKVQCIL (SEQ ID NO:558); and/or GADDFVPVLVFLIK (SEQ ID NO:559). The translation product of this gene shares sequence homology with human ras inhibitor and yeast VPS9p which is thought to be important in golgi vacuole transport.

This gene is expressed primarily in T cells and melanocytes and to a lesser extent in a variety of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, dysfunction and disorders involving T cells and melanocytes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ras inhibitor indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating signal transduction; diagnosis and treatment of disorders involving T cells and melanocytes.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 90**

This gene maps to chromosome 9 and therefore polypeptides of the invention can be used in linkage analysis as a marker for chromosome 9. The translation product of this gene shares sequence homology with neuronal olfactomedin-related ER localized protein which is thought to be important in influence the maintenance, growth, or differentiation of chemosensory cilia on the apical dendrites of olfactory neurons. In specific embodiments, polypeptides of the invention comprise the sequence: SARASTQPPAGQHGPC (SEQ ID NO:561); MPGRWRWQRDMHPARKLLSLL FLILMGTELTQD (SEQ ID NO:562); SAAPDSLLRSSKGSTRGSL (SEQ ID NO:563); AAIVWRGKSESRIAKTPGI (SEQ ID NO:564); FRGGGTLVLPPTHT PEWLIL (SEQ ID NO:567); PLGITLPLGAPETGGGD (SEQ ID NO:565); and/or CAAETWKGSQRAGQLCALLA (SEQ ID NO:566).

This gene is expressed in pineal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological and endocrinological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neurological or endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 323 as residues: Leu-20 to Ala-26, Arg-32 to Arg-39, Thr-104 to Gly-112.

5 The tissue distribution and homology to olfactomedin-related protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for maintenance, growth, or differentiation of neuron cells in pineal gland, therefore, may be useful for diagnosis and treatment of neurological disorders in pineal gland.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 91**

10 This gene is expressed primarily in prostate and apoptotic T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, prostate disease and T cell dysfunction. Similarly, polypeptides and  
15 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate cancer, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial  
20 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for detect abnormal activity in prostate and T cells  
25 or probably treatment of this abnormality.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 92**

This gene is expressed primarily in prostate and to a lesser extent in smooth muscle cells, fibroblasts, and placenta.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders in prostate or vascular system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes  
35 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prosate or vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain

tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating function of prostate or highly vascularized tissues, e.g. placenta.

#### 10 FEATURES OF PROTEIN ENCODED BY GENE NO: 93

This gene is expressed primarily in embryos and fetal tissues stage human and to a lesser extent in a wide variety of other proliferative tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders in embryonic development and cell proliferation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the embryonic tissues and proliferative cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of abnormalities in developing and proliferative cells and organs.

#### 30 FEATURES OF PROTEIN ENCODED BY GENE NO: 94

The translation product of this gene shares sequence homology with transformation related protein which is thought to be important in transformation.

This gene is expressed primarily in female reproductive tissues, i.e., breast cancer cells, placenta, and ovary and to a lesser extent in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, cancer or dysfunction of reproductive tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproduction system,

5 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the

10 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 327 as residues: Ser-50 to Pro-61.

The tissue distribution and homology to transformation related protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of conditions caused by transformation, i.e. tumorigenesis in

15 reproductive organs, e.g. breast, placenta, and ovary.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 95**

This gene is expressed primarily in testes, rhabdomyosarcoma, infant brain and to a lesser extent in some tumors and highly vascularized tissues.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumorigenesis, abnormal angiogenesis, and/or neurological disorders. , Similarly, polypeptides and antibodies directed to these polypeptides are useful in

25 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the tumor tissues or vascular tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

30 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 328 as residues: Arg-46 to Trp-54, Pro-60 to Ile-69, Asn-116 to Ala-122, Arg-147 to Lys-153, Ser-158 to Glu-170, Ile-399 to

35 Ser-405, Pro-486 to Met-499, Pro-502 to Asp-508.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for a range of disease states including treatment of

tumor or vascular disorders and the treatment of neurological disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder.

## 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 96

This gene maps to chromosome 7 and therefore polynucleotides of the present invention can be used in linkage analysis as a marker for chromosome 7. The translation product of this gene is homologous to the *Clostridium perfringens* enterotoxin (CPE) receptor gene product and shares sequence homology with a human ORF specific to prostate and a glycoprotein specific to oligodendrocytes both of which are tissue specific proteins. (See e.g., Katahira et al., J Cell Biol. 136(6):1239-1247 (1997). PMID: 9087440; UI: 97242441.

This gene is expressed primarily in pancreas tumor and ulcerative colitis and to a lesser extent in several tumors and normal tissues.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, pancreatic disorder, ulcerative colitis, tumors and food poisoning. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system or tumorigenic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 329 as residues: Gly-147 to Met-152, Cys-177 to Lys-188.

30 The tissue distribution and homology to prostate and oligodendrocyte-specific protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for marker of diagnosis or treatment of disorder in pancreas, ulcerative colitis, and tumors. Furthermore, identity to the human receptor for *Clostridium perfringens* enterotoxin indicates that the soluble portion of this receptor could be used in the treatment of food poisoning associated with *Clostridia perfringens* by blocking the activity of perfringens enterotoxin.



**FEATURES OF PROTEIN ENCODED BY GENE NO: 97**

The translation product of this gene shares sequence homology with ATPase which is thought to be important in metabolism.

- 5 This gene is expressed primarily in testes and several hematopoietic cells and to a lesser extent in other tissues.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemia and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 330 as residues: Leu-37 to Ala-42.

The tissue distribution and homology to ATPase indicates that polynucleotides and polypeptides corresponding to this gene are useful for marker of diagnosis and treatment of leukemia and other hematopoietic disorders.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 98**

- In specific embodiments, polypeptides of the invention comprise the sequence: MRSARPSLGCLPSWAFSQUALNI (SEQ ID NO:568); LLGLKGLAPAEISAVCE KGNFN (SEQ ID NO:569); VAHGLAWSYYIGYLRILPELQARIR (SEQ ID NO:570); TYNQHYNLLRGAVSQRC (SEQ ID NO:571); ILLPLDCGVPDNLISM ADPNIRFLDKLPQQTGDRAGIKDRVYSN (SEQ ID NO:572); SIYELLENGQRAGT CVLEYATPLQTLFAMSQYSQAGFSGEDRLEQ (SEQ ID NO:573); AKLFCRTLE DILADAPESQNNCRLLIAYQEPADDSSFSLSQEVLRLRQEEKEEVTGSLKTSAPV PSTSTMSQEPPELLISGMEKPLPLRTDFS (SEQ ID NO:574); and/or LLGLKGLA PAEISAVCEKGNFNVAHGLAWSYYIGYLRILPEL (SEQ ID NO:575).

- 35 Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in prostate BPH and to a lesser extent in bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, benign prostatic hypertrophy or prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male urinary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 331 as residues: Ile-60 to Asn-69, Leu-106 to Asp-112, Glu-130 to Gly-136, Phe-160 to Glu-167, Pro-184 to Cys-190, Glu-197 to Ser-202, Arg-215 to Glu-221, Thr-237 to Pro-242.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of benign prostatic hypertrophy or prostate cancer.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 99**

This gene is expressed primarily in salivary gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders or injuries of the salivary gland. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of glandular tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of disorders of, or injuries to the salivary gland or other glandular tissue.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 100**

This gene maps to chromosome 15, accordingly, polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 15. The translation product of this gene shares sequence homology with a *C.elegans* gene of unknown function. In specific embodiments, polypeptides of the invention comprise the sequence: DPRVRLNSLTCKHIFISLTQ (SEQ ID NO:583); TMKLLKLRNIV KLSLYRHFTN (SEQ ID NO:576); TLILAVAASIVFIWTTMKFRI (SEQ ID NO:577); VTCQSDWRELWVDDAIWRLLFSMILFVI (SEQ ID NO:578); MVLWR PSANNQRFAFSPLSEEEEEDEQ (SEQ ID NO:580); KEPMLKESFEGMKMRS TKQEPNGNSKVNKAQEDDL (SEQ ID NO:584); and/or KWVEENVPSVTDVALP ALLDSDEERMITHFERSKME (SEQ ID NO:582). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in thyroid and to a lesser extent in osteoclastoma, kidney medulla, and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, thyroid dysfunction or cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 333 as residues: Lys-107 to Leu-124, Glu-150 to Thr-159, Pro-173 to Asp-179, Ser-192 to Ser-201.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of thyroid dysfunction or cancer.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 101**

This gene maps to chromosome 16, therefore polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 16. In specific embodiments, polypeptides of the invention comprise the sequence:

IRHELTVLRDTRPACA (SEQ ID NO:585); and/or MDFXMALIYD (SEQ ID NO:586). Polynucleotides encoding these polypeptides are also encompassed by the invention.

5 This gene is expressed primarily in kidney cortex and to a lesser extent in adult brain, corpus colosum, hippocampus, and frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disorders. Similarly, polypeptides and antibodies directed to  
10 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial  
15 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of neurological  
20 disorders.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 102

In specific embodiments, polypeptides of the invention comprise the sequence:  
MQEMMRNQDRALSNLESIPGGYNA (SEQ ID NO:587); LRRMYTDIQEPMLSA  
25 AQEQF GGNPF (SEQ ID NO:588); ASLVSNNTSSGEGSQPSRTENRDPLPNPWAP  
QT (SEQ ID NO:589); SQSSSASSGTASTVGGTTGSTASGTSGQSTTAPNLVPGV  
GASMFNTPG MQSLLQQTENPQLMQNMLSAPY (SEQ ID NO:590);  
MRSMMQSLSQNPDLAAQMMLNNPLFAGNPQLQEOMRQQLPTFLQQ (SEQ ID  
NO:591); MQNPDTLSAMSNPRAMQALLQIQQLQTLATEAPGLIPGFTPGLG  
30 ALGSTGGSSGTNGSNATPSENTSPTAGT (SEQ ID NO:592); TEPGHQQFI  
QQMLQALAGVNPQLQNPEVRFQQLEQLSAMGFLNREANLQALATGGDINAA  
IERLLGSQPS (SEQ ID NO:593); RNPAMMQEMMRNQDRALSNLESIPGGY  
NALRRMYTDIQEPMLSAA (SEQ ID NO:594); GNPFAASLVSNNTSS (SEQ ID  
NO:595); ENRDPLPNPWA (SEQ ID NO:595); GKILKDQDTLSQHGHD (SEQ ID  
35 NO:597); GLTVHLVIKTQNRP (SEQ ID NO:598); SELQSQMQRQLLSNPPEMM  
(SEQ ID NO:599); PEISHMLNNPDIMR (SEQ ID NO:600); and/or  
RQLIMANPQMQLIQRNP (SEQ ID NO:601). Polynucleotides encoding these

polypeptides are also encompassed by the invention.

This gene is expressed primarily in breast.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of tumor systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of some types of breast cancer.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 103**

The translation product of this gene shares sequence homology with secreted serine proteases and lysozyme C precursor, which is thought to be important in bacteriolytic function. In specific embodiments, polypeptides of the invention comprise the sequence: NLCHVDCQDLLNP NLLAGIHCAKRIVS (SEQ ID NO:602); LDGFEGYSLSDWLCLAFVESKFN (SEQ ID NO:603); NENADGSFDYGLFQINSHYWCN (SEQ ID NO:604); and/or NLCHVDCQDLLNP NLLAGIHCAKRIVS (SEQ ID NO:605). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, infection. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 336 as residues: Ile-62 to Phe-70, Asn-78 to Asn-84.

The tissue distribution and homology to lysozyme C precursor indicates that polynucleotides and polypeptides corresponding to this gene are useful for boosting the monocyte-macrophage system and enhance the activity of immunoagents.

#### 10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 104**

This gene is expressed primarily in apoptotic T-cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of some immune disorders.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 105**

The translation product of this gene shares sequence homology with ARI protein of Drosophila (accession 2058299; EMBL: locus DMARIADNE, accession X98309), which is thought to be important in axonal path-finding in the central nervous system. In specific embodiments, polypeptides of the invention comprise the sequence IREVNEVIQNPAT (SEQ ID NO:606); ITRILLSHFNWDKEKLMERYF DGNLEKLFA (SEQ ID NO:607); NTRSSAQDMPCQICYLNYPNSYF (SEQ ID NO:608); TGLECGHKFCMQCWSEYLTTKIMEEGMGQTISCPAHG (SEQ ID NO:614); CDILVDDNTVMRLITDSKVKLKYQHLITNSFVECNRLKWKCPAPD CHHVVKVQYPDAKPV (SEQ ID NO:609); CDILVDDNTVMRLITDSK

VKLKYQHLITNSFVECNRLWKWCPAPDCHHVVKV (SEQ ID NO:610);  
 GCNHMVCRNQNKAEFCWVCLGPWEPHGS AWYNCNRYNEDDAKAARDAQE  
 RSRAALQRYL (SEQ ID NO:611); FYCNRYMNHMQSLRFEHKLYAQVKQ  
 KMEEMQQHNMSWIEVQFLKKAVDVLCQCRATLMT (SEQ ID NO: 612);  
 5 YVFAFYLLKNNQSIIFENNQADLENATEVLSGYLERDISQDSLQDIKQKVQDKY  
 RYCESR (SEQ ID NO:613) Polynucleotides encoding these polypeptides are also  
 encompassed by the invention.

This gene is expressed primarily in adult brain, and to a lesser extent in  
 endometrial tumor, melanocytes, and infant brain.

10 Therefore, polynucleotides and polypeptides of the invention are useful as  
 reagents for differential identification of the tissue(s) or cell type(s) present in a  
 biological sample and for diagnosis of diseases and conditions, which include, but are  
 not limited to, diseases or injuries involving axonal path development. Similarly,  
 polypeptides and antibodies directed to these polypeptides are useful in providing  
 15 immunological probes for differential identification of the tissue(s) or cell type(s). For  
 a number of disorders of the above tissues or cells, particularly of the central nervous  
 system, expression of this gene at significantly higher or lower levels may be routinely  
 detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g.,  
 serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample  
 20 taken from an individual having such a disorder, relative to the standard gene  
 expression level, i.e., the expression level in healthy tissue or bodily fluid from an  
 individual not having the disorder.

The tissue distribution and homology to ARI protein indicates that  
 polynucleotides and polypeptides corresponding to this gene are useful for treatment of  
 25 disease states or injuries involving axonal path development, including  
 neurodegenerative diseases and nerve injury.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 106**

The translation product of this gene shares sequence homology with cytochrome  
 30 b561 [Sus scrofa] which is thought to be an integral membrane protein of  
 neuroendocrine storage vesicles of neurotransmitters and peptide hormones.

This gene is expressed primarily in frontal cortex and to a lesser extent in  
 rhabdomyosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as  
 35 reagents for differential identification of the tissue(s) or cell type(s) present in a  
 biological sample and for diagnosis of diseases and conditions, which include, but are  
 not limited to, neurological disorders. Similarly, polypeptides and antibodies directed to

these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 339 as residues: Ser-18 to Pro-24.

The tissue distribution and homology to cytochrome b561 [*Sus scrofa*] indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of neurological disorders. This gene may also be important in regulation of some types of cancers.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 107

In specific embodiments, polypeptides of the invention comprise the sequence: MWGYLFVDAAWNFLGCLICGW (SEQ ID NO:615); MHFISSGNVSAIRSSILL RXSLSYLGNCRLRVSAIFVYFLLFLLLS (SEQ ID NO:616); and/or MDQALRGSPSE GFSTDPSPQVGRQIPSFPPWRRLVLPKASGCFLEREWLVCVFKLRTRPGAEA HAYNSSILGGRGKGIT (SEQ ID NO:617). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in pancreas tumor and to a lesser extent in cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, pancreatic tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred



epitopes include those comprising a sequence shown in SEQ ID NO: 340 as residues: Pro-22 to Phe-33.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of pancreatic tumors.

5

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 108**

This gene maps to chromosome 17 and therefore polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 17. In specific embodiments, polypeptides of the invention comprise the sequence:

10 MLPALASCCHFSPPEQAARLKKLQEQEKQKVEFRKRMEKEVSDFIQDSGQIK  
KKFQPMNKIERSILHDVVEVAGLTSFSFGEDDDCRYVMIFKKEFAPSDEELDSY  
RRGEEWDPQKAEKRNXXELAQRQ (SEQ ID NO:618); EEEAAQQGPVVV  
SPASDYKDKYSHLIGKGAAKDAAHMLQANKTYGCXPVANKRDRSIEEAMNE  
IRAKKRLRQSGE (SEQ ID NO:619); PPRRPAQLPLTPGAGQGAGRDKAAAIRA  
15 HPGAPPLNHLLP (SEQ IDNO:620); AVPQAGGKQVFDLSPLELGYVRGMCVCV  
(SEQ ID NO:621) and/or MLPALASCCHFSPPEQAARLKKLQEQEKQKVEFRK  
RMEKEVSDFIQDSGQIKKFQPMNKIERSILHDVVEVAGLTSFSFGEDDDCRYV  
MIFKKEFAPSDEELDSYRRGEEWDPQKAEKRNXXELAQRQEEEEAAQQGPVVV  
SPASDYKDKYSHLIGKGAAKDAAHMLQANKTYGCXPVANKRDRSIEEAMNE  
20 IRAKKRLRQSGE (SEQ ID NO:622). Polynucleotides encoding these polypeptides  
are also encompassed by the invention. The translation product of this gene shares  
sequence homology with FSA-1 which may play a role as a structural protein  
component of the acrosome.

This gene is expressed primarily in fetal kidney and sperm.

25

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male reproductive disorders, especially involving acrosomal dysfunction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in  
30 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or  
35 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an

individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 341 as residues: Glu-8 to Asn-35.

The tissue distribution and homology to FSA-1 indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of infertility due to  
5 acrosomal disfunction of sperm.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 109**

This gene is expressed primarily in pituitary and to a lesser extent in epididymus.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for  
15 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an  
20 individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 342 as residues: Met-1 to Trp-6.

Because the gene is found in both pituitary and epididymus, this indicates that  
25 polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of male reproductive disorders. This may involve a secreted peptide produced in the pituitary targeting the epididymus.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 110**

30 In specific embodiments, polypeptides of the invention comprise the sequence: LLCPVLNSGXSWNFPHPSPQEYSFHGFHSTRLWI (SEQ ID NO:623); and/or PSTPWFLFLLGLTCPFSTSHPRWDSIPP (SEQ ID NO:624). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in resting T-cells.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, T-cell disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of certain immune disorders, especially those involving T-cells.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 111**

This gene is expressed primarily in cerebellum and whole brain and to a lesser extent in infant brain and fetal kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 344 as residues: Asp-48 to Gly-55.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neurological disorders.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 112**

The translation product of this gene shares sequence homology with yeast mitochondrial ribosomal protein homologous to ribosomal protein s15 of E.coli which

is thought to be important in the early assembly of ribosomes (See Accession No. M38016). This gene maps to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in developmental tissues.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, development of cancers and tumors in addition to healing wounds. Similarly, polypeptides and antibodies directed to these polypeptides are useful in  
10 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and developmental expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or  
15 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ribosomal protein s15 of *E. coli* indicates that polynucleotides and polypeptides corresponding to this gene are useful for  
20 diseases related to the assembly of ribosomes in the mitochondria which is important in the translation of RNA into protein. Therefore, this indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of multiple tumors as well as in healing wounds which are thought to be under similar regulation as developmental tissues. Protein, as well as, antibodies directed against the  
25 protein have utility as tumor markers, in addition to immunotherapy targets, for the above listed tumors and tissues.

### **FEATURES OF PROTEIN ENCODED BY GENE NO: 113**

The translation product of this gene shares sequence homology with human  
30 poliovirus receptor precursors which are thought to be important in viral binding and uptake. Preferred polypeptide fragments comprise the following amino acid sequence:  
ELISISNVALADEGEYTCSTFTMPVRTAKSLVTVLGIPQKPIITGYKSSLREKDT  
ATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFTVSSSVTFQVTR  
EDDGASIVCSVNHESLKGADRSTSQRIEVLPTAMIRPDPPHPREGQKLLHHC  
35 EGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGS  
YKAYYTLNVND (SEQ ID NO:625). Also preferred are polynucleotide fragments encoding these polypeptide fragments (See Accession No. gnllPID1002627).

This gene is expressed almost exclusively in human brain tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, susceptibility to viral disease and diseases of the CNS especially cancers of that system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 346 as residues: Leu-26 to Asp-37, Lys-53 to Ser-59.

The tissue distribution and homology to poliovirus receptor precursors indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and prevention of diseases that involve the binding and uptake of virus particles for infection. It might also be helpful in genetic therapy where the goal is to insert foreign DNA into infected cells. With the help of this protein, the binding and uptake of this foreign DNA might be aided. In addition, it is expected that over expression of this gene will indicate abnormalities involving the CNS, particularly cancers of that system.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 114**

The translation product of this gene shares sequence homology with YO87\_CAEEL hypothetical 28.5 KD protein ZK1236.7 in chromosome III of *Caenorhabditis elegans* in addition to alpha-1 collagen type III (See Accession No. gil537432). One embodiment for this gene is the polypeptide fragment(s) comprising the following amino acid sequence: VPELPDRVHQLHQA VQG CALGRPGFPGGPTH SGHHKSHPGPAGGDYNRCDRPGQVHLHNPRGTGRRGQLHPTAGPGVHRRACPSQQLPHRLGPGVPCPSLTPVLPSWTQSWCG LPGYTSSS (SEQ ID NO:630). An additional embodiment is the polynucleotide fragment(s) encoding these polypeptide fragments

This gene is expressed primarily in brain cells and to a lesser extent in activated B and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegeneration and immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 347 as residues: Glu-34 to Glu-39, Gly-51 to Ser-72, Ala-88 to Glu-93, Gln-100 to Val-105.

The tissue distribution and homology to YO87\_CAEEL hypothetical 28.5 KD protein ZK1236.7 in chromosome III of *Caenorhabditis elegans* as well as to a conserved alpha-1 collagen type III protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons' Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorders. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 115**

The translation product of this gene shares sequence homology with alpha 3 type IX collagen which is thought to be important in hyaline cartilage formation via its ability to uptake inorganic sulfate by cells (See Accession No. gil975657). One embodiment of this gene is the polypeptide fragment comprising the following amino acid sequence: SLRRPRSAAXQTLTTLSSVSSASSALPGSREPCDPRAPPPR SGSAASCCSCCSCPRRRAPLRSPRGSKRRIRQREVVDLYNGMCLQGPGAGVPG RDGSPGANGIPGTPGIPGRDGFKGKGECLRESFEESWTPNYKQCSWSSLNY GIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSPG LPIEAIYLDQGSPEMNSTINIHTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKG DASTGWNSVSRIIIIEELPK (SEQ ID NO:634). An additional embodiment are the

polynucleotide fragments encoding this polypeptide fragment.

This gene is expressed primarily in smooth muscle and to a lesser extent in synovial tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as  
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias i.e., spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid and autoimmune  
10 disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily  
15 fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to alpha 3 type IX collagen indicates that  
20 polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of diseases associated with the mutation in this gene which leads to the many different types of chondrodysplasias. By the use of this product, the abnormal growth and development of bones of the limbs and spine could be routinely detected or treated in utero since the protein or muteins thereof could affect epithelial cells early in  
25 development and later the chondrocytes of the developing craniofacial structure.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 116**

The translation product of this gene shares sequence homology with retrovirus-related reverse transcriptase which is thought to be important in viral replication. One  
30 embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence: TKKENC RPASLMNIDTKILNKILMNQ (SEQ ID NO:640). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments (See Accession No. pirlA25313IGNHUL1).

This gene is expressed primarily in human meningima.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, retroviral diseases such as AIDS, and possibly certain cancers due to transactivation of latent cell division genes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to retrovirus-related reverse transcriptase indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of diseases and maladies associated with retroviral infection since a functional reverse transcriptase (RT) or RT-like molecule is an integral component of the retroviral life cycle.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 117

The translation product of this gene shares sequence homology with an unknown gene from *C. elegans*, as well as weak homolog with mammalian metaxin, a gene contiguous to both thrombospondin 3 and glucocerebrosidase, is known to be required for embryonic development. Preferred polypeptide fragments comprise the following amino acid sequence: MCNLPIKVVCRAAEYMSPSGKVPXXHVGNGQ VVSELGPVQFVKAKGHSLSDGLEEVQKAEMKAYMELVNNMLLTAELYLQWC DEATVGXITHXRYGSPYPWPLXHILAYQKQWEVKRKXKAIGWGKKTLTDQVLE DVDQCCQALSQRLGTQPYFFNKQPTELDALVFGHLYTILTTQLTNDELSEKVKN YSNLLAFCRRI EQHYFEDRGKGRLS (SEQ ID NO:641); MCNLPIKVVCRAAE YMSPSGKVPXXHVGNGQVVSELGPVQFVK (SEQ ID NO:642). Also preferred are polynucleotide fragments encoding these polypeptide fragments (See Accession No. gil1326108).

This gene is expressed primarily in fetal tissues and to a lesser extent in hematopoietic cells and tissues, including spleen, monocytes, and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer; lymphoproliferative disorders; inflammation; chondrosarcoma, and Gaucher disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification



of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and embryonic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression in embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation or cellular division. Additionally, the expression in hematopoietic cells and tissues indicates that this protein may play a role in the proliferation, differentiation, and survival of hematopoietic cell lineages. Thus, this gene may be useful in the treatment of lymphoproliferative disorders, and in the maintenance and differentiation of various hematopoietic lineages from early hematopoietic stem and committed progenitor cells.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 118**

The translation product of this gene shares sequence homology with reverse transcriptase which is important in the synthesis of a cDNA chain from an RNA molecule, and is a method whereby the infecting RNA chains of retroviruses are transcribed into their DNA complements. One embodiment for this gene is the polypeptide fragment comprising the following amino acid sequence:  
 MXXXNSHITIFTLNVNGLNAPNERHRLANWIQSQDQVCCIQETHLTGRDTHRL  
 KIKGWRKIYQANGKQKK (SEQ ID NO:647). An additional embodiment is the polynucleotide fragments comprising polynucleotides encoding these polypeptide fragments (See Accession No. gil2072964).

This gene is expressed primarily in skin and to a lesser extent in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer, hematopoietic disorders; inflammation; disorders of immune surveillance. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the epidermis and/or hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and

wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 5       The tissue distribution and homology to reverse transcriptase indicates that polynucleotides and polypeptides corresponding to this gene are useful for cancer therapy. Expression in the skin also indicates that this gene is useful in wound healing and fibrosis. Expression by neutrophils also indicates that this gene product plays a role in inflammation and the control of immune surveillance (i.e. recognition of viral
- 10       pathogens). Reverse transcriptase family members are also useful in the detection and treatment of AIDS.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 119**

- 15       The translation product of this gene shares sequence homology with reverse transcriptase which is important in the synthesis of a cDNA copy of an RNA molecule, and is a method whereby a retrovirus reverse-transcribes its genome into an inheritable DNA copy.

      This gene is expressed primarily in the frontal cortex of brain.

- 20       Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer and neurodegenerative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
- 25       of the above tissues or cells, particularly of the CNS and peripheral nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
- 30       the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

      The tissue distribution and homology to reverse transcriptase suggest that this is useful in the treatment of cancer and AIDS. The expression in brain indicates that it plays a role in neurodegenerative disorders and in neural degeneration.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 120**

One embodiment of this gene has homology to a hypothetical protein in *Schizosaccharomyces pombe* (See Accession No. 2281980). Another embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:  
5 IYHLHSWIFFHFKRAFCMCFITMKVIAHCSKLRKCXNAQISVFCTTLTASYPT  
(SEQ ID NO:651). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments. This gene maps to chromosome 18, and therefore, may be used as a marker in linkage analysis for chromosome 18.

10 This gene is expressed primarily in adult hypothalamus and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative disorders; endocrine function; and vertigo. Similarly,  
15 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, CNS and peripheral nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded  
20 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides  
25 corresponding to this gene are useful for the treatment and diagnosis of neurodegenerative disorders; diagnosis of tumors of a brain or neuronal origin; treatments involving hormonal control of the entire body and of homeostasis, behavioral disorders, such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and  
30 panic disorder. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 121**

35 The translation product of this gene shares sequence homology with the human IRLB protein which is thought to be important in binding to a c-myc promoter element and thus regulating its transcription (See Accession No. gi33969). This gene maps to

chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in brain and breast and to a lesser extent in a variety of hematopoietic tissues and cells.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer of the brain and breast; lymphoproliferative disorders; neurodegenerative diseases. Similarly, polypeptides and antibodies directed to these  
10 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the CNS, breast, and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial  
15 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of cancer of the  
20 brain, breast, and hematopoietic system. In addition, it may be useful for the treatment of neurodegenerative disorders, as well as disorders of the hematopoietic system, including defects in immune competency and inflammation. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and immunotherapy targets for the above listed tumors and tissues.

25

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 122**

The translation product of this gene shares sequence homology with an ATP synthase, a key component of the proton channel that is thought to be important in the translocation of protons across the membrane.

30 This gene is expressed primarily in T cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, T cell lymphoma. Similarly, polypeptides and antibodies directed to these  
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or

lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ATP synthase indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of defects in proton transport, homeostasis, and metabolism, as well as the diagnosis and treatment of lymphoma. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 123**

This gene maps to chromosome 15, and therefore, may be used as a marker in linkage analysis for chromosome 15.

This gene is expressed primarily in a variety of fetal tissues, including fetal liver, lung, and spleen, and to a lesser extent in a variety of blood cells, including eosinophils and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer (abnormal cell proliferation); T cell lymphomas; and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetus and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of conditions involving cell proliferation. Expression of this gene in fetal tissues, as well as in a variety of blood cell lineages indicates that it may play a role in either cellular proliferation; apoptosis; or cell survival. Thus it may be useful in the management and

treatment of a variety of cancers and malignancies. In addition, its expression in blood cells suggest that it may play additional roles in hematopoietic disorders and conditions, and could be useful in treating diseases involving autoimmunity, immune modulation, immune surveillance, and inflammation..

5

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 124**

This gene is expressed primarily in placenta and to a lesser extent in pineal gland and rhabdomyosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as  
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental, endocrine, and female reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For  
15 a number of disorders of the above tissues or cells, particularly of the [insert system where a related disease state is likely, e.g., immune], expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
20 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 357 as residues: Leu-69 to Val-76.

The tissue distribution indicates that polynucleotides and polypeptides  
25 corresponding to this gene are useful for diagnosis and treatment of disorders in development. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and immunotherapy targets for the above listed tumors and tissues.

#### **30 FEATURES OF PROTEIN ENCODED BY GENE NO: 125**

This gene is expressed primarily in benign prostatic hyperplasia.

Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of benign prostatic hyperplasia. Similarly,  
35 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive

system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of benign prostatic hyperplasia. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and immunotherapy targets for the above listed tumors and tissues.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 126**

This gene is expressed primarily in apoptotic T-cells and to a lesser extent in suppressor T cells and ulcerative colitis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases involving premature apoptosis, and immunological and gastrointestinal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of disorders involving inappropriate levels of apoptosis, especially in immune cell lineages. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases (such as AIDS), and leukemia.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 127**

This gene is expressed primarily in Raji cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and T cell autoimmune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 360 as residues: Asp-23 to Gly-29.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammation and T cell autoimmune disorders. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases (such as AIDS), and leukemia.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 128**

The translation product of this gene shares sequence homology with an *C. elegans* coding region C47D12.2 of unknown function (See Accession No. gnl|PIDle348986). One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence: EDDGFNRSIHEVILKNITWY SERVLTEISLGSLLLLVVIRTIQYNMTRTRDKYLHTNCLAALANMSAQFRSLHQY AAQRIISLFSLLSKKHNVLEQATQSLRGSLSNDVPLPDYAQDLNVIEEVIRMM LEIINSLTNSLHHNPNLVALLYKRDLFEQFRTHPSFQDIMQNIDLVISFFSSRLL QAGS (SEQ ID NO:657); EDDGFNRSIHEVILKNITWYSERVLTEISLGSLLLLVV (SEQ ID NO:658); RTIQYNMTRTRDKYLHTNCLAALANMSAQFRSLHQYAAQ RIISLFSLLSKKHNVLEQATQSLRGSLSNDVPLPDY AQD (SEQ ID NO:661); SCLTNSLHHNPNLVALLYKRDLFEQFRTHPSFQD IMQNIDLVISFFSSRLLQAGS (SEQ ID NO:660). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments. This gene maps to



chromosome 18, and therefore, may be used as a marker in linkage analysis for chromosome 18.

This gene is expressed primarily in smooth muscle and to a lesser extent in fetal liver.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, atherosclerosis and other cardiovascular and hepatic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing  
10 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample  
15 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of circulatory system  
20 disorders such as atherosclerosis, hypertension, and thrombosis. In addition, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). In addition the  
25 expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various wound-healing models and/or tissue trauma.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 129

30 The translation product of this gene shares sequence homology with a ribosomal protein which is thought to be important in cellular metabolism, in addition to the *C.elegans* protein F40F11.1 which does not have a known function at the current time (See Accession No. gnl|PID|e244552). Preferred polypeptide fragments comprise the following amino acid sequence:

35 MADIQTERAYQKQPTIFQNKKRVLGETGKEKLPRVTNKNIGLGFKDT  
PRLLRGTYIDKKCPFTGNVSIRGRILSGVVTQDEDAEDHCHPPRLSALHPQVQ  
PLREAPQEHVCTPVPL LQGRPDR (SEQ ID NO:662); MKMQRTTIVIRRDYLH

YIRKYNRFEKRHKNSVHLSPCFRDVGIGDIVTVGECRPLSKTVRFNVLKVTK  
 AAGTKKQFQKF (SEQ ID NO:663); MADIQTERAYQKQPTIFQNKKRVLLGET  
 GK (SEQ ID NO:664); HCHPPRLSALHPQVQPLREAPQEHVCTPVPL LQGRPDR  
 (SEQ ID NO:666); NIGLGFKDTPRRLLRGTIDKKCPFTGNVSIRGRILSGVVTO  
 5 (SEQ ID NO:669); MKMQRTVIRRDYLHYIRKYNRFEKRHKNSVHLS (SEQ  
 ID NO:667); CFRDVGIGDIVTVGECRPLSKTVRFNVLKVTKAAGTKKQFQKF  
 (SEQ ID NO:668). Also preferred are polynucleotide fragments encoding these  
 polypeptide fragments.

10 This gene is expressed primarily in Wilm's tumor and to a lesser extent in  
 thymus and stromal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as  
 reagents for differential identification of the tissue(s) or cell type(s) present in a  
 biological sample and for diagnosis of diseases and conditions, which include, but are  
 not limited to, diseases affecting RNA translation. Similarly, polypeptides and  
 15 antibodies directed to these polypeptides are useful in providing immunological probes  
 for differential identification of the tissue(s) or cell type(s). For a number of disorders  
 of the above tissues or cells, particularly of the Wilm's tumors, expression of this gene  
 at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,  
 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial  
 20 fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
 such a disorder, relative to the standard gene expression level, i.e., the expression level  
 in healthy tissue or bodily fluid from an individual not having the disorder. Preferred  
 epitopes include those comprising a sequence shown in SEQ ID NO: 362 as residues:  
 Thr-11 to Asp-20.

25 The tissue distribution and homology to a ribosomal protein indicates that  
 polynucleotides and polypeptides corresponding to this gene are useful for diseases  
 affecting RNA translation.

### FEATURES OF PROTEIN ENCODED BY GENE NO: 130

30 The translation product of this gene shares sequence homology with a yeast  
 DNA helicase which is thought to be important in global transcriptional regulation (See  
 Accession No. gnllPIDe243594). One embodiment for this gene is the polypeptide  
 fragments comprising the following amino acid sequence: IFYDSDWNPTVDQQA  
 MDRAHRLGQTKQVTVYRLICKGTIEERILQRAKEKSEIQRMVISG (SEQ ID  
 35 NO:670); TRMIDLLEEYMVYRKHTYXRLDGSSKISERRDMVADFQNRNDI  
 FVLLSTRAGGLGINLTAXDTVHF (SEQ ID NO:671); TRMIDLLEEYMVYRK  
 HTYXRLDGSSKISERRDM (SEQ ID NO:674); RRDMVADFQNRNDIFVLL

STRAGGLGINLTAXDTVHF (SEQ ID NO:675) , IFYDSDWNPTVDQQAMD  
RAHRLGQTKQVTYRLICKG (SEQ ID NO:676); RLICKGTIEERILQRAK  
EKSEIQRMVISG (SEQ ID NO:678). An additional embodiment is the polynucleotide  
fragments encoding these polypeptide fragments.

5        This gene is expressed primarily in amygdala.

         Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, diseases and disorders of the brain. Similarly, polypeptides and  
10       antibodies directed to these polypeptides are useful in providing immunological probes  
for differential identification of the tissue(s) or cell type(s). For a number of disorders  
of the above tissues or cells, particularly of the central nervous system, expression of  
this gene at significantly higher or lower levels may be routinely detected in certain  
tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,  
15       urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an  
individual having such a disorder, relative to the standard gene expression level, i.e.,  
the expression level in healthy tissue or bodily fluid from an individual not having the  
disorder.

         The tissue distribution and homology to a DNA helicase indicates that  
20       polynucleotides and polypeptides corresponding to this gene are useful for diseases  
affecting RNA transcription, particularly developmental disorders and healing wounds  
since the later are though to approximate developmental transcriptional regulation.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 131**

25       This gene is expressed primarily in prostate and to a lesser extent in amygdala  
and pancreatic tumors.

         Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
30       not limited to, prostate enlargement and gastrointestinal disorders, particularly of the  
pancreas and gall bladder. Similarly, polypeptides and antibodies directed to these  
polypeptides are useful in providing immunological probes for differential identification  
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,  
particularly of the reproductive system, expression of this gene at significantly higher or  
35       lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded  
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or  
another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of prostate diseases, including benign prostatic hyperplasia and prostate cancer. In addition, the tissue distribution in tumors of the pancreas indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tissues where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 132**

This gene is expressed primarily in adult lung and to a lesser extent in hypothalamus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, pulmonary diseases and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the pulmonary and respiratory systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of pulmonary and respiratory disorders such as emphysema, pneumonia, and pulmonary edema and emboli. In addition, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental

disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 133**

5        This gene is expressed primarily in human liver.

         Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cirrhosis of the liver and other hepatic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

         The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of liver disorders such as cirrhosis, jaundice, and Hepatitis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

#### **25        FEATURES OF PROTEIN ENCODED BY GENE NO: 134**

         This gene is expressed primarily in fetal kidney and to a lesser extent in fetal liver and spleen.

         Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, development and regeneration of liver and kidney and immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive and excretory systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 367 as residues: Pro-70 to Arg-77, Tyr-102 to Thr-107.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the kidney and liver, such as cirrhosis, kidney failure, kidney stones, and liver failure, hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells. In addition the expression in fetus would suggest a useful role for the protein product in developmental abnormalities, fetal deficiencies, pre-natal disorders and various wound-healing models and/or tissue trauma.

#### 15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 135**

This gene is expressed primarily in brain, bone marrow, and to a lesser extent in placenta, T cell, testis and neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative and immunological diseases and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 368 as residues: Met-1 to His-6.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, the gene or gene product may also

play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, or sexually-linked disorders.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 136

5 Translation product of this gene is homologous to the human WD repeat protein HAN11. Preferred polypeptide fragments comprise the following amino acid sequence:

MSLHGKRKEIYKYEAPWTVYAMNWSVRPDKRFRLLALGSFVEEYNNKVQLVG  
 LDEESSEFICRNTFDHPYPTTKLMWIPDTKGVYPDLLATSGDYLRVWRVGETET  
 10 RLECLLNNNKNSDFCAPLTSFDWNEVDPYLLGTSSIDTTCTIWGLETGQVLGRV  
 NLVSGHVKTQLIAHDKEVYDIAFSRAGGGGRDMFASVGADGSVRMFDLRHLEH  
 STIYEDPQHHPLLRLCWNKQDPNYLATMAMDGMEVVILDVRVPAHLXPGTTIE  
 HVSMALLGPHIHPATSALQRM TTRLSSGTSSKCPEPLRTL SWPTQLXGEINN VQ  
 WASTQPELSPSATTAWRYSECSVGGAVPTRQGLLYFLPLPHPQS (SEQ ID  
 15 NO:679); MSLHGKRKEIYKYEAPWTVYAMNWSVRPDKRFRLLALGSFV  
 EEYNNKVQLVGLDEESSEFICRNTFDHPYPTTKLMWIPDTKGVYPDLLATSGDY  
 LRVWRVGETETRLECLLNNNKNSDFCAPLTSFDWNEVDPYLL (SEQ ID  
 NO:680); SFDWNEVDPYLLGTSSIDTTCTIWGLETGQVLGRVNLVSGHVK  
 TQLIAHDKEVYDIAFSRAGGGGRDMFASVGADGSVRMFDLRHLEHSTIYEDPQH  
 20 HPLLRLCWNKQDPNYLATMAMDGMEVVILDVRVPAHLXPGTTI (SEQ ID  
 NO:681); VGADGSVRMFDLRHLEHSTIYEDPQHHPLLRLCWNKQDPNYLA  
 TMAMDGMEVVILDVRVPAHLXPGTTIEHVSMALLGPHIHPATSALQRM TTRL  
 SGTSSKCPEPLRTL SWPTQLXGEINN VQWASTQPELSPSATTAWRYSECSV  
 GAVPTRQGLLYFLPLPHPQS (SEQ ID NO:682). Also preferred are polynucleotide  
 25 fragments encoding these polypeptide fragments.

This gene is expressed primarily in placenta, embryo, T cell and fetal lung and to a lesser extent in endothelial, tonsil and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
 30 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological and developmental diseases in addition to cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the  
 35 immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or

cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 369 as residues: Gly-19 to Gln-28, Pro-36 to Phe-42.

5       The tissue distribution in tumors of colon, ovary, and breast origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above  
10 listed tumors and tissues. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

#### 15   **FEATURES OF PROTEIN ENCODED BY GENE NO: 137**

This gene is expressed primarily in TNF and INF induced epithelial cells, T cells and kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
20 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammatory conditions particularly inflammatory reactions in the kidney. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of renal  
25 system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an  
30 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 370 as residues: Thr-67 to Gly-72, Gln-132 to Ala-145, Arg-150 to Pro-157.

The tissue distribution indicates that the protein products of this gene are useful for treating the damage caused by inflammation of the kidney.



**FEATURES OF PROTEIN ENCODED BY GENE NO: 138**

This gene maps to chromosome 1, and therefore, may be used as a marker in linkage analysis for chromosome 1 (See Accession No. D63485).

5 This gene is expressed primarily in breast cancer and colon cancer and to a lesser extent in thymus and fetal spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers, especially of the breast and colon tissues. Similarly,  
10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,  
15 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tumors of colon and breast origins indicates that  
20 polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 139**

This gene maps to chromosome 17, and therefore, can be used as a marker for linkage analysis from chromosome 17.

This gene is expressed primarily in CD34 positive cells, and to lesser extent in activated T-cells and neutrophils.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunologically related diseases and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing  
35 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and hematopoietic system, expression of this gene at significantly higher or lower levels

may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in CD34, T-cell and neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of hematopoietic disorders and immunologically related diseases, such as anemia, leukemia, inflammation, infection, allergy, immunodeficiency disorders, arthritis, asthma, immune deficiency diseases such as AIDS.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 140

This gene was recently cloned by another group, who called the gene KIAA0313 gene. (See Accession No. d1021609.) Preferred polypeptide fragments comprise the amino acid sequence:

LYATATVISSPSTEXLSQDQGDRA SLDAADSGRGSWTSCSSGSHDNIQTIQ  
HQRSWETLPFGHTHFDYSGDPAGLWASSSHMDQIMFSDHSTKYNRQNSRES  
LEQAQSRASWASSTGYWGEDSEGDGTIKRRGGKDV SIEAESSSLTSVTTEETK  
PVPMPAHIAVASSTTKGLIARKEGRYREPPPTPPGYIGIPITDFPEGHSH PARKP  
PDYNVALQSRMRVARSSDTAGPSSVQQPHGHPTSSRPVNKPQWHKXNESDPR  
LAPYQSQGFSTEEDEDEQVSAV (SEQ ID NO:683); HMDQIMFSDHSTKYNRQ  
NSRESLEQAQSRASWASSTGYWGE (SEQ ID NO:684); SVTTEETKPVPMP  
AHIAVASSTTKGLIARKEGRYREPPPTPPGYIGIPITD (SEQ ID NO:685); and  
VALQSRMRVARSSDTAGPSSVQQPHGHPTSSRPVNKPQW

HKXNESDPR LAPYQSQGF (SEQ ID NO:686). Also preferred are polynucleotide fragments encoding these polypeptide fragments. This gene maps to chromosome 4, and therefore, may be used as a marker in linkage analysis for chromosome 4 (See Accession No. AB002311 ).

This gene is expressed primarily in ovarian cancer, tumors of the Testis, brain, and colon.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, ovarian, testicle, brain and colon cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male and female reproductive systems,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,  
5 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tumors of colon, ovary, testis, and brain origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where  
10 expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 141**

15 This gene is expressed primarily in spleen and colon cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, colon cancer and immunological disorders. Similarly, polypeptides and  
20 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the gastrointestinal tract and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g.,  
25 serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tumors of colon, ovary, and breast origins indicates  
30 that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues.

35

**FEATURES OF PROTEIN ENCODED BY GENE NO: 142**

Translation product is homologous to T cell translocation protein, a putative zinc finger factor (See Accession No. 340454), as well as to the G-protein coupled receptor TM5 consensus polypeptide (See Accession No. R50734). Preferred polypeptide

5 fragments comprise the following amino acid sequence:

CLLFVVFVSLGMRCLEFWTIVYNVLYLKHKCNVLLCYHLCSI (SEQ ID NO:687);

ACSKLIPAFEMVMRAKDNVYHLDCFACQLCNQRXCVDKFFLKNNXXLCQT

DYEEGLMKEGYAPXVR (SEQ ID NO:688). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

10 This gene is expressed primarily in fetal brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological disorders including brain cancer. Similarly, polypeptides

15 and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Central Nervous System, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,

20 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides

25 corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with

30 the developing embryo.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 143**

Translation product for this gene has significant homology to the Fas ligand, which is a cysteine-rich type II transmembrane protein/tumor necrosis factor receptor

35 homolog. Mutations within this protein have been shown to result in generalized lymphoproliferative disease leading to the development of lymphadenopathy and autoimmune disease (See Medline Article No. 94185175). Preferred polypeptide

fragments comprise the following amino acid sequence:

SALSEPGAPDRRRPCPESVPRRPDDEQWPPPTALCLDVAPLPPSS (SEQ ID NO:689). Also preferred are polynucleotide fragments encoding these polypeptide fragments (See Accession No. 473565).

5 This gene is expressed primarily in osteoblasts, lung, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoblast-related, pulmonary, neurological, and immunological  
10 diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded  
15 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 376 as residues: Trp-33 to Thr-40, Lys-  
20 45 to Ile-63.

The tissue distribution in osteoblasts, lung, and brain combined with its homology to the Fas ligand indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as,  
25 antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. Because the Fas ligand gene is known to be expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including asthma, immune deficiency diseases such as AIDS  
30 and leukemia, and various autoimmune disorders including lupus and arthritis.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 144

This gene shares sequence homology with a 21.5 KD transmembrane protein in the SEC15-SAP4 intergenic region of yeast. (See Accession No. 1723971.) Preferred  
35 polypeptide fragments comprise the amino acid sequence:

AHASESGERWWACCGVRFGRLSIEAIGRSCCHDGPGLVANRGRFRFKWAIEL  
SGPGGGSRGRSDRSGQGDSLYPVGYLDKQVPDTSVQETDRILVEKRCWDIAL

GPLKQIPMNLFIMYMAGNTISIFPTMMVCMMAWRPIQALMAISATFKMLESSSQ  
KFLQGLVYLIGNLMGLALAVYKCQSMGLLPHTHASDWLAFIEPPERMEFSGG  
GLLL (SEQ ID NO:691); PVGYLDKQVPDTSVQETDRILVEKRCWDIALGPLKQ  
IPMNLFI (SEQ ID NO:693); and ATFKMLESSSQKFLQGLVYLIGNLMGLALAV  
5 YKCQSMGLLPHTHASD (SEQ ID NO:692). Also preferred are polynucleotide  
fragments encoding these polypeptide fragments.

This gene is expressed primarily in osteoclastoma, hemangiopericytoma, liver,  
lung.

Therefore, polynucleotides and polypeptides of the invention are useful as  
10 reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, osteoclastoma, hemangiopericytoma, liver and lung tumors. Similarly,  
polypeptides and antibodies directed to these polypeptides are useful in providing  
immunological probes for differential identification of the above tissue(s) or cell  
15 type(s). For a number of disorders of the above tissues or cells, particularly of the lung  
and liver systems, expression of this gene at significantly higher or lower levels may be  
routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily  
fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or  
cell sample taken from an individual having such a disorder, relative to the standard  
20 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an  
individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides  
corresponding to this gene are useful for diagnosing osteoclastoma,  
hemangiopericytoma, liver and lung tumors.

25

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 145**

Translation product of this gene shares homology with the glucagon-69 gene  
which may indicate this gene plays a role in regulating metabolism. (See Accession No.  
A60318) One embodiment for this gene is the polypeptide fragments comprising the  
30 following amino acid sequence:  
PTTKLDIMEKKKHIQIRFPSFYHKLVDSEGRMRKRETRREDSDTKHNL (SEQ ID  
NO:694). An additional embodiment is the polynucleotide fragments encoding these  
polypeptide fragments.

This gene is expressed primarily in brain, kidney, colon, and testis.

35 Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, brain, kidney, colon, and testicular cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, neurological, circulatory, and gastrointestinal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in tumors of brain, kidney, colon, and testis origins, indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioral disorders such as Alzheimer's Disease, Parkinson's Disease, Huntingtons Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder and panic disorder. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system.

## 25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 146**

The translation product of this gene shares sequence homology with goliath protein which is thought to be important in the regulation of gene expression during development. Protein may serve as a transcription factor. One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:

30 TEHIIAVMITELRGKDILSYLEKNISVQMTIAVGTRMPPKNFSRGSLVFVSISFIV  
LMISSAWLIFYFIQKIRYTNARDRNQRRLLGDAAKKAISKLTTRTVKKGDKETD  
PDFDHCAVCIESYKQNDVVRILPCKHVFHKSCVDPWLSEHCTCPMCKLNILKA  
LGIV (SEQ ID NO:695); TEHIIAVMITELRGKDILSYLEKNISVQMTIAVGTRMP  
PKNFSRGSLVFVSISFIVLM IISSAWLIFYF (SEQ ID NO:697); SISFIVLMISSA  
35 WLIFYFIQKIRYTNARDRNQRRLLGDAAKKAISKLTTRTVKKGDKE (SEQ ID  
NO:698); VKKGDKETDPDFDHCAVCIESYKQNDVVRILPCKHVFHKSCVDP

WLSEHCTCPMCKLNILKALGIV (SEQ ID NO:699). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments (See Accession No. 157535). Moreover, another embodiment is the polynucleotide fragments encoding these polypeptide fragments:

- 5 MTHPGTEHIIA VMITELRGKDILSYLEKNISVQMTIAVGTRMPPKNFSRGS  
LVFVSISFIVLMISSAWLIFYFIQKIRYTNARDRNQRR LGDAAKKAISKLTTRTV  
KKGDKETDPDFDHCAVCIESYKQNDVVRILPCKHV FHKSCVDPWLSEHCTCP  
MCKLNILKALGIVPNLPCTDNVAFD MERLTRTQAVNRRSALGDLAGDNSLGL  
PLRTSGISPLPQDGELTPRTGEINIAVTKEWFIIASFGLLSALTLCYMIIRATASLN  
10 ANEVEWF (SEQ ID NO:696); MTHPGTEHIIA VMITELRGKDILSYLEKNISVQMTIAVGTRMPPKNFSRGS  
LVFVSISFIVLMISSAWLIFYFIQKIRYTNARDRNQRR LGDAAKKAISKLTTRTVKKGDKE  
TDPDFDHCAVCIESYKQNDVVRILPCKHV FHKSCVDPWLSEHCTCPMCKLNIL  
KALGIVPNLPC (SEQ ID NO:701); TQAVNRRSALGDLAGDNSLGL EPLRTSGI  
15 SPLPQDGELTPRTGEINIAVTKEWFIIASFGLLSALTLCYMIIRATASLN ANEVEWF  
(SEQ ID NO:702); PLHGVADHLGCDPQTRFFVPPNIKQWIAL LQRGNCTF  
KEKISR AAFHNAVAVVIYNNKSKEEPVTMTHPGTEHIIA VMITELRGKDILSYLE  
KNISVQMTIAVGTRMPPKNFSRGS LVFVSISFIVLMISSAWLIFYFIQKIRYTN  
RDRNQRR LGDAAKKAISKLTTRTVKKGDKETDPDFDHCAVCIESYKQNDVVR  
20 LPCKHV FHKSCVDPWLSEHCTCPMCKLNILKALGIVPNLPCTDNVAFD MERLTRTQAVNRRSALGDL  
AGDNSLGL EPLRTSGISPLPQDGELTPRTGEINIAVTKEWFIIASFGLLSALTLCYMIIRATASLN  
ANEVEWF (SEQ ID NO:703); and  
HGVADHLGCDPQTRFFVPPNIKQWIAL LQRGNCTFKEKISR AAFHNAVAVVIY  
NNKSKEE (SEQ ID NO:704). An additional embodiment is the polynucleotide  
25 fragments encoding these polypeptide fragments. When tested against Jurkat cell lines,  
supernatants removed from cells containing this gene activated the GAS pathway.  
Thus, it is likely that this gene activates immune cells through the JAKS/STAT signal  
transduction pathway.

- 30 This gene is expressed primarily in macrophage, breast, kidney and to a lesser  
extent in synovium, hypothalamus and rhabdomyosarcoma.

- Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, schizophrenia and cancer. Similarly, polypeptides and antibodies directed  
35 to these polypeptides are useful in providing immunological probes for differential  
identification of the tissue(s) or cell type(s). For a number of disorders of the above  
tissues or cells, particularly of the immune and neural system, expression of this gene at



significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to zinc finger protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of schizophrenia, kidney disease and other cancers. The tissue distribution in macrophage, breast, and kidney origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of tumors within these tissues, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 147

The translation product of this gene shares sequence homology with HNP36 protein, an equilibrative nucleoside transporter, which is thought to be important in gene transcription as well as serving as an important component of the nucleoside transport apparatus (See Accession No. 1845345). One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:

MSGQGLAGFFASVAMICAIASGSELSESAFGYFITACAVIILTIICYLGLPRLEFYR  
 YYQQLKLEGPGEQETKLDLISKGEEPRAGKEESGVSVSNSQPTNESHSHKAILK  
 NISVLAFSVCFI TITIGMFPAVTVEVKSSIAGSSTWERYFIPVSCFLT FNIFDWLG  
 RSLTAVFMWPGKDSRWLPSWXLARLVFVPLLLCNIKPRRYLTVVFEHDAWFI  
 FFMAAFASFNGYLASLCMCFGPKKVKPAEAETAEPSPSSCVVWHWGLFS  
 PSCSGQLCDKGWTEGLPASLPVCLLPARGDPEWGGFFF (SEQ ID  
 NO:705); MSGQGLAGFFASVAMICAIASGSELSESAFGYFITACAVIILTIIC  
 YLGLPRLEFYRYYQQLKLE GPGEQETKLDLISKGEEPRAGKEESGVSVSNSQ  
 PTNESHSHI (SEQ ID NO:706); SGVSVSNSQPTNESHSHKAILKNISVLAFSVCFI  
 TITIGMFPAVTVEVKSSIAGSSTWERYFIPVSCFLT FNIFDWLGRS (SEQ ID  
 NO:707), TIGMFPAVTVEVKSSIAGSSTWERYFIPVSCFLT FNIFDWLGRSLTAVF  
 MWPGKDSRWLPSWXLARLVFVPLLLCNIK PRRYLTVVFEHDA (SEQ ID  
 NO:708); FGPKKVKPAEAETAEPSPSSCVVWHWGLFSPSCSGQLCDK

GWTEGLPASLPVCLLPSPARGDPEWSSGGFFF (SEQ ID NO:709). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in eosinophils and aortic endothelium and to a lesser extent in umbilical vein endothelial cell and thymus.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential  
10 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
15 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to HNP36 protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of blood neoplasias and other hematopoietic disease.

20

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 148**

This gene is expressed primarily in breast cancer cell lines, thymus stromal cells, and ovary.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, endocrine and female reproductive system diseases including breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell  
30 type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard  
35 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of endocrine disorders. In addition, the tissue distribution in tumors of thymus, ovary, and breast origins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of these tumors, in addition to other tumors where expression has been indicated. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tumors and tissues

#### 10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 149**

Translation product of this gene has homology to pmt1 and pmt 2, two conserved schizosaccharomyces pombe genes. One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:

15 DDDGFEIVPIEDPAKHRILDPEGLALGAVIASSKKAKRDLIDNSFNRYTFNEDEG  
ELPEWVFVQEEKQHRIRQLPVGKKEVEHYRKRWREINARPIXXXXXXXXXXXXX  
XXXXXXXXLEQTRKKAEEVVNTVDIXRTRES (SEQ ID NO:710);  
DDGFEIVPIEDPAKHRILDPEGLALGAVIASSKKAKRDLIDNSFNRYTF (SEQ  
ID NO:711); KRWREINARPIXXXXXXXXXXXXXXXXXXXXLEQTRKKAEE  
AVVNTVDIXRTRES (SEQ ID NO:712). An additional embodiment is the  
20 polynucleotide fragments encoding these polypeptide fragments (See Accession No.  
e1216734).

This gene is expressed primarily in retina and ovary and to a lesser extent in breast cancer cell, epididymus and osteosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as  
25 reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, neuronal growth disorders, cancer and reproductive system disorders.  
Similarly, polypeptides and antibodies directed to these polypeptides are useful in  
providing immunological probes for differential identification of the tissue(s) or cell  
30 type(s). For a number of disorders of the above tissues or cells, particularly of the  
neural and reproductive system, expression of this gene at significantly higher or lower  
levels may be routinely detected in certain tissues (e.g., cancerous and wounded  
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or  
another tissue or cell sample taken from an individual having such a disorder, relative to  
35 the standard gene expression level, i.e., the expression level in healthy tissue or bodily  
fluid from an individual not having the disorder. Preferred epitopes include those  
comprising a sequence shown in SEQ ID NO: 382 as residues: Met-1 to Gly-7.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis or treatment of reproductive system disease and cancers.

## 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 150

One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:

MIKDKGRARTALTSSQPAHLCPENPLLHLKAAVKEKKRNKKKKKTIGSPKRIQS  
 PLNNKLLNSPAKTLPGACGSPQKLIDGFLKHEGPPAEKPLEELSASTSGVPGLS  
 10 SLQSDPAGCVRPPAPNLAGAVEFNDVKTLLEWITTISDPM EEDILQVVKYCTD  
 LIEEKDLEKLDLVIKYMKRLMQQSVE SVWNMAFD FILDNVQVVLQQTYGSTLK  
 VT (SEQ ID NO:713); MIKDKGRARTALTSSQPAHLCPENPLLHLKAAVKE  
 KKRNNKKKKKTIGSPKRIQ (SEQ ID NO:714); KRIQSPLNNKLLNSPAKT  
 LPGACGSPQKLIDGFLKHEGPPAEKPLEELSASTSGVPGLSSLQSDPAGCVRPP  
 15 APNLAGAVEFNDVKTLLEWITTISDPM (SEQ ID NO:715);  
 TISDPM EEDILQVVKYCTDLIEEKDLEKLDLVIKYMKRLMQQSVE  
 SVWNMAFD FILDNVQVVLQQTYGSTLKVT (SEQ ID NO:716). An additional  
 embodiment is the polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in 12 week embryo and to a lesser extent in  
 20 hemangiopericytoma and frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as  
 reagents for differential identification of the tissue(s) or cell type(s) present in a  
 biological sample and for diagnosis of diseases and conditions, which include, but are  
 not limited to, growth disorders and hemangiopericytoma. Similarly, polypeptides and  
 25 antibodies directed to these polypeptides are useful in providing immunological probes  
 for differential identification of the tissue(s) or cell type(s). For a number of disorders  
 of the above tissues or cells, particularly of the circular and neural system, expression  
 of this gene at significantly higher or lower levels may be routinely detected in certain  
 tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,  
 30 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an  
 individual having such a disorder, relative to the standard gene expression level, i.e.,  
 the expression level in healthy tissue or bodily fluid from an individual not having the  
 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID  
 NO: 383 as residues: Leu-4 to Lys-11.

35 The tissue distribution indicates that polynucleotides and polypeptides  
 corresponding to this gene are useful for the treatment of growth disorders,  
 hemangiopericytoma and other soft tissue tumors.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 151**

The translation product of this gene has been found to have homology to a human DNA mismatch repair protein PMS3. Preferred polypeptide fragments comprise the following amino acid sequence: FCHDCKFPEASPAMNCEP (SEQ ID NO:717). Also preferred are polynucleotide fragments encoding these polypeptide fragments (See Accession No. R95250).

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, lymphoma, immunodeficiency diseases, and cancers resulting from genetic instability. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 384 as residues: Met-1 to Lys-6.

The tissue distribution in neutrophils and the sequence homology indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of Hodgkin's lymphoma, since the elevated expression and secretion by the tumor mass may be indicative of tumors of this type. Additionally the gene product may be used as a target in the immunotherapy of the cancer. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia. Furthermore, its homology to a known DNA repair protein would suggest gene may be useful in establishing cancer predisposition and prevention in gene therapy applications.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 152**

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, infectious diseases and lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of inflammation and infectious diseases.

#### 15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 153**

One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence:

MASSVPAGGHTRAGGIFLIGKLDLEASLFKSFQWLPFVLRKKC

NFFCWDSSAHSPLHPLSASCSAPACHASDTHLLYPSTRALCPSIFAWLVAPHS

20 VFRTNAPGPTPSSQSSPVFPVFPVSFMALIVCXLVCC (SEQ ID NO:720);

MASSVPAGGHTRAGGIFLIGKLDLEASLFKSFQWLPFVLRKKCNFFCWDSSAH

SLPLHPLSASCSAPACHA (SEQ ID NO:721);FAWL VAPHSVFRTNAPGPTPS

SQSSPVFPVFPVSFMALIVCXLVCC (SEQ ID NO:722). An additional embodiment is the polynucleotide fragments encoding these polypeptide fragments.

25 This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and infectious disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred

epitopes include those comprising a sequence shown in SEQ ID NO: 386 as residues: Ser-11 to Pro-17.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of infectious diseases and inflammation.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 154**

This gene is expressed in multiple tissues including ovary, uterus, adipose tissue, brain, and the liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, uterine, ovarian, brain, and liver cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the female reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnostic or therapeutic uses in the treatment of the female reproductive system, obesity, and liver disorders, particularly cancer in the above tissues.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 155**

This gene maps to chromosome 3, and therefore, may be used as a marker in linkage analysis for chromosome 3 (See Accession No. D87452).

This gene is expressed in multiple tissues including brain, aortic endothelial cells, smooth muscle, pituitary, testis, melanocytes, spleen, neutrophils, and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological disorders including immunodeficiencies, cancers of the brain and the female reproductive system, as well as cardiovascular disorders, such as

atherosclerosis and stroke. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and immune systems, expression of this gene at

5 significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution suggest that polynucleotides and polypeptides corresponding to this gene are useful in treatment/detection of disorders in the nervous system, including schizophrenia, neurodegeneration, neoplasia, brain cancer as well as cardiovascular and female reproductive disorders including cancer within the above tissues.

#### 15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 156**

The translation product of this gene shares sequence homology with the human gene encoding cytochrome b561 (See Accession No. P10897). Cytochrome b561 is a transmembrane electron transport protein that is specific to a subset of secretory vesicles

20 containing catecholamines and amidated peptides. This protein is thought to supply reducing equivalents to the intravesicular enzymes dopamine-beta-hydroxylase and alpha-peptide amidase. Preferred polypeptides of the invention comprise the amino acid sequence:

MAMEGYWRFLALLGSALLVGFLSVIFALVWVLHYREGLGWDGSALEFNWHP  
 25 VLMVTGFVFIQGLAIIVYRLPWTWKCSKLLMKSIHAGLNAVAAILAISVVAVFE  
 NHNVNNIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFLMPIHV  
 YSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPEGVFVNTLGLLLVFGALIF  
 WIVTRPQWKRPKEPNSTILHPNGGTEQGARGSMPAYSGNNMDKSDSEL  
 NSEVAARKRNALDEAGQRSTM (SEQ ID NO:724); as well as antigenic fragments

30 of at least 20 amino acids of this gene and/or biologically active fragments. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in anergic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

35 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune system and metabolism related diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological



probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product or RNA of this gene is useful for treatment or diagnosis of immune system and metabolic diseases or conditions including Tay-Sachs disease, phenylketonuria, galactosemia, various porphyrias, and Hurler's syndrome.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 157**

The translation product of this gene shares sequence homology with collagen which is important in mammalian development. This gene also shows sequence homology with bcl-2. (See Accession No. P80988.) Preferred polypeptide fragments comprise the amino acid sequence: PGRAGSPGSLQLPAEPGHPAGNLAPLTSRPQPLCRIPAVPG (SEQ ID NO:725). Also preferred are polynucleotide sequences encoding this polypeptide fragment.

This gene is expressed primarily in HL-60 tissue culture cells and to a lesser extent in liver, breast, and uterus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunological diseases, hereditary disorders involving the MHC class of immune molecules, as well as developmental disorders and reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and reproductive system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those

comprising a sequence shown in SEQ ID NO: 390 as residues: Ser-39 to Gly-46, Leu-49 to Ala-62.

The tissue distribution and homology to collagen indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hereditary MHC disorders and particularly autoimmune disorders including rheumatoid arthritis, lupus, scleroderma, and dermatomyositis, as well as many reproductive disorders, including cancer of the uterus, and breast tissues.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 158**

10 This gene is expressed primarily in the amygdala region of the brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, a variety of brain disorders, particularly those effecting mood and personality. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and/or diagnosis of a variety of brain disorders, particularly bipolar disorder, unipolar depression, and dementia.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 159**

30 This gene is expressed in a variety of tissues and cell types including brain, smooth muscle, kidney, salivary gland and T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers of a variety of organs including brain, smooth muscle, kidney, salivary gland and T-cells and cardiovascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the central nervous, urinary, salivary, digestive, and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in brain, smooth muscle, and T-cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of various neurological, and cardiovascular disorders, but not limited to cancer within the above tissues. Additionally the gene product may be used as a target in the immunotherapy of the cancer. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 160**

The translation product of this gene shares sequence homology with collagen which is thought to be important in cellular interactions, extracellular matrix formation, and has been found to be an identifying determinant in autoimmune disorders. Moreover, this gene shows sequence homology with the yeast protein, Sls1p, an endoplasmic reticulum component, involved in the protein translocation process in Yeast *Yarrowia lipolytica*. (See Accession No. 1052828; see also J. Biol. Chem. 271, 11668-11675 (1996).) With mouse, this same region shows sequence homology with the heavy chain of kinesin. (See Accession No. 2062607.) Recently, suppression of the heavy chain of kinesin was shown to inhibit insulin secretion from primary cultures of mouse beta-cells. (See Endocrinology 138 (5), 1979-1987 (1997).) Moreover, kinesin was found associated with drug resistance and cell immortalization. (See 468355.) Thus, it is likely that this gene also act as a genetic suppressor elements.

This gene is expressed primarily in the greater omentum and to a lesser extent in a variety of organs and cell types including gall bladder, stromal bone marrow cells, lymph node, liver, testes, pituitary, and thymus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the endocrine, gastrointestinal, and immunological systems, including autoimmune disorders and cancers in a variety of organs and cell types.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and gastrointestinal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 393 as residues: Asn-27 to Leu-47, Gln-81 to Lys-88, Asp-93 to Lys-102, Asn-107 to Leu-116, Met-129 to Glu-141, Glu-150 to Asp-157, Lys-176 to Glu-185, Glu-333 to Tyr-349, Cys-393 to Leu-403, Gln-423 to Gly-429.

The tissue distribution in within various endocrine and immunological tissues combined with the sequence homology to a conserved collagen motif indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis of various autoimmune disorders including, but not limited to, rheumatoid arthritis, lupus erythematosus, scleroderma, dermatomyositis. Because the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 161**

This gene has homology to the tissue inhibitor of metalloproteinase 2. Such inhibitors are vital to proper regulation of metalloproteins such as collagenases (See Accession No. P16368). In addition, this gene maps to chromosome 17, and therefore, may be used as a marker in linkage analysis for chromosome 17 (See Accession No. P16368).

This gene is expressed primarily in several types of cancer including osteoclastoma, chondrosarcoma, and rhabdomyosarcoma and to a lesser extent in several non-malignant tissues including synovium, amygdala, testes, placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, various types of cancer, particularly cancers of bone and cartilage, as well as various autoimmune disorders. Similarly, polypeptides and antibodies directed

to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the musculoskeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,  
5 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in various cancers and the sequence homology to a  
10 collagenase inhibitor indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

15

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 162**

This gene is homologous to the mitochondrial ATP6 gene and therefore is likely a homolog of this gene family (See Accession No. X76197).

This gene is expressed primarily in brain tissue.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, a variety of brain disorders, including Down's syndrome, depression, Schizophrenia, and epilepsy. Similarly, polypeptides and antibodies directed to these  
25 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal  
30 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in brain tissue indicates this gene is useful for diagnosis of various neurological disorders including, but not limited to, brain cancer.  
35 Additionally the gene product may be used as a target in the immunotherapy of cancer in the brain as well as for the diagnosis of metabolic disorders such as obesity Tay-Sachs disease, phenylketonuria and Hurler's Syndrome.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 163**

This gene is expressed primarily in placenta, neutrophils, and microvascular endothelial cells and to a lesser extent in multiple tissues including brain, prostate, spleen, thymus, and bone.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neutropenia and other diseases of the immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in placenta indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis various female reproductive disorders. Additionally the gene product may be used as a target in the immunotherapy of various cancers. Because the gene is expressed in some cells of lymphoid and endocrine origin, the natural gene product may be involved in immune functions and metabolism regulation, respectively. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 164**

This gene is expressed primarily in neutrophils, monocytes, bone marrow, and fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune system disorders including, but not limited to, autoimmune disorders such as lupus, and immunodeficiency disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
 5 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in various immune system tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis of various immunological disorders such as Hodgkin's lymphoma, arthritis,  
 10 asthma, immune deficiency diseases such as AIDS, and leukemia.

### FEATURES OF PROTEIN ENCODED BY GENE NO: 165

The translation product of this gene shares sequence homology with dystrophin which is thought to be defective in both Duchene and Becker Muscular Dystrophy.  
 15 Preferred polypeptide fragments comprise the following amino acid sequence:  
 MKLLGECSSSIDSVKRLEHKLKEEEESLPGFVNLHSTETQTAGVIDRWELLQAQ  
 ALSKELRMKQNLQKWQQFNSDLNSIWAWLGDTEEELEQLQRLELSTDIQTIELQ  
 IKKLKELQKAVDHRKAILLSINLCSPEFTQADSKESRDLQDRLXQMNGRWDRV  
 CSLLEEWRGLLQDALMQCQGFHEMSHGLLLMLENIDRRKNEIVPIDSNLDAEIL  
 20 QDHHKQLMQIKHELLESQLRVASLQDMSCQLLVNAEGTDCLEAKEKVHVIGNR  
 LKLLLKEVSRHIKELEKLLDVSSSQDLSSWSSADELDTSGSVSPXSGRSTPNR  
 QKTPRGKCSLSQPGPSVSSPHSRSTKGGSDSSLSEXPGRSGRGFLFRVLRAA  
 LPLQLLLLLLIGLACLVPMSEEDYSCALSNNFARSFHPMLRYTNGPPPL (SEQ ID  
 NO:726); MKLLGECSSSIDSVKRLEHKLKEEEESLPGFVNLHSTETQTAGVIDR  
 25 WELLQAQALSKELRMKQNLQKWQQFNSDLNSIWAWLGDTEEELEQLQRLELS  
 TDIQTIELQIK (SEQ ID NO:727); KLKELQKAVDHRKAILLSINLCSPEFTQADSK  
 ESRDLQDRLXQMNGRWDRVCSLLEEWRGLLQDALMQCQGFHEMSHGLLLML  
 ENIDRRKNEIVPIDSNLDAEILQDHHKQLMQIKHELLESQLRVASLQDMSCQL  
 (SEQ ID NO:728); QDMSCQLLVNAEGTDCLEAKEKVHVIGNRLKLLLKEVS  
 30 RHIKELEKLLDVSSSQDLSSWSSADELDTSGSVSPXSGRSTPNRQKTPRGKCS  
 LSQPGPSVSSPHS (SEQ ID NO:729); DSSLSEXPGRSGRGFLFRVLRAAL  
 PLQLLLLLLIGLACLVPMSEEDYSCALSNNFARSFHPMLRYTNGPPPL (SEQ ID  
 NO:730). Also preferred are polynucleotide fragments encoding these polypeptide  
 fragments. Furthermore, this gene maps to chromosome 6, and therefore, may be used  
 35 as a marker in linkage analysis for chromosome 6 (See Accession No. N62896).

This gene is expressed in numerous tissues including the heart, kidney, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, musculoskeletal disorders including Muscular Dystrophy and cardiovascular diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscle tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to dystrophin indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of Muscular Dystrophy and other muscle disorders.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 166**

This gene is expressed primarily in human cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the central nervous system, including Alzheimer's Disease, Parkinson's Disease, ALS, and mental illnesses. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 399 as residues: Pro-20 to Gly-26, Leu-37 to Pro-42, His-57 to Gly-63.

The tissue distribution indicates that the protein products of this gene are useful for treatment/diagnosis of diseases of the central nervous system and may protect or



enhance survival of neuronal cells by slowing progression of neurodegenerative diseases.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 167**

5 Preferred polypeptides encoded by this gene comprise the following amino acid sequence:

MKLLICGNYLAPSHSESSRRCCLLCFYPLCLEINFGMKVFLSMPFLVLFQ

SLIQED (SEQ ID NO:731). Polynucleotides encoding such polypeptides are also provided. This gene is believed to reside on chromosome 15. Therefore polynucleotides  
10 derived from this gene are useful in linkage analysis as chromosome 15 markers.

This gene is expressed primarily in human testes tumor and to a lesser extent in normal human testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
15 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the testes, particularly cancer, and other reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of  
20 the male reproductive tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily  
25 fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for treatment/diagnosis of testicular diseases including cancers.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 168**

30 This gene is expressed primarily in fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, conditions affecting hematopoietic development and metabolic diseases.  
35 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the

hepatic system, and fetal hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 401 as residues: His-7 to Trp-17, Leu-19 to Lys-27, Pro-33 to Gly-44, Lys-68 to Gly-74, Lys-85 to Cys-95.

The tissue distribution indicates that the protein products of this gene are useful for treatment/diagnosis of diseases of the developing liver and hematopoietic system, and act as a growth differentiation factor for hematopoietic stem cells.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 169

The polypeptide encoded by this gene is believed to be a membrane bound receptor. The extracellular domain of which is expected to consist of the following amino acid sequence:

RILLVKYSANEENKYDYLPPTTVNVCSELVKLVFCVLVSFCVIKKDHQSRNLKY  
 ASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAVIFS NFSIITALLFRIV  
 LKXRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFFSPSNSCLL  
 FRNECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI  
 YNEKILKEGNQLTEXIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGH  
 S (SEQ ID NO:732). Thus, preferred polypeptides encoded by this gene comprise the extracellular domain as shown above. It will be recognized, however, that deletions of either end of the extracellular domain up to the first cysteine from the N-terminus and the first cysteine of the C-terminus, is expected to retain the biological functions of the full-length extracellular domain because the cysteines are thought to be responsible for providing secondary structure to the molecule. Thus, deletions of one or more amino acids from either end (or both ends) of the extracellular domain are contemplated. Of course, further deletions including the cysteines are also contemplated as useful as such polypeptides is expected to have immunological properties such as the ability to evoke and immune response. Polynucleotides encoding all of the foregoing polypeptides are provided.

This gene is expressed primarily in human osteoclastoma and to a lesser extent in hippocampus and chondrosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, cancers, particularly those of the bone and connective tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 402 as residues: Met-1 to Cys-6, Ala-41 to Tyr-49, Lys-76 to Lys-84.

The tissue distribution indicates that the protein products of this gene are useful for diagnosis of cancers of the bone and connective tissues, and may act as growth factors for cells involved in bone or connective tissue growth.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 170**

Preferred polypeptides encoded by this gene comprising the following amino acid sequence:

NSVPNLQTLAVLTEAIGPEPAIPRXPREPPVATSTPATPSAGPQPLPTGTV

LVPGGPAPPCLGEAWALLPPCRPSLTSCFWSPRPSPWKETGV (SEQ ID NO:733). Polynucleotides encoding such polypeptides are also provided herein.

This gene is expressed primarily in hematopoietic progenitor cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the blood including cancer and autoimmune disorders.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the blood/circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 403 as residues: Gln-4 to His-10, Pro-25 to His-32.

The tissue distribution indicates that the protein products of this gene are useful for diagnosis of diseases involving growth differentiation of hematopoietic cells.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 171**

5 Preferred polypeptides encoded by this gene comprise the following amino acid sequences: ALQLAFYPDAVEEWLEENVHPSLQRLQXLLQDLSEVSAPP (SEQ ID NO:734); and/or CHPPALAGTLLRTPEGRAHARGLLLEAGGA (SEQ ID NO:735). Polynucleotides encoding such polypeptides are also provided. The protein product of this gene shares sequence homology with metallothionines. Thus, polypeptide encoded  
10 by this gene are expected to have metallothionine activity, such activities are known in the art and described elsewhere herein.

This gene is expressed primarily in kidney cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
15 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the kidney including cancer and renal dysfunction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal system,  
20 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the  
25 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 404 as residues: Ser-47 to Gln-52.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of diseases of the kidney including kidney failure.

30

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 172**

This gene is expressed primarily in 12 week old early stage human.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
35 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the developing embryo, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 405 as residues: Gln-31 to Thr-43, Gly-51 to Ser-58, Pro-65 to Pro-72.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of developmental problems with fetal tissue. The gene may be involved in vital organ development in the early stage, especially hematopoiesis, cardiovascular system, and neural development.

#### 15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 173**

The translation product of this gene shares sequence homology with TGN38, an integral membrane protein previously shown to be predominantly localized to the trans-Golgi network (TGN) of cells.

This gene is expressed primarily in developing embryo and to a lesser extent in cancer tissues including lymphoma, endometrial, prostate and colon.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental abnormalities and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the developing fetus, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 406 as residues: His-65 to Ser-72, Pro-82 to Gly-91, Pro-98 to Glu-118, Ser-126 to Gly-166, Pro-180 to Asp-188, Tyr-209 to Lys-214, Gln-220 to Leu-228.

The tissue distribution and homology to an integral membrane protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for

diagnosis of cancers and developmental abnormalities where aberrant expression relates to an abnormality.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 174**

5       The translation product of this gene shares sequence homology with a dnaJ heat shock protein from E. coli which is allelic to sec63, a gene that affects transit of nascent secretory proteins across the endoplasmic reticulum in yeast.

      This gene is expressed primarily in Hodgkin's lymphoma and to a lesser extent in testes.

10       Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer. Similarly, polypeptides and antibodies directed to these  
15       polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or  
20       another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 407 as residues: Thr-13 to Trp-21, Arg-74 to Asp-81.

      The tissue distribution and homology to dnaJ indicates that polynucleotides and  
25       polypeptides corresponding to this gene are useful as a diagnostic for cancer including Hodgkin's lymphoma.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 175**

      This gene is expressed primarily in endothelial cells and to a lesser extent in  
30       bone marrow stromal cells.

      Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases involving angiogenic abnormalities including diabetic  
35       retinopathy, macular degeneration, and other diseases including arteriosclerosis and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for treating diseases where an increase or decrease in angiogenesis is indicated and as a factor in the wound healing process.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 176**

The translation product of this gene shares sequence homology with MAT8 (mouse) which is thought to be important in regulating chloride conductance in cells (particularly in the breast) by modulating the response mediated by cAMP and protein kinase C to extracellular signals.

This gene is expressed primarily in amniotic cells and hematopoietic cells including macrophages, Neutrophils, T cells, TNF induced aortic endothelium and to a lesser extent in testes, TNF induced epithelial cells, and smooth muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammatory responses mediated by T cells, macrophages, and/or neutrophils particularly those involving TNF, and also cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 409 as residues: Thr-19 to Ala-33, Leu-54 to Asp-82, Pro-89 to Ala-97, Pro-100 to Lys-125, Ser-127 to Phe-135, Gly-164 to Leu-169, Cys-173 to Arg-178.

The tissue distribution and homology to mat-8 indicates that polynucleotides and polypeptides corresponding to this gene are useful for modifying inflammatory

responses to cytokines such as TNF and thus modifying the duration and/or severity of inflammation. Polynucleotides and polypeptides derived from this gene are thought to be useful in the diagnosis and treatment of cancer.

## 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 177

This gene is expressed primarily in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, vascular restenosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases associated with vascular response to injury such as vascular restenosis following angioplasty..

## FEATURES OF PROTEIN ENCODED BY GENE NO: 178

One embodiment of the claimed invention comprises:

MRPDWKAGAGPGGPPQKPAPSSQQRKPPARPSAAAAIAVAAAEERLRQRN  
RLRLEEDKPAVERCLEELVFGDVENDEALLRRLRGPRVQEHEDSGDSEVENEAKGNFPPQKKPV  
WVDEEDEDEEMVDMMNRRFRKDMKNASESKLSKDNLKKRLKEEFQHAMGGVPAWAETTKRKTSSDDESEEDDLLQRTGNFISTSTSLPRG  
ILKMKNQCQHANARPTVARISICAVPSRCTDCDGCWD (SEQ ID NO:737); or  
CLEELVFGDVENDEALLRRLRGPRVQEHEDSGDSEVENEAKGNFPPQKKPV  
WVDEEDEDEEMVDMMNRRFRKDMKNASESKLSKDNLKKRLKEEFQHAMG  
GVPWAETTKRKTSSDDESEEDDLLQRTGNFISTSTSLPRGILKMKNQCQHA  
NARPTVARISICAVPSRCTDCDGC (SEQ ID NO: 738). LKEKIVRSFEVSPDGS  
FLLINGIAGYLHLLAMKTKELIGSMKINGRVAASTFSSDSKKVYASSGDGEVYV  
WDVNSRKCLNRFVDEGSLYGLSIATSRNGQYVACGSNCGVVNIYNQDSCLQE  
TNPKPIKAIMNLVTGVTSLTFNPTTEILAIASEKMKEAVRLVHLPSCTVFNSFPVI  
KNKNISHVHTMDFSPRSGYFALGNEKGKALMYRLHHYSDF (SEQ ID NO:739);



and/or KINGRVAASTFSSDSKKVYASSGDGEVYVWDVNSRKCLNRFVDEGSL  
YGLSIATSRNGQYVACGSNCGVVNIYNQDSCLQETNPKPIKAIMNLVTGVTSLT  
FNPTTEILAIASEKMKEAVRLVHLPSCTVFSNFPVIKNKNISHVHTMDFSPRS  
GFALGNEKGKAL (SEQ ID NO:740).

- 5 This gene is expressed primarily in epididymus and endometrial tumors and to a lesser extent in T cell lymphoma and cell lines derived from colon cancer.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, tumors of the reproductive organs including testis and endometrial cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 411 as residues: Ser-67 to Lys-72, Val-87 to Leu-93, Tyr-128 to Pro-141, Asp-204 to Gly-210.

The tissue distribution indicates that the protein products of this gene are useful for treating tumors of the endometrium or epithelial tumors of the reproductive system.

## 25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 179**

Preferred polypeptides encoded by this gene comprise the following amino acid sequence:

- MRILQLILLALATGLVGGETRIIKGFECKLHSQPWQAALFEKTRLLCGATLIAPR  
WLLTAAHCLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDH  
30 RNDIMLVKMASPV SITWAVRPLTLSSRCVTAGTSCSFPAGAARPDPSYACLTPC  
DAPTSPSLSTRSVRTPATPSQTPWCVPACRKGARTPARVTPGALWSVTSLFKA  
LSPGARIRVRSPESLVSTRKSANMWTGSRRR (SEQ ID NO:741); ETRIIKGFEC  
KLHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRYIVHLGQHNLQKEE  
GCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV SITWAVRPLTLSSR  
35 CVTAGTSCSFPAGAARPDPSYACLTPCDAPTSPSLSTRSVRTPATPSQTPWCVP  
ACRKGARTPARVTPGALWSVTSLFKALSPGARIRVRSPESLVSTRKSANMWTG

SRRR (SEQ ID NO:742); or CKLHSQPWQAALFEKTRLLCGATLIAPRWLLT  
AAHCLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNS

(SEQ ID NO:743). The translation product of this gene shares sequence homology  
with neuropsin a novel serine protease which is thought to be important in modulating  
extracellular signaling pathways in the brain. Owing to the structural similarity to other  
serine proteases the protein products of this gene are expected to have serine protease  
activity which may be assayed by methods known in the art and described elsewhere  
herein.

This gene is expressed primarily in endometrial tumor and to a lesser extent in  
colon cancer, benign hypertrophic prostate, and thymus.

Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, cancers of the endometrium or colon and benign hypertrophy of the  
prostate. Similarly, polypeptides and antibodies directed to these polypeptides are  
useful in providing immunological probes for differential identification of the tissue(s)  
or cell type(s). For a number of disorders of the above tissues or cells, particularly of  
the urogenital or reproductive systems, expression of this gene at significantly higher or  
lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded  
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or  
another tissue or cell sample taken from an individual having such a disorder, relative to  
the standard gene expression level, i.e., the expression level in healthy tissue or bodily  
fluid from an individual not having the disorder. Preferred epitopes include those  
comprising a sequence shown in SEQ ID NO: 412 as residues: Gly-12 to Ser-22, Pro-  
34 to Ser-53.

The tissue distribution and homology to serine proteases indicates that  
polynucleotides and polypeptides corresponding to this gene are useful for diagnosing  
or treating hyperproliferative disorders such as cancer of the endometrium or colon and  
hyperplasia of the prostate.

### **FEATURES OF PROTEIN ENCODED BY GENE NO: 180**

Preferred polypeptide encoded by this gene comprise the following amino acid  
sequence: VLQGRYFSPILEMRRLRPEGXXNLPGGsRAQKEPRQDLTLVLWPHC  
PHFAMTRSYPVKQCMVQGSFYCIFKGPVQNWNC (SEQ ID NO:744).

Polynucleotides encoding such polypeptide are also provided.

This gene is expressed primarily in fetal brain

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, identifying and expanding stem cells in the CNS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for detecting and expanding stem cell populations in the (or of the) central nervous system.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 181**

This gene is expressed primarily in early stage human brain and a stromal cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental abnormalities of the CNS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 414 as residues: Gln-42 to Gln-47, Gln-54 to Pro-60.

The tissue distribution indicates that the protein products of this gene play a role in the development of the central nervous system. Therefore this gene and its products

are useful for diagnosing or treating developmental abnormalities of the central nervous system.

#### FEATURES OF PROTEIN ENCODED BY GENE NO: 182

5 Preferred polypeptides encoded by this gene comprise the following amino acid sequence:

MPIIDQVNPELHDFMQSAEVTIFALSWLITWFGHVLSDFRHVVRLYDF  
 FLACHPLMPIYFAAVIVLYREQEVLDCDCDMASVHLLSQIPQDLPYETLISRXE  
 TFLFSFPHPNLLGRPLPNSKLRGRQPLLSKTLSWHQPSRGLIWCCGSGXRGLL  
 10 RPEDRTKDVLT KPRTNRFVKLAVMGLTVALGAAALAVVKSALWAPKFQLQL  
 FP (SEQ ID NO:745); or CPEFFIPATLPCPFVFAFTSEASSRAYLTQRGPGGLAQ  
 NLMPLPVGFWMGSLPPPWCWRKWVSEACSCFC (SEQ ID NO:746) These

polypeptides are structurally similar to various TGF-beta family members. Thus, this polypeptide is expected to have a variety of activities in the modulation of cell growth  
 15 and proliferation.

This gene is expressed primarily in osteoclastoma, microvascular endothelium, and bone marrow derived cell lines.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
 20 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematological diseases particularly involving aberrant proliferation of stem cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of  
 25 the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an  
 30 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 415 as residues: Ser-33 to Ala-39.

The tissue distribution indicates that the protein products of this gene is useful for treating disorders of the progenitors of the immune system. Applications include in vivo expansion of progenitor cells, ex vivo expansion of progenitor cells, or the  
 35 treatment of tumors of the circulatory system, such as lymphomas.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 183**

This gene maps to chromosome 17 and therefore, polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 17. In specific embodiments, polypeptides of the invention comprise the sequence:

- 5 GFGSVSAAGRRSGGTWQPVQ (SEQ ID NO:747); PGGLAVGSRWWSRSLT (SEQ ID NO:748); LEPSRQRRPRRRGGTSRPETDQRAKCWRQL (SEQ ID NO:749); and/or VCLRCQNRMEN (SEQ ID NO:750). In further specific embodiments, polypeptides of the invention comprise the sequence: MAACTARRPGR GQPLVVPVADXGPVAKAALCAAXAGAFSPASTTTTRHLSSNRNPEGKVLETV
- 10 GVFEVPKQNGKYETGQLFLHSIFGYRGVVLFPWQARLXDRDVASAAPEKAEN PAGHGSKEVKGKTHTYQVLIDARDCPHISQRSQTEAVTFLANHDDSRALYAIP GLDYVSHEDILPYTSTDQVPIQHELPERFLLYDQTKAPPFVARETLRAWQEKNH PWLELSDVHRETTENIRVTVIPFYMGMREAQNSHVYWWRYCIRLENLSDSDVVQ LRERHWRIFSLSGTLETVRGRGVVGREPVLSKEQPAFQYSSHVSLQASSGHMW
- 15 GTRFRFERPDGSHFDVRIPPFSLSENKDEKTPPSGLHW (SEQ ID NO:751); MAACTARRPGRGQPLVVPVADXGPVAKAALCAA (SEQ ID NO:752); VLETVG VFEVPKQNGKYETGQLFLHSIFGYRGVVL (SEQ ID NO:757); GLDYVSHEDILPYTST (SEQ ID NO:758); DVHRETTENIRVTVIPFYM (SEQ ID NO:759); WWRYCIRLENLSDSDVQLRER (SEQ ID NO:760); and/or PAFQYSS
- 20 HVSLQASSGHMWGTRFRER (SEQ ID NO:761). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in gall bladder, prostate, and fetal brain, and to a lesser extent in a few tumor and fetal tissues.

- 25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, growth related disorders such as cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
- 30 of the above tissues or cells, particularly of the prostate, gall bladder, and fetal brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
- 35 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of growth-related disorders, such cancers.

## 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 184

In specific embodiments, polypeptides of the invention comprise the sequence:SLCCPEGAEGC (SEQ ID NO:762) and/or QLKKTTHYDRPCP (SEQ ID NO:763). Polynucleotides encoding these polypeptides are also encompassed by the invention.

10 This gene is expressed primarily in stromal cell, tonsil, and glioblastoma and to a lesser extent in some other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are  
15 not limited to, immune and inflammatory disorders and glioblastoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the stromal cells, tonsil, and glioblastoma expression of this gene at significantly higher or lower levels  
20 may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Additionally, it is believed that the  
25 product of this gene regulates pancreatic cell differentiation into beta cells. Accordingly, polynucleotides and polypeptides of the invention are useful in the treatment of insulin-dependent diabetes mellitus and associated conditions e.g. pancreatic hypofunction and the prevention, as well as the treatment of undifferentiated type pancreatic cancers. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 417 as  
30 residues: Pro-27 to Ala-32.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune and inflammatory disorders and glioblastoma.

## 35 FEATURES OF PROTEIN ENCODED BY GENE NO: 185

This gene is expressed primarily in hepatocellular carcinoma and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, liver diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the liver, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 418 as residues: Gly-32 to Lys-39.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of liver diseases.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 186**

This gene is expressed primarily in hippocampus and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neuronal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hippocampus, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal disorders.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 187**

This gene is expressed primarily in bone cancer and hippocampus and to a lesser extent in osteoclastoma and other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, bone-related disorders and neuronal diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, osteoclast, and hippocampus, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of bone-related disorders and neuronal diseases.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 188**

This gene maps to chromosome 4 and therefore polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 4.

This gene is expressed primarily in neuronal tissues such as hippocampus, spinal cord, and hypothalamus and to a lesser extent in a few other tissues such as ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neuronal diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuronal tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal disorders.



**FEATURES OF PROTEIN ENCODED BY GENE NO: 189**

This gene maps to chromosome 10, therefore, polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 10.

- 5 This gene is expressed primarily in neuronal tissues and immune tissues, and to a lesser extent in a few other tissues such as skin tumor, lung etc.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neuronal and immune-related disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuronal and immune-related tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 422 as residues: Pro-19 to Asp-25.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal and immune-related disorders.

**25 FEATURES OF PROTEIN ENCODED BY GENE NO: 190**

The translation product of this gene shares sequence homology with human N33, a gene located in a homozygously deleted region of human metastatic prostate cancer which is thought to be important in prevention of prostate cancer. In specific embodiments, polypeptides of the invention comprise the sequence:

- 30 AQRKKEMVLSEKVSQ LMEWTNKR PVIRMGDKFRRLVKAPPRNYSVIVMFTA  
LQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEGSDVFQMLNM  
NSAPTFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNMA  
ARWRFWCVSVT (SEQ ID NO:765); MVVALLIVCDVPSAS (SEQ ID NO:766);  
AQRKKEMVLSEKVSQ L (SEQ ID NO:767); MEWTNKR PVIRMGDKF (SEQ  
35 ID:768); RRLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRY  
SSAFTNRIFFA (SEQ ID NO:769); MVDFDEGSDVFQMLNMNSAPTFINFPAGK  
GKP (SEQ ID NO:770); KRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPN

(SEQ ID NO:771); and/or YAGPLMLGLLLA VIGGLVYLRRVIWNFSLIKLDGLLQL  
CVLCLL (SEQ ID NO:772). Polynucleotides encoding these polypeptides are also  
encompassed by the invention.

5 This gene is expressed primarily in infant adrenal gland prostate cell line and to  
a lesser extent in a few other tissues like liver, smooth muscle etc.

Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, prostate cancer and endocrine disorders. Similarly, polypeptides and  
10 antibodies directed to these polypeptides are useful in providing immunological probes  
for differential identification of the tissue(s) or cell type(s). For a number of disorders  
of the above tissues or cells, particularly of the prostate and adrenal gland, expression  
of this gene at significantly higher or lower levels may be routinely detected in certain  
tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,  
15 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an  
individual having such a disorder, relative to the standard gene expression level, i.e.,  
the expression level in healthy tissue or bodily fluid from an individual not having the  
disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID  
NO: 423 as residues: Pro-34 to Gly-43, Arg-113 to Pro-120.

20 The tissue distribution and homology to N33 indicates that polynucleotides and  
polypeptides corresponding to this gene are useful for diagnosis and treatment for  
prostate cancer and endocrine disorders.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 191**

25 This gene is expressed primarily in T cell and to a lesser extent in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as  
reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, immune disorders. Similarly, polypeptides and antibodies directed to  
30 these polypeptides are useful in providing immunological probes for differential  
identification of the tissue(s) or cell type(s). For a number of disorders of the above  
tissues or cells, particularly of the immune, expression of this gene at significantly  
higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and  
wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal  
35 fluid) or another tissue or cell sample taken from an individual having such a disorder,  
relative to the standard gene expression level, i.e., the expression level in healthy tissue

or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 424 as residues: Trp-3 to Phe-9.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders.

5

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 192**

This gene maps to chromosome 6, therefore, polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 6. Neural activity and neurotrophins induce synaptic remodeling in part by altering gene expression. This gene is believed to be a glycosylphosphatidylinositol-anchored protein encoded by a hippocampal gene and to possess neural activity. This molecule is believed to be expressed in postmitotic-differentiating neurons of the developing nervous system and neuronal structures associated with plasticity in the adult. Message of this gene is believed to be induced by neuronal activity and by the activity-regulated neurotrophins BDNF and NT-3. The product of this gene is believed to stimulate neurite outgrowth and arborization in primary embryonic hippocampal and cortical cultures and to act as a downstream effector of activity-induced neurite outgrowth. In specific embodiments, polypeptides of the invention comprise the sequence: DAVFKGFSDCLLKLGD (SEQ ID NO:773); CQEGAKDMWDKLRKESKNLN (SEQ ID NO:774); VLLVLSAALATWLSF (SEQ ID NO:775); MGLKLNGRYISLILAVQIAYLVQAVR AAGKCDVFKGFSDCLLKLGD (SEQ ID NO:776); PAAWDDKTNIKTVCTYW EDFHSCTVTALTDCQEGAKDMWDKLRKESKNLNIQGSFELCGSGNGAAGSL LPAFPVLLVLSAALATWLSF (SEQ ID NO:777); and/or MGLKLNGRYISLILAVQIAYLVQAVRAAGKCDVFKGFSDCLLKLGDXXXXXPAAWDDKTNIKTVCTYWEDFHSCTVTALTDCQEGAKDMWDKLRKESKNLNIQGSFELCGSGNGAAGSLLPAFPVLLVLSAALATWLSF (SEQ ID NO:778). Polynucleotides encoding this polypeptide are also encompassed by the invention.

This gene is expressed primarily in human placenta, endometrial tumor and tissues of the central nervous system (CNS).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, relating to reproductive disorders, cancers and neurological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and neurological disorders, expression of this gene at significantly higher

35

or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 425 as residues: Asp-47 to Asp-63, His-75 to Tyr-80, Pro-83 to Tyr-89.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of reproductive disorders such as endometrial tumors. Expression of this gene in tissues of the CNS and its strong homology to Neuritin suggest that the protein product from this gene may also be used in the treatment and diagnosis of neurological disorders and in the regeneration of neural tissues, e.g., following injury.

#### 15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 193**

The translation product of this gene shares sequence homology with tenascin which is thought to be important in development. The translation product of this gene is believed to be a ligand of the fibroblast growth factor family. FGF ligand activity is known in the art and can be assayed by methods known in the art and disclosed elsewhere herein.

This gene is expressed primarily in endometrial tumors, and other types of tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 426 as residues: Gly-29 to Glu-34, Arg-71 to Arg-76, Thr-176 to Cys-182, Gly-184 to Glu-199.

The tissue distribution and homology to tenascin indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers.

## 5 FEATURES OF PROTEIN ENCODED BY GENE NO: 194

In specific embodiments, polypeptides of the invention comprise the sequence: MNSAAGFSHLDRRERVCLKGESFEKQPRCASTLC (SEQ ID NO:779).

Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in fetal human lung and neutrophils.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, lung development and respiratory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes  
15 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the respiratory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual  
20 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in fetal lung and neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis  
25 and treatment of lung and immunity related diseases, for example, lung cancer, viral, fungal or bacterial infections (e.g. lesions caused by tuberculosis), inflammation (e.g. pneumonia), metabolic lesions etc.

## FEATURES OF PROTEIN ENCODED BY GENE NO: 195

30 This gene is expressed primarily in breast lymph node.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immunal disorders. Similarly, polypeptides and antibodies directed to  
35 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at

significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immunal disorders.

#### 10 FEATURES OF PROTEIN ENCODED BY GENE NO: 196

This gene maps to chromosome 5 and accordingly, polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 5. The translation product of this gene shares sequence homology with human M-phase phosphoprotein 4 which is thought to be important in phosphorylation and signal transduction processes. In specific embodiments, polypeptides of the invention comprise the sequence: TIYPTEELQAVQKIVSITERALKLVSD (SEQ ID NO:780); RALKGVLRV GVLAKGLLLRGDRNVNLVLLC (SEQ ID NO:781); ALAALRHAKWFQARAN GLQSCVIIIRILDLCQRVPTWS (SEQ ID NO:782); GDALRRVFECISSGIL (SEQ ID NO:783); LAFRQIHKVLGMDPLP (SEQ ID NO:784); and/or TIYPTEELQAVQ KIVSITERALKLVSDSLSEHEKNKNKEGDDKKEGGKDRALKGVLRVGVLAGG LLLRGDRNVNLVLLCSEKPSKTLLSRIAENLPKQLAVISPEKYDIKCAVSEAAIL NSCVEPKMQVTITLTSPIIREENMREGDVTSGMVKDPPDVLDRQKCLDALAALR HAKWFQARANGLQSCVIIIRILDLCQRVPTWSDFPSWAMELLVEKAISSASSP QSPGDALRRVFECISSGILKGSPGLLDPEKDPFDLATMTDQQREDITSSAQFA LRLLAFRQIHKVLGMDPLPQMSQRFNIHNNRKRRRSDGVDGFEGGKDKK DYDNF (SEQ ID NO:785). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in Human Hippocampus and to a lesser extent in Prostate, Human Frontal Cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders related to reproductive system and nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system and nervous system, expression of this gene at significantly higher or lower

levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to human M-phase phosphoprotein 4 indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of reproductive and nervous system disorders.

#### 10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 197**

In specific embodiments, polypeptides of the invention comprise the sequence: MGSQHSAAARPSSCRRKQEDDRDG (SEQ ID NO:786); LLAEREQEEAIAQFPYVEFTGRDSITCLTC (SEQ ID NO:787); and/or QGTGYIPTEQVNELVALIPHSDQRLRPQRTKQYV (SEQ ID NO:788).

15 Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in Human Primary Breast Cancer and to a lesser extent in Human Adult Spleen, Hodgkin's Lymphoma I, Salivary Gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer and immunal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 430 as residues: Ser-126 to Gly-138.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and immunal disorders.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 198**

This gene is expressed primarily in monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, blood cell disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of blood cell disorders.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 199**

This gene is expressed primarily in Human Ovary and Synovia and to a lesser extent in Human 8 Week Whole Embryo.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, reproductive and developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and developmental system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of reproductive and developmental disorders.



**FEATURES OF PROTEIN ENCODED BY GENE NO: 200**

This gene maps to chromosome 8 and therefore polynucleotides of the invention can be used in linkage analysis as a marker for chromosome 8. The translation product of this gene shares limited sequence homology with collagen proline rich domain.

This gene is expressed primarily in CNS.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 433 as residues: Pro-35 to Asp-41.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neurological diseases.

**25 FEATURES OF PROTEIN ENCODED BY GENE NO: 201**

Translation product of this gene shares homology with a mammalian histone H1a protein. One embodiment for this gene is the polypeptide fragments comprising the following amino acid sequence: ARLNVGRESLKREMLKSQGVKVSESPMGAR HSSWPEGAAFCCKKVQGAQMOPPPRR (SEQ ID NO:789); ARLNVGRESLKR EML (SEQ ID NO:790); LKSQGVKVSESPMGARHSSW (SEQ ID NO:791); AFCCKKVQGAQMOPPPRR (SEQ ID NO:792). An additional embodiment is the polynucleotide fragments encoding these polypeptide (See Accession No. pirlS24178) fragments.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at  
5 significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders. Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in vital immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such  
15 as AIDS, and leukemia.

#### **FEATURES OF PROTEIN ENCODED BY GENE NO: 202**

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as  
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential  
25 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having  
30 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders. Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for  
35 immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 203**

This gene is expressed primarily in Neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as  
5 reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, infectious disorders, immune disorders, and cancers. Similarly,  
polypeptides and antibodies directed to these polypeptides are useful in providing  
immunological probes for differential identification of the tissue(s) or cell type(s). For  
10 a number of disorders of the above tissues or cells, particularly of the immune system,  
expression of this gene at significantly higher or lower levels may be routinely detected  
in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum,  
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from  
an individual having such a disorder, relative to the standard gene expression level, i.e.,  
15 the expression level in healthy tissue or bodily fluid from an individual not having the  
disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID  
NO: 436 as residues: Thr-31 to Lys-36.

The tissue distribution indicates that polynucleotides and polypeptides  
corresponding to this gene are useful for diagnosis and treatment of infectious  
20 disorders, immune disorders, and cancers. Since the gene is expressed in cells of  
lymphoid origin, the natural gene product may be involved in immune functions.  
Therefore it may be also used as an agent for immunological disorders including  
arthritis, asthma, immune deficiency diseases such as AIDS, and leukemia. Protein, as  
well as, antibodies directed against the protein may show utility as a tumor marker  
25 and/or immunotherapy targets for the above listed tumors and tissues.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 204**

This gene maps to chromosome 16 and therefore polynucleotides of the  
invention can be used in linkage analysis as markers for chromosome 16. The  
30 translation product of this gene shares sequence homology with lactate dehydrogenase  
which is thought to be important in lactate metabolism.

This gene is expressed primarily in human tonsils and to a lesser extent in  
Spleen, and Neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as  
35 reagents for differential identification of the tissue(s) or cell type(s) present in a  
biological sample and for diagnosis of diseases and conditions, which include, but are  
not limited to, immune disorders, infectious disorders, and cancers. Similarly,

polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune disorders, infectious disorders, and cancers, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 437 as residues: Gly-7 to Ser-12.

The tissue distribution and homology to lactate dehydrogenase gene indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders, infectious disorders, and cancers.

#### 15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 205**

The translation product of this gene shares sequence homology with Gcap1 protein which is developmentally regulated in brain.

This gene is expressed primarily in placenta and endometrial tumor and to a lesser extent in several other tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, vasculogenesis/angiogenesis and tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system and tumors, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to Gcap1 protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorder or dysfunction of vascular system of tumorigenesis.

**FEATURES OF PROTEIN ENCODED BY GENE NO: 206**

In specific embodiments, polypeptides of the invention comprise the sequence MPYAQWLAENDRFEEAQKAFHKAGRQREA (SEQ ID NO:799); VQVLEQLTNNAVAESRFNDAAYYYWMLSMQCLDIAQD (SEQ ID NO:794);  
 5 PAQKDTMLGKFYHFQRLAELYHGYHAIHRHTEDP (SEQ ID NO: 795); FSVHRPETLFNISRFLHSLPKDTPSGISKVKILFT (SEQ ID NO:800); LAKQSKALGAYRLARHAYDKLRGLYIP (SEQ ID NO:796); ARFQKSIELG TLTIRAKPFHDSEELVPLCYRCSTNN (SEQ ID NO: 797); and/or PLLNNLGNVC INCRQPFISSASSYDVLHLVEFYLEEGITDEEAISLIDLEVLPRKRDDRQLEICKQQ  
 10 LPDSCG (SEQ ID NO:798). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a  
 15 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male reproductive and endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and endocrine systems,  
 20 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the  
 25 disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of male reproductive and endocrine disorders.

**30 FEATURES OF PROTEIN ENCODED BY GENE NO: 207**

This gene is expressed in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are  
 35 not limited to, lung diseases such as cystic fibrosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the respiratory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual  
5 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 440 as residues: Tyr-49 to Cys-54.

The tissue distribution indicates that polynucleotides and polypeptides  
10 corresponding to this gene are useful for detection and treatment of disorders associated with developing lungs particularly in premature infants where the lungs are the last tissues to develop. The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of lung tumors since the gene may be involved in the regulation of cell division,  
15 particularly since it is expressed in fetal tissue. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and immunotherapy targets for the above listed tumors and tissues.

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO. X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO. Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
1	HLHDS67	97979 03/27/97	Uni-ZAP XR	11	2526	427	2526	458	458	234	1	30	31	30
2	HLHDZ58	97979 03/27/97	Uni-ZAP XR	12	1131	1	1131	129	129	235	1	14	15	115
3	HLMMJ13	97979 03/27/97	Lambda ZAP II	13	941	39	941	62	62	236	1	44	45	102
3	HLMMJ13	97979 03/27/97	Lambda ZAP II	218	941	39	941	245	245	441	1	35	36	41
4	HLTEI25	97979 03/27/97	Uni-ZAP XR	14	843	1	843	155	155	237	1	19	20	42
5	HMSJX24	97979 03/27/97	Uni-ZAP XR	15	1018	1	1018	90	90	238	1	18	19	36
6	HNFD65	97979 03/27/97	Uni-ZAP XR	16	661	1	661	76	76	239	1	28	29	127
7	HNHDX07	97979 03/27/97	Uni-ZAP XR	17	553	1	553	106	106	240	1	23	24	66
8	HNHGC82	97979 03/27/97	Uni-ZAP XR	18	869	1	869	101	101	241	1	21	22	68
9	HNHGO09	97979 03/27/97	Uni-ZAP XR	19	959	1	959	176	176	242	1	21	22	44
10	HOUBE18	97979 03/27/97	Uni-ZAP XR	20	1446	1	1446	101	101	243	1	27	28	50
11	HOUDL69	97979 03/27/97	Uni-ZAP XR	21	1471	579	1460	692	692	244	1	31	32	42

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO.	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO.	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
12	HPMF171	97979 03/27/97	Uni-ZAP XR	22	1402	242	1402	401	401	245	1	32	33	60
13	HPMGQ55	97979 03/27/97	Uni-ZAP XR	23	1047	1	1047	164	164	246	1	26	27	35
14	HPQAC69	97979 03/27/97	Lambda ZAP II	24	990	1	988	82	82	247	1	20	21	37
15	HPTBB03	97979 03/27/97	Uni-ZAP XR	25	1208	350	1173	398	398	248	1	29	30	210
16	HPTWA66	97979 03/27/97	pBluescript	26	1922	1381	1922	24	24	249	1	33	34	547
16	HPTWA66	97979 03/27/97	pBluescript	219	575	1	575	148	148	442	1	22	23	65
17	HPTWC08	97979 03/27/97	pBluescript	27	1951	1422	1874	219	219	250	1	19	20	299
18	HRGCZ46	97979 03/27/97	Uni-ZAP XR	28	3989	2635	3989		2748	251	1	16	17	39
19	HSADV34	97979 03/27/97	Uni-ZAP XR	29	3735	2966	3735	272	272	252	1	30	31	594
19	HSADV34	97979 03/27/97	Uni-ZAP XR	220	3018	1929	3018	26	26	443	1	1	2	156
20	HSDFW61	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	30	1667	59	1625	138	138	253	1	32	33	130
21	HSDGP60	97974 04/04/97	Uni-ZAP XR	31	1408	1	1408	285	285	254	1			20



Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		209080 05/29/97												
22	HSOAI55	97974 04/04/97 209080	Uni-ZAP XR	32	2031	1273	2031	1285	1285	255	1	29	30	30
		05/29/97												
23	HSQEO84	97974 04/04/97 209080	Uni-ZAP XR	33	971	13	971	91	91	256	1	19	20	218
		05/29/97												
23	HSQEO84	97974 04/04/97 209080	Uni-ZAP XR	221	968	8	968	86	86	444	1	20	21	56
		05/29/97												
24	HSXAM05	97974 04/04/97 209080	Uni-ZAP XR	34	1792	369	1792	470	470	257	1	26	27	49
		05/29/97												
25	HSXAS67	97974 04/04/97 209080	Uni-ZAP XR	35	896	1	896	96	96	258	1	32	33	121
		05/29/97												
26	HTDAF28	97974 04/04/97 209080	pSport1	36	912	1	912	38	38	259	1	22	23	87
		05/29/97												
27	HTEGQ64	97974	Uni-ZAP XR	37	1382	67	1382	271	271	260	1			25

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
28	HTGEU09	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	38	872	1	872	74	74	261	1	18	19	28
29	HTOAM21	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	39	812	1	812	41	41	262	1	30	31	43
30	HTPBW79	209511 12/03/97	Uni-ZAP XR	40	1515	118	1507	302	302	263	1	24	25	362
30	HTSEV09	97974 04/04/97 209080 05/29/97	pBluescript	222	1404	1	1265	92	92	445	1	19	20	415
31	HJPCD40	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	41	704	22	704		117	264	1	18	19	127
32	HTWBY48	97974 04/04/97 209080 05/29/97	pSport1	42	1094	1	1094	32	32	265	1	34	35	53
33	HTWC146	97974 04/04/97	pSport1	43	1821	892	1647	56	56	266	1	26	27	28

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		209080 05/29/97												
34	HTXGI75	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	44	1024	30	1024		167	267	1	20	21	25
35	HWTFB59	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	45	983	779	983	85	85	268	1	30	31	221
35	HWTFB59	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	223	707	488	707	514	514	446	1	41	42	64
36	HADAE74	97974 04/04/97 209080 05/29/97	pSport1	46	2421	664	1587	710	710	269	1			2
37	HAGFB60	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	47	840	1	840	97	97	270	1	30	31	48
38	HATEF60	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	48	2432	1193	2246	1491	1491	271	1	17	18	51
39	HBMSN25	97974	Uni-ZAP XR	49	1742	1165	1742	1207	1207	272	1	23	24	31

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		04/04/97 209080 05/29/97												
40	HCDAR68	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	50	1487	181	1455	325	325	273	1	35	36	56
41	HCE3J79	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	51	1328	251	1328	525	525	274	1			21
42	HMDAN54	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	52	1856	725	1853	928	928	275	1	33	34	50
43	HCECA49	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	53	1558	310	1408	393	393	276	1			1
44	HCEEC15	97974 04/04/97 209080 05/29/97	Uni-ZAP XR	54	948	1	948	9	9	277	1	23	24	65
45	HCESE40	97974 04/04/97 209080 05/29/97	pBluescript	55	990	99	990	193	193	278	1	32	33	256

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
45	HCESF40	97974 04/04/97 209080 05/29/97	pBluescript	224	1384	99	1384	193	193	447	1	32	33	205
46	HCFMV39	97974 04/04/97 209080 05/29/97	pSport1	56	1603	1	1296	96	96	279	1	29	30	102
47	HCM SX86	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	57	1052	5	786	12	12	280	1	28	29	32
48	HCNAP62	97975 04/04/97 209081 05/29/97	Lambda ZAP II	58	814	1	558	93	93	281	1	22	23	42
49	HCRAF32	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	59	1215	257	1215		356	282	1	19	20	20
50	HCUDC07	97975 04/04/97 209081 05/29/97	ZAP Express	60	478	1	478	147	147	283	1	36	37	69
51	HCWBB42	97975 04/04/97 209081	ZAP Express	61	618	1	618	212	212	284	1	35	36	74

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
52	HDTAB05	97975 04/04/97 209081 05/29/97	PCMV/Sport 2.0	62	751	1	751	257	257	285	1	21	22	32
53	HE2AV74	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	63	780	283	780		433	286	1			16
54	HE2AY71	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	64	588	21	588	169	169	287	1			16
55	HE2GS36	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	65	774	272	774	445	445	288	1			37
56	HE2OF09	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	66	1866	1313	1866	1596	1596	289	1			11
57	HE6EU50	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	67	1152	117	686	237	237	290	1	20	21	34
58	HE9HU17	97975 04/04/97	Uni-ZAP XR	68	2483	1577	2448	1620	1620	291	1			14

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
59	HE9ND48	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	69	536	1	536	83	83	292	1	36	37	43
60	HEBBW11	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	70	865	647	865		388	293	1	30	31	135
61	HELDY74	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	71	932	1	932	201	201	294	1	17	18	33
62	HEMAE80	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	72	996	1	945	12	12	295	1	24	25	136
63	HEEBA88	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	73	785	464	785	356	356	296	1	29	30	57
64	HFGAB89	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	74	1069	196	1047	295	295	297	1	32	33	34
65	HFVHY45	97975	pBluescript	75	831	1	831		89	298	1	30	31	76

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
66	HGBA193	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	76	590	1	590	233	233	299	1	38	39	94
67	HGBBQ69	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	77	1274	1	1273	105	105	300	1	24	25	43
68	HHFCF08	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	78	1133	4	1042	175	175	301	1	23	24	30
69	HHFHJ59	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	79	661	1	661	192	192	302	1	29	30	112
70	HHFHR32	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	80	1378	1	1378		358	303	1			13
71	HHGCN69	97975 04/04/97 209081 05/29/97	Lambda ZAP II	81	1440	298	1440	532	532	304	1	23	24	34



Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
72	HHGDOI3	97975 04/04/97 209081 05/29/97	Lambda ZAP II	82	1381	766	1371	993	993	305	1	23	24	34
73	HHFPD63	97975 04/04/97 209081 05/29/97	Uni-ZAP XR	83	1706	182	1644	257	257	306	1	24	25	81
74	HHSEG23	97976 04/04/97	Uni-ZAP XR	84	573	1	573	160	160	307	1	18	19	71
75	HJPV06	97976 04/04/97	Uni-ZAP XR	85	684	199	684	323	323	308	1	27	28	33
76	HKIXL73	97976 04/04/97	pBluescript	86	1036	591	1036	690	690	309	1	32	33	114
77	HKMNC43	97976 04/04/97	pBluescript	87	908	1	908	139	139	310	1	18	19	108
78	HMEJE31	97976 04/04/97	Lambda ZAP II	88	655	1	655	165	165	311	1	33	34	64
79	HMSKS35	97976 04/04/97	Uni-ZAP XR	89	1102	1	1102	228	228	312	1	26	27	49
80	HNF AE54	97976 04/04/97	Uni-ZAP XR	90	1533	665	1518	347	347	313	1	26	27	293
81	HNFJH45	97976 04/04/97	Uni-ZAP XR	91	575	1	575	275	275	314	1	30	31	67
82	HNGBT31	97976 04/04/97	Uni-ZAP XR	92	639	1	639	224	224	315	1	28	29	104

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
83	HNGIN60	97976 04/04/97	Uni-ZAP XR	93	744	1	744	225	225	316	1	43	44	70
84	HNGIG84	97976 04/04/97	Uni-ZAP XR	94	526	1	526	268	268	317	1	29	30	38
85	HNHDW42	97976 04/04/97	Uni-ZAP XR	95	426	1	426	168	168	318	1	28	29	71
86	HNHFL57	97976 04/04/97	Uni-ZAP XR	96	844	1	844	98	98	319	1	25	26	61
87	HOGAR52	97977 04/04/97 209082	PCMVSPORT 2.0	97	1985	453	1985	533	533	320	1	17	18	285
88	HOSBZ55	97977 04/04/97 209082	Uni-ZAP XR	98	1416	69	1416	246	246	321	1	32	33	54
89	HOSDI92	97977 04/04/97 209082	Uni-ZAP XR	99	1935	141	772		274	322	1	20	21	58
90	HPBCU51	97977 04/04/97 209082	pBluescript SK-	100	599	1	599	86	86	323	1	27	28	119
91	HPCAL49	97977 04/04/97 209082	Uni-ZAP XR	101	784	1	784		280	324	1	18	19	43

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
92	HPFCR13	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	102	1035	602	1035	859	859	325	1	32	33	58
93	HPHAC83	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	103	2218	840	2182	1035	1035	326	1	17	18	17
94	HPMBQ32	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	104	1351	1	1351	18	18	327	1	23	24	86
95	HPWAN23	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	105	2066	51	2052	270	270	328	1	29	30	537
95	HPWAN23	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	226	2057	1	1954	220	220	449	1	29	30	315
96	HRDFB85	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	106	1705	23	1697	233	233	329	1	21	22	201
97	HRGBR28	97977 04/04/97	Uni-ZAP XR	107	1167	611	1167	53	53	330	1	1	2	263

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		209082 05/29/97												
98	HSKGN81	97977 04/04/97 209082 05/29/97	pBluescript	108	1907	151	1432	353	353	331	1	23	24	260
98	HSKGN81	97977 04/04/97 209082 05/29/97	pBluescript	227	2084	335	2084	537	537	450	1	19	20	23
99	HSPAH56	97977 04/04/97 209082 05/29/97	pSport1	109	611	1	576	229	229	332	1	25	26	47
100	HE8EU04	209746 04/07/98	Uni-ZAP XR	110	2632	294	2632	337	337	333	1	25	26	333
100	HSXBT86	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	228	2143	53	1096	235	235	451	1			9
101	HSXCS62	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	111	2249	1	1953	90	90	334	1	18	19	199
102	HTEFU09	97977 04/04/97 209082	Uni-ZAP XR	112	2198	228	2158	400	400	335	1			23

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
103	HTKEM35	97977 04/04/97 209082	Uni-ZAP XR	113	1043	40	1043	320	320	336	1	20	21	142
		05/29/97												
104	HTGEP89	97977 04/04/97 209082	Uni-ZAP XR	114	703	1	703	285	285	337	1	29	30	94
		05/29/97												
105	HTGEW91	97977 04/04/97 209082	Uni-ZAP XR	115	3684	526	1338	584	584	338	1	24	25	37
		05/29/97												
106	HTOEY16	97977 04/04/97 209082	Uni-ZAP XR	116	1965	127	1915	202	202	339	1	27	28	38
		05/29/97												
107	HTPCN79	97977 04/04/97 209082	Uni-ZAP XR	117	503	1	503		1	340	1	7	8	70
		05/29/97												
108	HTSGM54	97977 04/04/97 209082	pBluescript	118	1133	316	1069		423	341	1	12	13	84
		05/29/97												
109	HTSHE40	97977 04/04/97	pBluescript	119	1101	118	956	218	218	342	1	31	32	89

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		209082 05/29/97												
110	HTWAF58	97977 04/04/97 209082 05/29/97	Lambda ZAP II	120	282	1	282	137	137	343	1	25	26	48
111	HTWBY29	97977 04/04/97 209082 05/29/97	pSport1	121	2635	1593	2489	1654	1654	344	1	25	26	55
112	HUKFC71	209007 04/28/97 209083 05/29/97	Lambda ZAP II	122	994	1	932		272	345	1	15	16	221
113	HCE3Q10	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	123	1542	1	1542	143	143	346	1	25	26	63
114	HCEVR60	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	124	1390	82	1390	127	127	347	1	32	33	153
115	HDTAW95	209007 04/28/97 209083 05/29/97	PCMVSPORT 2.0	125	1288	412	1288	571	571	348	1			16
116	HE6EL90	209007	Uni-ZAP XR	126	1517	1	1452	243	243	349	1			9

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		04/28/97 209083 05/29/97												
117	HELBUE29	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	127	1073	198	1073		776	350	1			13
118	HERAH36	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	128	300	155	300	202	202	351	1			17
119	HFXBW82	209007 04/28/97 209083 05/29/97	Lambda ZAP II	129	1275	1	1275	56	56	352	1	23	24	61
120	HHPTD20	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	130	472	51	472		243	353	1			32
121	HIBED17	209007 04/28/97 209083 05/29/97	Other	131	1950	284	1927	395	395	354	1	72	73	245
122	HLTER03	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	132	990	1	990	78	78	355	1	22	23	34

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
123	HOABL56	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	133	1720	565	1720	660	660	356	1	18	19	21
124	HPMC192	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	134	705	28	705	106	106	357	1	28	29	98
125	HPWAZ95	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	135	323	1	323	88	88	358	1	27	28	78
126	HRGBR18	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	136	582	1	582	16	16	359	1	17	18	30
127	HSUBW09	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	137	1021	1	1021	153	153	360	1	32	33	56
128	HUKCO64	209007 04/28/97 209083 05/29/97	Lambda ZAP II	138	1777	439	1777	521	521	361	1			2
129	H6EAA53	209007 04/28/97 209083	Uni-ZAP XR	139	643	303	643	313	313	362	1	7	8	31



Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
130	HAGAI11	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	140	1220	1	1220		127	363	1	16	17	27
131	HAGAO39	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	141	721	1	721		415	364	1			14
132	HALSK07	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	142	1468	125	1468	210	210	365	1	29	30	33
133	HALSQ59	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	143	300	4	300	101	101	366	1	22	23	66
134	HAIBP89	unknown 05/18/98	Uni-ZAP XR	144	2243	173	2243	311	311	367	1	27	28	317
134	HBCGB91	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	229	1025	409	1025	624	624	452	1	20	21	25
135	HBMTD81	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	145	1082	163	1082	357	357	368	1			30

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
136	HBXGK12	209008 04/28/97 209084 05/29/97	ZAP Express	146	4313	1153	4313	1313	1313	369	1	18	19	42
137	HFKFJ07	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	147	1183	1	1183	149	149	370	1	41	42	254
138	HCQA140	209008 04/28/97 209084 05/29/97	Lambda ZAP II	148	734	1	734	285	285	371	1			19
139	HCWHZ24	209008 04/28/97 209084 05/29/97	ZAP Express	149	1405	1	1405	108	108	372	1	34	35	63
140	HE2GT20	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	150	2890	1178	2890	1178	1178	373	1	31	32	39
141	HE3EY43	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	151	2399	1181	2399	1265	1265	374	1	30	31	34
142	HFCEB37	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	152	802	352	802		487	375	1			10

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
143	HFTCT67	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	153	461	24	461	145	145	376	1	37	38	63
144	HGLAM46	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	154	2388	818	2388	648	648	377	1			18
145	HHGBR15	209008 04/28/97 209084 05/29/97	Lambda ZAP II	155	642	322	642	400	400	378	1			4
146	HIAAU36	209008 04/28/97 209084 05/29/97	pBluescript SK-	156	1251	583	1251		933	379	1	16	17	16
147	HUSIT49	209008 04/28/97 209084 05/29/97	pSport1	157	2127	247	2127	383	383	380	1	47	48	83
148	HKLAB16	209008 04/28/97 209084 05/29/97	Lambda ZAP II	158	1625	817	1625	1012	1012	381	1	18	19	20
149	HLMMU76	209008 04/28/97	Lambda ZAP II	159	1687	1307	1687	1296	1296	382	1	28	29	28

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
		209084 05/29/97												
150	HMSKQ35	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	160	1842	172	1463	319	319	383	1	30	31	33
151	HNHED86	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	161	770	1	770	30	30	384	1	31	32	46
152	HNHEI88	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	162	519	1	519	242	242	385	1	17	18	24
153	HNHFQ63	209008 04/28/97 209084 05/29/97	Uni-ZAP XR	163	753	1	753	164	164	386	1	17	18	67
154	HOECU83	209009 04/28/97	Uni-ZAP XR	164	1400	189	1400		508	387	1	22	23	33
155	HPTRC15	209009 04/28/97	pBluescript	165	2153	594	2153		611	388	1			13
156	HSKCP69	209009 04/28/97	Uni-ZAP XR	166	1251	219	1120			389	1			
156	HSKCP69	209009 04/28/97	Uni-ZAP XR	230	1250	223	1250	393	393	453	1	32	33	171
157	H6EAE26	209009	Uni-ZAP XR	167	882	48	882	155	155	390	1	33	34	153

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
158	HAGBX03	209009 04/28/97	Uni-ZAP XR	168	1208	1	1208	182	182	391	1			8
159	HAGDQ47	209009 04/28/97	Uni-ZAP XR	169	1307	1	1307	44	44	392	1	22	23	60
160	HAICP19	209009 04/28/97	Uni-ZAP XR	170	1624	89	1483	128	128	393	1	18	19	446
161	HAUAE83	209009 04/28/97	Uni-ZAP XR	171	2003	889	2003	1080	1080	394	1			23
162	HBHAD12	209009 04/28/97	Uni-ZAP XR	172	786	1	786		176	395	1	17	18	23
163	HBMTY28	209009 04/28/97	Uni-ZAP XR	173	1758	962	1758	1184	1184	396	1	27	28	34
164	HBMPV04	209009 04/28/97	Uni-ZAP XR	174	888	330	862		546	397	1			2
165	HCDDDB78	209009 04/28/97	Uni-ZAP XR	175	2379	750	2379	901	901	398	1	18	19	24
166	HCEQA68	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	176	1348	1	1348	12	12	399	1	28	29	78
167	HCEZS40	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	177	1502	178	1502	315	315	400	1			20
168	HCFNF11	209010	pSport1	178	1637	26	1607	152	152	401	1	44	45	257

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
169	HCRBL20	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	179	2911	1103	2858	192	192	402	1	32	33	424
169	HCRBL20	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	231	1811	20	1811	93	93	454	1	36	37	95
170	HCUBL62	209010 04/28/97 209085 05/29/97	ZAP Express	180	519	1	519	57	57	403	1	28	29	32
171	HDSAP81	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	181	968	320	968	476	476	404	1	27	28	79
172	HE2CT29	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	182	1128	1	1128	111	111	405	1	26	27	94
173	HE8MG65	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	183	2276	48	2276	88	88	406	1	37	38	257

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
173	HE8MG65	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	232	2271	56	2232	79	79	455	1	43	44	170
174	HE9FB42	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	184	2500	76	1693	518	518	407	1	1	2	623
175	HEMAM41	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	185	1337	60	1328	175	175	408	1	39	40	190
175	HEMAM41	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	233	1338	33	1327	175	175	456	1	32	33	91
176	HEMCV19	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	186	941	33	931	79	79	409	1	23	24	178
177	HEMDX17	209010 04/28/97 209085 05/29/97	Uni-ZAP XR	187	654	1	654	137	137	410	1			13
178	HE1AR54	209010 04/28/97 209085	Uni-ZAP XR	188	1848	454	1848	948	948	411	1	14	15	232

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
179	HETBX14	209010 04/28/97 209085	Uni-ZAP XR	189	1146	157	1146		74	412	1	14	15	53
180	HFGAB48	209010 04/28/97 209085	Uni-ZAP XR	190	906	156	906	245	245	413	1	30	31	32
181	HFKFI40	209010 04/28/97 209085	Uni-ZAP XR	191	1941	120	1002	213	213	414	1	18	19	218
182	HFXHN68	209010 04/28/97 209085	Lambda ZAP II	192	2118	777	2118	966	966	415	1	23	24	50
183	HGBFO79	209011 04/28/97	Uni-ZAP XR	193	1538	259	1538	273	273	416	1	23	24	49
184	HGLAM56	209011 04/28/97	Uni-ZAP XR	194	1098	68	1098		185	417	1	28	29	69
185	HHLBA89	209011 04/28/97	pBluescript SK-	195	1001	1	1001	324	324	418	1	25	26	39
186	HHPDW05	209011 04/28/97	Uni-ZAP XR	196	1443	1	1443	246	246	419	1	21	22	21
187	HHPSD37	209011 04/28/97	pBluescript	197	1282	66	1282	171	171	420	1	19	20	37



Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of NT Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
188	HHPSTF70	209011 04/28/97	pBluescript	198	951	26	951		162	421	1	16	17	34
189	HHSACK25	209011 04/28/97	Uni-ZAP XR	199	1740	1390	1740	1534	1534	422	1	19	20	31
190	HIASB53	209011 04/28/97	pBluescript	200	1707	401	1195	652	652	423	1	26	27	126
191	HIABZ65	209011 04/28/97	pBluescript SK-	201	779	1	779	23	23	424	1	26	27	68
192	HIPBB39	209011 04/28/97	Uni-ZAP XR	202	1617	188	1605	182	182	425	1	28	29	91
193	HLHSK94	209011 04/28/97	pBluescript	203	1974	1	1794	112	112	426	1	26	27	379
194	HLHTC70	209011 04/28/97	pBluescript	204	1057	229	1057	365	365	427	1	23	24	22
195	HLMIW92	209011 04/28/97	Lambda ZAP II	205	721	1	721	244	244	428	1	25	26	46
196	HLTCY93	209011 04/28/97	Uni-ZAP XR	206	2465	988	2465	1225	1225	429	1			4
197	HLTDB65	209011 04/28/97	Uni-ZAP XR	207	1480	1	1480		371	430	1	15	16	143
198	HMSHM43	209011 04/28/97	Uni-ZAP XR	208	872	1	872	35	35	431	1	18	19	36
199	HMSHQ24	209011 04/28/97	Uni-ZAP XR	209	1779	16	1779	148	148	432	1	24	25	36
200	HNF AH08	209011 04/28/97	Uni-ZAP XR	210	2110	592	2110	611	611	433	1	18	19	191

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
201	HNGAO10	209011 04/28/97	Uni-ZAP XR	211	938	1	938	107	107	434	1	27	28	30
202	HNGBE45	209011 04/28/97	Uni-ZAP XR	212	1551	1	1551	114	114	435	1	21	22	100
203	HNHAZ16	209011 04/28/97	Uni-ZAP XR	213	997	1	997	202	202	436	1	24	25	36
204	HNHCM59	209011 04/28/97	Uni-ZAP XR	214	1496	1	1132		165	437	1	28	29	41
205	HOSFM22	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	215	1308	501	1308		809	438	1			1
206	HPHAC88	97977 04/04/97 209082 05/29/97	Uni-ZAP XR	216	1705	384	1705	549	549	439	1	23	24	24
207	HCDEO95	209007 04/28/97 209083 05/29/97	Uni-ZAP XR	217	999	608	999	273	273	440	1	22	23	54

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5        The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

### Signal Sequences

- 15        Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, *Virus Res.* 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, *Nucleic Acids Res.* 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, *supra.*) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

- 25        In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., *Protein Engineering* 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results shown in Table 1.

- 35        As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., + or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

### 10 Polynucleotide and Polypeptide Variants

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

15 By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization

Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query

amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions,  
5 interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by deposited DNA clone can be  
10 determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and  
15 subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window  
20 Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity.  
25 For subject sequences truncated at the N- and C-termini, relative to the the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of  
30 the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are  
35 considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.



For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired  
5 residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence.  
10 This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query  
15 sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or  
20 activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in  
25 the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level.  
30 Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be  
35 deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., *J. Biol. Chem.* 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after

deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

### **Polynucleotide and Polypeptide Fragments**

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, or 2001 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity. More preferably, these polynucleotides can be used as probes or primers as discussed herein.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the

carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Particularly, N-terminal deletions of the polypeptide of the present invention can be described by the general formula m-p, where p is the total number of amino acids in the polypeptide and m is an integer from 2 to (p-1), and where both of these integers (m & p) correspond to the position of the amino acid residue identified in SEQ ID NO:Y.

Moreover, C-terminal deletions of the polypeptide of the present invention can also be described by the general formula 1-n, where n is an integer from 2 to (p-1), and again where these integers (n & p) correspond to the position of the amino acid residue identified in SEQ ID NO:Y.

The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues m-n of SEQ ID NO:Y, where m and n are integers as described above.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

### **Epitopes & Antibodies**

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an

epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')<sub>2</sub> fragments) which are capable of specifically binding to protein. Fab and F(ab')<sub>2</sub> fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

### **Fusion Proteins**

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the

polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

5        Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

10        Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final  
15        preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

20        Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG)  
25        can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

30        Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the  
35        fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D.

Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

#### 15 Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance



genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., *Basic Methods In Molecular Biology* (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein

after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

5

### **Uses of the Polynucleotides**

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

10

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

15

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

20

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

25

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

30

35

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are

more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage  
5 analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease  
10 could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural  
15 alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic  
20 polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic  
25 marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the  
30 region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991) ) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off  
35 of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model

systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of

unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

### Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell. Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine ( $^{125}\text{I}$ ,  $^{121}\text{I}$ ), carbon ( $^{14}\text{C}$ ), sulfur ( $^{35}\text{S}$ ), tritium ( $^3\text{H}$ ), indium ( $^{112}\text{In}$ ), and technetium ( $^{99\text{m}}\text{Tc}$ ), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example,  $^{131}\text{I}$ ,  $^{112}\text{In}$ ,  $^{99\text{m}}\text{Tc}$ ), a radio-opaque substance, or a material detectable by nuclear magnetic

resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human  
5 subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of <sup>99m</sup>Tc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The  
10 Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene  
15 expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to  
20 supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired  
25 response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such  
30 as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a  
35 recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

### **Biological Activities**

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

### **Immune Activity**

A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotide or polypeptide of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can

decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

5 A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation,  
10 differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis,  
15 glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune  
20 inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

25 A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The  
30 administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may  
35 inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic



shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

### **Hyperproliferative Disorders**

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

### **Infectious Disease**

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases

may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

- 5           Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, 10 Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., 15 Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, 20 Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

- Similarly, bacterial or fungal agents that can cause disease or symptoms and that 25 can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, 30 Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Pasteurellaceae Infections (e.g., Actinobacillus, Haemophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, 35 and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS

related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria,

5 Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

10 Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas.

15 These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or  
20 diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo  
25 therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

### **Regeneration**

A polynucleotide or polypeptide of the present invention can be used to  
30 differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion  
35 injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal

or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase  
5 regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue  
10 regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate  
15 nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease,  
20 Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

### **Chemotaxis**

25 A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular  
30 trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body.  
35 For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

5

### **Binding Activity**

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit  
10 (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural  
15 or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing  
20 the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results  
25 in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule  
30 activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

5 All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

10 Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with  
15 a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

#### **Other Activities**

20 A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic  
25 surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, cardiac  
30 rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

35 A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

**Other Preferred Embodiments**

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under  
5 stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which  
10 comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide  
15 sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at  
20 least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

25 A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide  
30 sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer  
35 as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method



comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

5 Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined  
10 from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95%  
15 identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

20 The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

25 Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous  
30 nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

35 The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95%

identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide

comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

### Examples

#### Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
Lambda Zap	pBluescript (pBS)
Uni-Zap XR	pBluescript (pBS)
Zap Express	pBK
lafmid BA	plafmid BA
pSport1	pSport1
pCMVSPORT 2.0	pCMVSPORT 2.0
pCMVSPORT 3.0	pCMVSPORT 3.0
pCR <sup>®</sup> 2.1	pCR <sup>®</sup> 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Altling-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Altling-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1

Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS-. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR<sup>®</sup>2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with <sup>32</sup>P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).)

The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25  $\mu$ l of reaction mixture with 0.5  $\mu$ g of the above cDNA template. A convenient reaction mixture is 1.5-5 mM  $MgCl_2$ , 0.01% (w/v) gelatin, 20  $\mu$ M each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., *Nucleic Acids Res.* 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.



This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then  
5 be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA  
10 synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

#### **Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide**

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR  
20 using primers selected for the cDNA sequence corresponding to SEQ ID NO:X., according to the method described in Example 1. (See also, Sambrook.)

#### **Example 3: Tissue Distribution of Polypeptide**

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by,  
25 among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P<sup>32</sup> using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is  
30 then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are  
35 mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

**Example 4: Chromosomal Mapping of the Polynucleotides**

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

**Example 5: Bacterial Expression of a Polypeptide**

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp<sup>r</sup>), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan<sup>r</sup>). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.<sup>600</sup>) of between 0.4 and 0.6. IPTG

(Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA

insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

- 5       The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

**Example 6: Purification of a Polypeptide from an Inclusion Body**

- 10       The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

- 15       Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

- 20       The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

- 25       The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

- 30       Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area

(e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant  $A_{280}$  monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commaissie blue stained 16% SDS-PAGE gel when 5  $\mu$ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

### **Example 7: Cloning and Expression of a Polypeptide in a Baculovirus**

#### **Expression System**

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five  $\mu$ g of a plasmid containing the polynucleotide is co-transfected with 1.0  $\mu$ g of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., *Proc. Natl. Acad. Sci. USA* 84:7413-7417 (1987). One  $\mu$ g of BaculoGold™ virus DNA and 5  $\mu$ g of the plasmid are mixed in a sterile well of a microtiter plate containing 50  $\mu$ l of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10  $\mu$ l Lipofectin plus 90  $\mu$ l Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm

tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

- 5        After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.)
- 10       After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in
- 15       35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

- To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection
- 20       ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 µCi of <sup>35</sup>S-methionine and 5 µCi <sup>35</sup>S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins
- 25       in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

### 30       **Example 8: Expression of a Polypeptide in Mammalian Cells**

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates

the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human HeLa, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., *J. Biol. Chem.* 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., *Biochem. et Biophys. Acta*, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., *Biotechnology* 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., *Biochem J.* 227:277-279 (1991); Bebbington et al., *Bio/Technology* 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., *Molecular and Cellular Biology*, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., *Cell* 41:521-530 (1985)). Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the



polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five  $\mu$ g of the expression plasmid pC6 is cotransfected with 0.5  $\mu$ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1  $\mu$ M, 2  $\mu$ M, 5  $\mu$ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200  $\mu$ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

**Example 9: Protein Fusions**

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

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GGGATCCGGAGCCCAAATCTTCTGACAAACTCACACATGCCCACCGTGCC
CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAACC
35 CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC

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AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG  
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC  
ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT  
GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT  
5 GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA  
GAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGG  
ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA  
GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC  
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC  
10 GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

**Example 10: Production of an Antibody from a Polypeptide**

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of  
15 the present invention is administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

20 In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell  
25 Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at  
30 about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line  
35 (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as

described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

It will be appreciated that Fab and F(ab')<sub>2</sub> and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')<sub>2</sub> fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

#### **Example 11: Production Of Secreted Protein For High-Throughput Screening Assays**

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a

- working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The
- 5 PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

- Plate 293T cells (do not carry cells past P+20) at  $2 \times 10^5$  cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x
- 10 Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

- The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in
- 15 Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of
- 20 transfections.

- Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off
- 25 PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

- While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of  $\text{CaCl}_2$  (anhyd); 0.00130 mg/L
- 30  $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ ; 0.050 mg/L of  $\text{Fe}(\text{NO}_3)_3 \cdot 9\text{H}_2\text{O}$ ; 0.417 mg/L of  $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ ; 311.80 mg/L of Kcl; 28.64 mg/L of  $\text{MgCl}_2$ ; 48.84 mg/L of  $\text{MgSO}_4$ ; 6995.50 mg/L of NaCl; 2400.0 mg/L of  $\text{NaHCO}_3$ ; 62.50 mg/L of  $\text{NaH}_2\text{PO}_4 \cdot \text{H}_2\text{O}$ ; 71.02 mg/L of  $\text{Na}_2\text{HPO}_4$ ; .4320 mg/L of  $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ ; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic
- 35 Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of

Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H<sub>2</sub>O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H<sub>2</sub>O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0  
 5 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H<sub>2</sub>O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H<sub>2</sub>O; 99.65 mg/ml of L-  
 10 Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 0.680 mg/L of Vitamin B<sub>12</sub>; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine;  
 15 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x  
 20 penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B  
 25 adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

30 It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an  
 35 activity in a particular assay.

**Example 12: Construction of GAS Reporter Construct**

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>Ligand</u>	<u>tyk2</u>	<u>JAKs</u> <u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>	<u>STATs</u>	<u>GAS(elements) or ISRE</u>
<u>IFN family</u>							
5	IFN- $\alpha$ /B	+	+	-	-	1,2,3	ISRE
	IFN-g.		+	+	-	1	GAS (IRF1>Lys6>IFP)
	IL-10	+	?	?	-	1,3	
<u>gp130 family</u>							
10	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS (IRF1>Lys6>IFP)
	IL-11(Pleiotrohic)	?	+	?	?	1,3	
	OnM(Pleiotrohic)	?	+	+	?	1,3	
	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
15	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
<u>g-C family</u>							
20	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP >>Ly6)(IgH)
	IL-7 (lymphocytes)	-	+	-	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
25	<u>gp140 family</u>						
	IL-3 (myeloid)	-	-	+	-	5	GAS (IRF1>IFP>>Ly6)
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS
30	<u>Growth hormone family</u>						
	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
	EPO	?	-	+	-	5	GAS(B-CAS>IRF1=IFP>>Ly6)
35	<u>Receptor Tyrosine Kinases</u>						
	EGF	?	+	+	-	1,3	GAS (IRF1)
	PDGF	?	+	+	-	1,3	
	CSF-1	?	+	+	-	1,3	GAS (not IRF1)
40							



To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5':GCGCCTCGAGATTTCCTCCGAAATCTAGATTTCCTCCGAAATGATTTCCTCCG  
AAATGATTTCCTCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5':CTCGAGATTTCCTCCGAAATCTAGATTTCCTCCGAAATGATTTCCTCCGAAATG  
ATTTCCCTCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC  
CTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGC  
CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGC  
CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT  
TGCAAAAAGCTT:3' (SEQ ID NO:5)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning  
5 site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules  
10 containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter  
15 construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

**Example 13: High-Throughput Screening Assay for T-cell Activity.**

The following protocol is used to assess T-cell activity by identifying factors,  
20 such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and  
25 Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately  
30 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to  
35 generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies)

with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

During the incubation period, count cell concentration, spin down the required number of cells ( $10^7$  per transfection), and resuspend in OPTI-MEM to a final  
5 concentration of  $10^7$  cells/ml. Then add 1ml of  $1 \times 10^7$  cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Gentamicin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

10 On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

15 Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12  
20 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples  
25 from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

**Example 14: High-Throughput Screening Assay Identifying Myeloid Activity**

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells.

- 5 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 10 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest  $2 \times 10^7$  U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

- 15 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM  $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$ , 1 mM  $\text{MgCl}_2$ , and 675 uM  $\text{CaCl}_2$ . Incubate at 37°C for 45 min.

- 20 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 25 These cells are tested by harvesting  $1 \times 10^8$  cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of  $5 \times 10^5$  cells/ml. Plate 200 ul cells per well in the 96-well plate (or  $1 \times 10^5$  cells/well).

- 30 Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

**Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.**

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes,  
5 EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or  
10 differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

15 The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

20 Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

25 To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker)  
30 containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

35 Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine

growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as  $5 \times 10^5$  cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to  $1 \times 10^5$  cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

#### **Example 16: High-Throughput Screening Assay for T-cell Activity**

NF- $\kappa$ B (Nuclear Factor  $\kappa$ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- $\kappa$ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- $\kappa$ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- $\kappa$ B is retained in the cytoplasm with I- $\kappa$ B (Inhibitor  $\kappa$ B). However, upon stimulation, I- $\kappa$ B is phosphorylated and degraded, causing NF- $\kappa$ B to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- $\kappa$ B include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- $\kappa$ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- $\kappa$ B would be useful in treating

diseases. For example, inhibitors of NF- $\kappa$ B could be used to treat those diseases related to the acute or chronic activation of NF- $\kappa$ B, such as rheumatoid arthritis.

To construct a vector containing the NF- $\kappa$ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- $\kappa$ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:  
 5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC  
 TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)

Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCC  
 ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCA  
 TCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTTCTCCGCCCCATGGCTGACT  
 AATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTC  
 CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:  
 3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2-promoter plasmid (Clontech) with this NF- $\kappa$ B/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- $\kappa$ B/SV40/SEAP cassette is removed from the above NF- $\kappa$ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF- $\kappa$ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF- $\kappa$ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

#### **Example 17: Assay for SEAP Activity**

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15  $\mu$ l of 2.5x dilution buffer into Optiplates containing 35  $\mu$ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50  $\mu$ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50  $\mu$ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

#### **Reaction Buffer Formulation:**

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6



23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

**Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability**

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO<sub>2</sub> incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50  $\mu$ l of 12  $\mu$ g/ml fluo-3 is added to each well. The plate is incubated at 37°C in a CO<sub>2</sub> incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100  $\mu$ l of buffer.

- 5 For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10<sup>6</sup> cells/ml with HBSS in a 50-ml conical tube. 4  $\mu$ l of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10<sup>6</sup> cells/ml, and dispensed into a microplate, 100  
10  $\mu$ l/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200  $\mu$ l, followed by an aspiration step to 100  $\mu$ l final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

- To measure the fluorescence of intracellular calcium, the FLIPR is set for the  
15 following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50  $\mu$ l. Increased emission at 530-nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca<sup>++</sup>  
20 concentration.

#### **Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity**

- The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase  
25 RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

- 30 Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members  
35 of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na<sub>3</sub>VO<sub>4</sub>, 2 mM Na<sub>4</sub>P<sub>2</sub>O<sub>7</sub> and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a

biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

- 5        The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg<sub>2+</sub> (5mM ATP/50mM MgCl<sub>2</sub>), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl<sub>2</sub>, 5 mM MnCl<sub>2</sub>, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the
- 10       components gently and preincubate the reaction mix at 30°C for 2 min. Initiate the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

- 15       Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as
- 20       above.

- Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of
- 25       tyrosine kinase activity.

#### **Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity**

- 30       As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase,
- 35       Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other

phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then  
5 rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C  
10 until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts  
15 filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and  
20 Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

25

**Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide**

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from  
30 these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

35 PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies).

The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

5 PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

10 Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

15 Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated  
25 disease.

#### **Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample**

30 A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

35 For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

#### **Example 23: Formulating a Polypeptide**

The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1  $\mu\text{g/kg/day}$  to 10  $\text{mg/kg/day}$  of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01  $\text{mg/kg/day}$ , and most preferably for humans between about 0.01 and 1  $\text{mg/kg/day}$  for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1  $\mu\text{g/kg/hour}$  to about 50  $\mu\text{g/kg/hour}$ , either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracisternally, intravaginally,

intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes  
5 of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules.

10 Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D- (-)-3-hydroxybutyric  
15 acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008;  
20 U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is  
25 formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are  
30 known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood  
35 of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.



The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

**Example 24: Method of Treating Decreased Levels of the Polypeptide**

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form.

- 5 Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

- 10 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

**Example 25: Method of Treating Increased Levels of the Polypeptide**

- 15 Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

- For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

**Example 26: Method of Treatment Using Gene Therapy**

- 25 One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long  
5 terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set  
10 forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to  
15 transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is  
20 then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media,  
25 containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is  
30 required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

**Example 27: Method of Treatment Using Gene Therapy - In Vivo**

Another aspect of the present invention is using *in vivo* gene therapy methods to treat disorders, diseases and conditions. The gene therapy method relates to the introduction of naked nucleic acid (DNA, RNA, and antisense DNA or RNA) sequences into an animal to increase or decrease the expression of the polypeptide of the present invention. A polynucleotide of the present invention may be operatively linked to a promoter or any other genetic elements necessary for the expression of the encoded polypeptide by the target tissue. Such gene therapy and delivery techniques and methods are known in the art, see, for example, WO90/11092, WO98/11779; U.S. Patent NO. 5693622, 5705151, 5580859; Tabata H. et al. (1997) *Cardiovasc. Res.* 35(3):470-479, Chao J et al. (1997) *Pharmacol. Res.* 35(6):517-522, Wolff J.A. (1997) *Neuromuscul. Disord.* 7(5):314-318, Schwartz B. et al. (1996) *Gene Ther.* 3(5):405-411, Tsurumi Y. et al. (1996) *Circulation* 94(12):3281-3290 (incorporated herein by reference).

The polynucleotide constructs of the present invention may be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, intestine and the like). These polynucleotide constructs can be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

The term "naked" polynucleotide, DNA or RNA, refers to sequences that are free from any delivery vehicle that acts to assist, promote, or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides may also be delivered in liposome formulations (such as those taught in Felgner P.L. et al. (1995) *Ann. NY Acad. Sci.* 772:126-139 and Abdallah B. et al. (1995) *Biol. Cell* 85(1):1-7) which can be prepared by methods well known to those skilled in the art.

The polynucleotide vector constructs of the present invention used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Any strong promoter known to those skilled in the art can be used for driving the expression of DNA. Unlike other gene therapies techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct of the present invention can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. *In vivo* muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked polynucleotide injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 g/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration. The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked polynucleotide constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The dose response effects of injected polynucleotide in muscle *in vivo* is determined as follows. Suitable template DNA for production of mRNA coding for the polypeptide of the present invention is prepared in accordance with a standard recombinant DNA methodology. The template DNA, which may be either circular or linear, is either used as naked DNA or complexed with

liposomes. The quadriceps muscles of mice are then injected with various amounts of the template DNA.

Five to six week old female and male Balb/C mice are anesthetized by intraperitoneal injection with 0.3 ml of 2.5% Avertin. A 1.5 cm incision is made on the anterior thigh, and the quadriceps muscle is directly visualized. The template DNA is injected in 0.1 ml of carrier in a 1 cc syringe through a 27 gauge needle over one minute, approximately 0.5 cm from the distal insertion site of the muscle into the knee and about 0.2 cm deep. A suture is placed over the injection site for future localization, and the skin is closed with stainless steel clips.

After an appropriate incubation time (e.g., 7 days) muscle extracts are prepared by excising the entire quadriceps. Every fifth 15  $\mu$ m cross-section of the individual quadriceps muscles is histochemically stained for protein expression. A time course for protein expression may be done in a similar fashion except that quadriceps from different mice are harvested at different times. Persistence of DNA in muscle following injection may be determined by Southern blot analysis after preparing total cellular DNA and HIRT supernatants from injected and control mice. The results of the above experimentation in mice can be used to extrapolate proper dosages and other treatment parameters in humans and other animals using naked DNA of the present invention.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference.

## Sequence Listing

### (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Human Genome Sciences, Inc., et al.
- (ii) TITLE OF INVENTION: 207 Human Secreted Proteins
- 10 (iii) NUMBER OF SEQUENCES: 800
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Human Genome Sciences, Inc.
- (B) STREET: 9410 Key West Avenue
- 20 (C) CITY: Rockville
- (D) STATE: Maryland
- (E) COUNTRY: USA
- 25 (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
- 30 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
- (B) COMPUTER: HP Vectra 486/33
- 35 (C) OPERATING SYSTEM: MSDOS version 6.2
- (D) SOFTWARE: ASCII Text
- 40 (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- 45 (B) FILING DATE:
- (C) CLASSIFICATION:
- 50 (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
- 55 (B) FILING DATE:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kenley K. Hoover

(B) REGISTRATION NUMBER: 40,302

(C) REFERENCE/DOCKET NUMBER: PZ007PCT

## (vi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504

(B) TELEFAX: (301) 309-8439

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGGATCCGGA GCCCAAATCT TCTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG 60  
AATTCGAGGG TGCACCGTCA GTCTTCCTCT TCCCCC AAA ACCCAAGGAC ACCCTCATGA 120  
TCTCCCGGAC TCCTGAGGTC ACATGCGTGG TGGTGGACGT AAGCCACGAA GACCCTGAGG 180  
TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG 240  
AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT 300  
GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA ACCCCCATCG 360  
AGAAAACCAT CTCCAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC 420  
CATCCCGGGA TGAGCTGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT 480  
ATCCAAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA 540  
CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG 600  
ACAAGAGCAG GTGGCAGCAG GGAACCTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC 660  
ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG TAAATGAGTG CGACGGCCGC 720  
GACTCTAGAG GAT 733

## (2) INFORMATION FOR SEQ ID NO: 2:



## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Trp Ser Xaa Trp Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCGCCTCGAG ATTTCCCCGA AATCTAGATT TCCCGAAAT GATTCCCCG AAATGATTTC 60  
CCCGAAATAT CTGCCATCTC AATTAG 86

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCGGCAAGCT TTTGCAAAG CCTAGGC 27

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTCGAGATTT CCCCAGAAATC TAGATTTCCC CGAAATGATT TCCCCGAAAT GATTCCCCG 60  
AAATATCTGC CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC CGCCCATCCC 120

180 GCCCCTAACT CCGCCAGTT CCGCCATTC TCGCCCAT GGCTGACTAA TTTTTTTAT  
240 TTATGCAGAG GCCGAGGCCG CTCGGCTC TGAGTATTC CAGAAGTAGT GAGGAGGCTT  
5 TTTTGGAGGC CTAGGCTTTT GCAAAAAGCT T 271

10 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

20 GCGCTCGAGG GATGACAGCG ATAGAACCCC GG 32

25 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

35 CGGAAGCTTC GCGACTCCCC GGATCCGCCT C 31

40

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

50 GGGGACTTTC CC 12

55

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

5 GCGGCCTCGA GGGGACTTTC CCGGGGACTT TCCGGGACT TTCCGGGACT TTCCATCCTG 60  
CCATCTCAAT TAG 73

10

(2) INFORMATION FOR SEQ ID NO: 10:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCGAGGGGA CTTTCCCGGG GACTTTCGGG GGACTTTCGG GGACTTTCCA TCTGCCATCT 60  
25 CAATTAGTCA GCAACCATAG TCCCGCCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 120  
CAGTTCGGCC CATCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG CAGAGGCCGA 180  
GGCCGCCTCG GCCTCTGAGC TATTCAGAA GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG 240  
30 CTTTTGCAAA AAGCTT 256

35

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2526 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

45 GACAGGCTAT CCGAGAATCT GAGAGCTGGG CCGGCAATT CCTCCAGYTA CCCTGTGAC 60  
CTAAGTCCAG TCACACATTT CCCAAAGTTT CTCITTGTCA TAACCCGTGT CTGGCTGGTT 120  
50 TTGRGGRCTT GAGAATGGGT CAGGGACTCC AGGCCAAGTC CAACAGAGAC CCCAAACCCA 180  
CCACACACCA GCAGCCACAA CCTCACCACC AACAAAGAGG ACTTTTGTGG GGCCACAAGT 240  
AAGAGGTCAT TTCTGGAATG GACTCAGACC TTAAACAGG AGAGTTGAGC ACTTCCAGKS 300  
55 AGTTTTTAAG CAAGGCATGG GGAACAGGGA ATAGAACCTT TCAAAGAGGT TGCCCAGAGA 360  
AAAGCTGGGC CTCTTGCAAT CGGCTTCCTT GGAGCAGCCT CTCTGGCAG AAAGCCATCA 420  
60 GGTGCTCAAT CATCTTCTCC TGGCCAAGGC TCTGACCATG CTTAGTACTG GAATAGAGGT 480

	GGCCAGGCCC CCAGCGACTC TTCTTGGCCT GATGTTTGTC CTCACAGGCA TGCCACGTGG	540
	CCTGAGATGA TTCAGAACAA ATCATGCTAA CTTTGAATCC ATCCAGCCAC TTGCAAATGA	600
5	TAATCAGAAG TCAGCTTGTT CACTGTTAGA AAGAACTAA CAAAAGAGAA CCCAGAGCAA	660
	TCTAGAATCT TTGAGTGCTT GGCTTTCCAA GGATACTGCG GAGACTCTGG CCAAGCTGAT	720
10	GAMCTTCTGA ARTGTCAC TG CACCATATG CAACAAGAAC CACCATTAC TGAGTAGCTA	780
	ATGGGTTTGG GGCCTGGGAC ATTCCATCTG AGGTCTCTCC TGAACATGTC ACTCCACAGC	840
	AGAGGACCGG TTGAGCTTA CCCAGAACCA CTCCTCCAGG AGAGCTGGAT GTTTTGGCTG	900
15	CAACACCTTG AGCACTGACT GCTATTGTTT AAAAAAGCC TTTGCTGCAT TCGGAGGACT	960
	GCCCCGTGCC CTGAGGTGAC TTCCTAATA TGTGGTTTCA TTAGCGAATT TATTTTTTGT	1020
20	GCTGGGTGGA CATTTGTATT TTGTTAGGTT GCTGTTTAA CTCAAGTTG CTGTGCTCTC	1080
	TGCAGCTACA AAACATCTTG GCATATTTAA GAKTGGCTTT TATAAATAGC TTTATTCTGA	1140
	TATTAATCAG ATTCCCAACT TTACTGAGAA TTAAGGACTG GGTACTTTA AAGAAATGCA	1200
25	AATAGCAATT GAAGAACCAC TGCTGCAGGT GGTAGCCCTG GCTAGACTGA ATTACACTAG	1260
	AAATCAGCCA GAAGGAAGCG TCCTTGGGAT CCCAGATCAC TCTTTTTTTT TTTTTTTTAA	1320
30	AAAGGGGAG CCCCTTGATG GCTCATCTCT CTGAATAACA GTTACGTCTT CATATCGATA	1380
	CCAGATGCCT TCTTCATCAT GCCACTGAAG CCACTCACCA CCTCAAGAA CATGCCAACC	1440
	TCTGTCAGAT TCACTTACCC ACAAACAAGG AGGCACGTTT GGCACAAAGT GTTGTCTCTC	1500
35	AGGTCCAAGT GGA CTCTACA GAGTGCTTGA CCTCAACACA CTGGATTCCA GGTGGACTGG	1560
	ACCAAGAGCA GGCAAAGACA CGGGAAGTGA AAACTCCAC AGGGTTTGGG GAATAGAAAT	1620
40	GAAAAGCCAC GTCATATAAC TCAAGAATAA ATGGTGTGTT GGAAATTTTA AAATTATCAT	1680
	CGAAGGTGGT GAACTATTT CAGGCCCAAA TGAAAGGAAA TCGCCAGTTG GGGATGAAAT	1740
	CACAGAGCCT GTGTTTTATG ATATGGTTGG ATGTCCACTG ATGAAATTTT AAAGGAGTTT	1800
45	CATTTTAAAA AGTGCGCATG ATTCTACATA TGAGAATTCT TTAGGCCAAG AAAGTGTCTT	1860
	TGGCTCAGAG GTGTTGGGAA TTAAAGCAGA GAGAAGCCAT TCGTGATGCT TAGAACCAAG	1920
50	GATGGTCATG TACACAAAGA CCATCGAGAC GGCCATTCTT GTTTACAAAA CACTTACCAA	1980
	GAAAGCACTT TGTAGGGGAA CTTTAGTAAG TTCTTCTCAT TTCATTATGT TTCTTCCAAG	2040
	GAAACAGGAG AGACTGAATT AATAATTCTC TCTTCTCTCT TAAGCACTTT TAAATAATA	2100
55	AAGTACATCT TGAAATTTGG GGGGCATCT CTGATTTAAA AAAAGAAAA GGCTGCTTGA	2160
	TGTATGTTAT GCAGAGACAC TCTGCCTCTG GTGGCTGCAG AGCAATACCC AAGCCTCAT	2220
60	TGGAAGGCTC AACATTGGA ATTGCATTT AATTGATTAA TCCTCAATTC ATGTGGCCTT	2280

ACGGGATGGT GGGTCTGGGA CCCCAATTCA TTCTTATCTG CCAAAGAATT ATCTAGAAGC 2340  
ACATCAAATA CCAGCACCCC ACCTGCACAA TGGGGGTGGA AAACTTTGT ATCCCTAAGC 2400  
5 ATATTATTTT ATAGTGTCTG CCATGCCATG TGGAAATACT TTATTTTAA CCTCAGGATT 2460  
TAAATAAAGT AAACACTATG ACATTTAAAA AAAAAAAAAA AAAACTCGAG GGGGGCCCGG 2520  
10 TACCCA 2526

15 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1131 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

25 CACTGCACCA GCTTTGTAT CTGTAAAATG ATGATAATAC CAACACCTTC TTCTTGGGGT 60  
ACTGAAGATG AGAGAACATG ATATGTGTAA AGTGCCCTCC ACAATACCCA GAACATAGCA 120  
AACATGTAAT GAATGTAGTA ATAGTAATTA TTTTATTTTC TTTTGATTCA GTTGGGACTA 180  
30 TGTTCAGCTG TAACAGAATA CCCAAAATAA CTGTTTAAA CAAATTAAAG TTTWGTGTG 240  
AAGTTTGTG ACGAATTCAG ACAATCCAGG GCTTTTATAG ATGCACCAGG ATCAGCAGGT 300  
35 ACAAAGGCAT CTTTCCTGAT TTCTGCCAGT CTCAATGCAT GGGTTGCAAT CCAGARTCCA 360  
RGATGGCAGT TCCAGCCCTG GTTACGCCCA TATTAGCACA CAGAAAGAAA GAGAAAGGGA 420  
TGTGCCTCTT CACTTTAATC ATAGCTCCCA CTAGATGCAC CCACTACTTC TGCTGATACT 480  
40 CCATTAGCTA ATGCTTGCTT ACATGGTCAC ACTTAGTTTC CAGAGAGACA TGTCTGGACA 540  
GTCATGTGCT CAATTAATAT CCAAGTGTCC AATTACTGAG AAAAAAGAA ACTAGCACCT 600  
45 TTGCTTGGTT GCATTCTCT TAGCATAAGC CACATTCTTT TTATGAAGTT GTCCTCAGTT 660  
ACTTGATGC CTCAGTTGTC CTTCAWITA GAAAWGCYCC TKGGACAYCC TGAAWCTGAC 720  
TTCTTTTGTG ATCAGCACCA TCACTACCAC TGCCYTCTTC AAAGCCACCA CGTCTGTCC 780  
50 CCAGGATGGT TGCAACAACC ACCATAGGGA CTTTTGCCT TCTACTTCCA CACAATAGNC 840  
CAGAGTAAGC TTTTGAAAT GTAGGTCAGA TCATGTCTCT CTCCTCTCT TCAAAACCCT 900  
55 CCCGATGGCT TTTTATATTA CTCAAAGAA AACCTAAAAC TTTGCTGTGA GATCTATGTG 960  
ACCCGGCTTA TTCTTCTCT TACTTTATCT CTGTATTGCT CTTCTCACT CTACTCCAGC 1020  
CATCCACCT CTTGCTGCT TGTCTATAC TCCTAAAAGA AGTTCAGTCT TCCCTTATGA 1080  
60

TATTGCACT TAAATAGAA AAAAAAAAAA AAAAAAACT CGAGGGGGGC C

1131

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(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 941 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

15

GGCAGGAGTA GCATTTCATT TAATCTGCAG GTATATTCTC CCAACAGTTT ATTGTCATGT 60  
GATGTCCTCA GCCAAGATTG TRAGGCAGAG AGGAGCTGTC CCAACCTACT ATACCACCGA 120  
20 GGCTGGAGAG ATCATATTTT TGGTATTAAA CTGGAGTCTC TCCATCCTTC ACATTGTTGA 180  
TGTCTCTGT AGCAAACCGG AAAAGTCAGT GACAGAAGAT GCCGCTAGCG GTTTGAGCCA 240  
GAGAATGACA GCTCTGGTTT GGAGAAAAGG GCCGGATGGT GGCTCTAGAA AGCCCATCCT 300  
25 TCTGCTCTTC TTTTCTCTCC CCCTTATATT GTGCTTTCAT TCATTTCATC ATTCATCAAA 360  
CATTTGTTGA GCACCTAATA TGTGTCAAGC TCTGTGCTAG CCTCTGGAAA ACCTGCCCTC 420  
30 ATGTAGCTCA CTGTGGAGTA GGAGAAACAA TGACTACACT ATGATAAGCA CGGGTTGTCA 480  
GGGTCTCACA GAGCAGTGGC CCCTCATCCA GACCGATGAG GTCAAAGAAG GCATCCAGGC 540  
GAGGATGGTG TCAGAGCTAA CTGAAGAATG AGAGGGAGCT GCACCASCAG GGGTTGGAAC 600  
35 TGAAGGTGGC AGTGCCCTGA GTCTTGATTC CAGCAGAGGG AGAGCAGTCT GTGAAAAGGC 660  
ACCAAGGGTG GGAGAGGGCA GAGCACATGG AGGAACTTCA GGTAGTTCTG GATGCCSCTG 720  
40 GGGCAAAGCT AGAGAGGTAA GAAGAATCTA CAAATGTTCC TCGAGTTACA TGAACCTCCA 780  
TCCCAATAAA CCCATTGGAA ACGAAAAATT TAAGTCAGAA GTGCATTTAA GGCTGGTCCG 840  
AGTAGAATGA TTTTACAAC GAATTGATCA CAACCACTTA CAGATGTCTT TGTTCCTTCT 900  
45 CCACTCCCAC TGCTTCACCT GACTAGCCTT TAAAAA A 941

50

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 843 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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CNAGGGATAA CCCCAAAGNT GGGAAATAAA CCCTCAATTA AAGGGGGAAC CAAAAAGCTG 60  
GGAAGTTCCC CCCCGCGGTG GCGGCCNGNT CTAGGAAC TA GTGAATCCC CCGGGGCTGC 120  
AGGGAATTCG GCACGGAGTG GGAATGTTGT TTGTATGATA CTATTTCCAC AAWATGCATT 180  
GAGACTTGGT KTGTGGCCTA GGACATGGTC AATTCTTITYT AAATATTCCG TGAATTTCTT 240  
TAGTGCATAT TCTCCGATGG GGGCTGTGGG GACAGAGTTC TAAATATGCC CATTAGATTA 300  
AATCTCTTCA TTCTGTGCT CACATCTTCT ATATCCTTAT TAATCTGTCA ATCTCTTCAA 360  
GAGAGGTGTT ATTAAAATCT CTCACTGTAT GTGTCACTTT GCCCTTAAAA TTCTGATGAT 420  
TTGCTTTATA AATGTTTATA ACCATTTTCC AGGAAGAACA TTAAAGAACT TTCCATTGGC 480  
ATTATCCAGT TTCCCTCAAA ATACTGGTTT TTTTATTTT GGCTNCTAAG CAGCTATGAA 540  
TCCAGTTTCT CAGAAGCCCT TGTCTCAAGG CATTTGTTTC CAGATTACCT TGTTAGCATC 600  
CACACTATGG GCTATTTTAG AAAACAAAA AAAGTATCAA AATCATATAG CTATGATTTT 660  
CCTGTGCTTG AAGGAGCCTT AAAGCTCATC TAGTCCAGCC AGTATTTGTT CATCCAAATT 720  
CTGCCAAGAA ATCTCTATTG TCAAGATATT CTTTACCATC TTTGGGACAT TCTCATTATT 780  
AGAAACAAAT CCTAAGAAGA AATTCTGCCA TAKACAACCC ATCCGTCTTT TAAAAAATAA 840  
AAA 343

- 35 (2) INFORMATION FOR SEQ ID NO: 15:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1018 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

45  
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55  
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CTGTAATTTT TAATTTTCAT ATACCGTGCT TTGATCTTAA TTTTATTTT TGAGTTCTCT 60  
GAAGTTTACA TATACAGAGT GCTTCAGGAA TGATCATTTT GTTATTATTC ATGCTTCTTA 120  
ACAATGTTGT TTTAGTCCAA GAAGATAATT GCCAGAGAAA GAATACAGTG CAGGAAAGAA 180  
GARGCTGGAG CCAGTGGTGA AGARGGATTG AGARGACAGA CATGTGGGA ATGAAATCAT 240  
GAATAATCGT GTTTTGAAT TGTCCAAAAA CTTCTACAAA CCATGAAATG TTGGAGTTTA 300  
AATCTAATTG TTGAAAAATT CCCACATTC CTTGTATCCC TTAGGTTGAG CATAATCCA 360  
CATCCGTGGA CTGATGCACT TCCCAAGAGG GGGCCTCATT AACTCTCCG AGGCAGCAGC 420  
AGCAAGGGCA CCCCTCCTT TCCCCCACA CCCCAATTCT CATGGCTCTT CTTTCTCTCA 480  
TCTCATGCTT AGGTTAGAAA AGGCACAAG GTAAGGAAGC CCTTGGGAAT AGGCTGAATC 540

5 TGGCTATCTA ATTTGGTGCC AAATACTTAA TGTGCTTGAA TTTAAAAACA GCAAACATGT 600  
AGAAAGGTAA TTATAATTAT GAGGCCAGTT CTTTAAGCTA GCTTTTTC CCCTCTCAA 660  
CAGCATATTG GCTTGGATGT CAGCAGGAGA AAGTGTTTTT TGCAATACAC ATAATGCATA 720  
TATGGTCCTG TTAGCAATCT ATAGAAAATA GATATTGCTC ATTAAGGTAA ATATTTTGT 780  
10 TGATGAATGA TCTGGAATGG TCTGGACTTG TTGTGTGAAC AGGAAATTGC TCTGTAGGCT 840  
TTGACTTGTG AGGTAAAGAG TGAGGCTGGT AAGATTAATT AAAGTAAATA CTGTGACAAT 900  
AGGATGTCAA AACCAAAAAC GTGTTTCTGA AACTCAAGGA ATTAATGACA CATAGGGAAG 960  
15 TTTTGGCCAT ATTAAGCATA GAGTAGGAGA GGCAAGTCAA GAATAAAAAA AAAAAAAA 1018

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(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 661 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTTAAGAAAT TAGTGAATCC CCGGNTGCAG GGAATTCGGC ACGAGGAGGA GGCCGTCAGC 60  
TGGCAGGAGC GCAGGATGGC AGCTGYTCCC CCGGGTTGCA CCCCCCAGY TCTGCTGGAC 120  
35 ATAAGYTGGT TAACAGAGAG CCTGGGAGCT GGGCAGCCTG TACCTGTGGA GTGCCGACAC 180  
CGCCTGGAGG TGGCTGGGCC AAGGAAGGG CCTCTGAGCC CAGCATGGAT GCCTGCCTAT 240  
GCCTGCCAGC GCCCTACGCC CCTCACACAC CACAACACTG GCCTMTCCGA GCTGCTGGAG 300  
40 CATGGAGTGT GTGAGGAGGT GGAGAGAGTT CGGCGCTCAG AGAGGTACCA GACCATGAAG 360  
GTGCGCAGGG CAGGGCTCGG ACCTACCCCA GGAATGTCCT GCCCTGGGAA TGACAACACA 420  
45 GTCCACACCA TGCACGGGGA GGCAAACAGG GGCAGCTGAC CCAGCCCAGG GGTGAGANGA 480  
GGTCTTGCCG AGGAAGTGGC AGCTAAGCTG ATACCTGATA TGCACWAGKC AGCCARGYGG 540  
AGACAGGCAA GGAAGAAGCT TGTTTTGAGG ACAGAAATTT CTAGATCACT CAGCACCATC 600  
50 TGGCTTTTGG GCCTTTTGT TTTATTTGT TTTTGAGACG GGGTCTCGCT CTGTCGCCCA 660  
N 661

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(2) INFORMATION FOR SEQ ID NO: 17:

60 (i) SEQUENCE CHARACTERISTICS:



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- (A) LENGTH: 553 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGCACAGGGC TATTTGCCCC TCTCTCCACA TGACAGAACT GCTCTAAGTT TCTTTGCTGC 60  
TCTTCTCAGC TGTCAGACGG CTTGCTGCTT GTTTTCCACA CCACCATGTC TATCTTTGC 120  
TGTCCCTWAC TCTGCCTGTT TTTTTCCTTT TGTATTTCTT CTGGCTCTTG TCCCTTTTCC 180  
CACGTGTCWC AGCTTTCCTT TATTGCCACT TTCAGTCAGA GCAGTCCTGT GCTTCTGGTG 240  
CCGGCATAACA ATACTTACTT GAGTTTCTTG GCTTTTCTTG ACTGTGCATC TCTTACTTCA 300  
ACATAGGAAT AGCCTGTCAT AGAATTTCTC CAGTTCAGG GCTCAAGAGG GAGAGTGCCA 360  
GAAAATTGAG ACTGTTTTCC CTGTCTTGGA TTGAATTCAT AAAGCAAAC CAGTGTGTTGT 420  
GTGAGGGTTT GCTGTGTCAT GCCTATAGGT TGTGTGGGTG CAAACCTATA GAATCCAGCC 480  
TGCGAAAAGA AAGRAACCAG AGAATANCAG CATCAGAACA ATGCTTGACA TCATTCTCA 540  
ATCAAGCAGT CCA 553

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(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 869 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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GGCACGAGCT GCCAACACTG AGGTCTTCGT GGCTTCTCAC ATCTAGATGT ATCCCTCTCA 60  
AATCTATCCT CTATCCAGGC ACCAGATTGA GGTATCTAAA ATGTCAACTT TCCAGTTACT 120  
CCTTCTTATA CTAGCCCAAT CAACTTACAA GATAAAGTCC AAGCCCCTTC ATATGACAAA 180  
CCACACCCTG CTAACTCTC CAGGTTTGAA TCCTTCATCT CCTACTTTAA ACTTTAAAC 240  
CCAGCAGCAC GAAAGTGTCT CCTATGCATG TTGCCATATG CGTCTCTCC ATCATGCATT 300  
TGCCTGAGCA AGATGTCTTG AGTTAACATC TTATCTTTA AGACTCATTG TGGTGGTAGA 360  
CAGCCTTTAA TAACGGATCC TTGGCCAGGC ACAGTGACTC ACACCTGTAA TCCAGAACT 420  
TTGAAAGGCC AAAGAAGGAA GAAAGCTTGA GGCCAGTAGT TTGAGACCAG CCTGGGAAAC 480  
AGAGAGATAT CCCATCTGTA CAAAAATTT AAAAAATAT TAGCAGGGAG TAGTGGCATG 540  
CACAAGTGGT CCCAGCTCCA TGGGAGASTG AGGTAGGAAC ATCACTTGAG CCCAGGAAGT 600

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276

CAAGGCTGCA GTGAACCATG ATCAGAACAT TGCANTCCAG CTTGGGTAAC AGAGTGAGAC 660  
CTTAGGTCAG AAAAATGAAT AAATAAGCAT AAAATTTTAA AAACCTAGCC AGGCATGGTG 720  
5 GCACACATCT GTGGTCCCTG CTACTTAGGA GGCTGAGGTG AGAGGATCCT TGAGCCCAGG 780  
AGGTCAACAC TACAGTGAGC TATGATTGTG CCACTAAACT CCAACCTGGG TGAAAAAGCA 840  
AAACCCTGCC AAAAAAAAAA AAAAAAAT 869  
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(2) INFORMATION FOR SEQ ID NO: 19:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 959 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGCGAGCCGA GATCGTGCCA TTGCACTCCA GCCTGGGCAA CAAGAGTGAA ACTCTGTCTC 60  
25 AAAAAAAAAA AATTATAATA CTATATGCCA TAAATGACA TTTCATATTT AAAGAGTTTT 120  
TTAAACTCT TGTATTCACTA TGCCATAATT TGAAACCCTA TTTCAGTGAA TGAGAATGGT 180  
30 ATCTGTTGTC CTCATTTTTT CATTTTTATC CTTAACAATT TCCACCACAG CCAGTGCATA 240  
TAATGGCAAT GACACCCAGG GATGGAATGA TAAGTCCAT CRCMGCTCAG TCAAGACGCA 300  
GACTTGATGT GGCCCCAACA ACAGTCAATA ATGGAGTCTC CAAAATAAAG CTCTATAGGA 360  
35 AAGGTAAATA CCCGCTGCAC AAGAAACCAC AGCATCTAGG TTCTAACCCC ATCTCTATGA 420  
AGAGCTTGCT GGGAGAGTTT TGACATTWAA CAATCTGTCT GATKGCCAAT TTTYTTCTTC 480  
40 TATAAATGA TAATGTTKGA YTCAAAGATC CAAAGTCAAT TCATGGTCTA AAACCTAATG 540  
ATTTTTTTAG GTTTTGKGAC ATTTCAGTGT AACTGTAGT AATTTATATC TTATTTTCCC 600  
ACTAATTTAG AAAAATATYT AAATGATCCT TAATTGGCAA TGGGTCCTAA GAATTTTGTT 660  
45 TTAAATCCCT GTTACCCAAA AGAGCCCTTT TTTGTATCTC GCAGTAGTTA CAAGGATCTT 720  
TCTAAATCTT AAAAAAAAAA AAAAAAGAAA GAAAGAAAAG AAAAGAAAAA AAGTCAGCCG 780  
50 GGCGTGGTGG CTCATGCCTG TAATCCCAGC ACTTTGGGAC CAAGGTGGAC AGATCACGAG 840  
GTCAGGAGAT GGAGACCATC CCGGCCAACA TGGAGAAACC CTGTCTCTAC TAAAAAAAAA 900  
AAAAACTCGA GGGGGGCCCG GTACCCAATN CGCCGGCTAG TGGTCGTAAA ACAATCAAA 959  
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(2) INFORMATION FOR SEQ ID NO: 20:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CGGGGCAGGG CTGTGTGGCA CCGCCAGGGA GCGGGCCAC CTGAGTCACT TTATTGGGTT 60  
10 CAGTCAACAC TTTCTTGCTC CCTGTTTCT CTCTGTGGG ATGATCTCAG ATGCAGGGGC 120  
TGGTTTGGG GTTTTCCTGC TTGTGCCAAG GGCTGGACAC TGCTGGGGG CTGGAAGCC 180  
15 CCTCCCTCC TGTCTTCTG TGGCTCCAT CCCCTCATGG GTGCTGCCAT CCTTCCTGGA 240  
GAGAGGGAGG TGAAAGCTGG TGTGAGCCCA GTGGGTCCC GCCACTCAC CCAGGAGCTG 300  
GCTGGCCAG GACCGGGAGA GGGAGCACTG CTGCCCTCCT GGCCCTGCTC CTTCCGAGT 360  
20 TAGGGGTGGA CCGAGCCTCG CTTCCCCAC TGTCTGGAG GGAAGGGAA GGAGGGGTC 420  
TTCAGGCTGG AGCCAGGCTG GGGGTGCTGG GTGAGAGAT GAGATTAGG GGTGCCTCA 480  
25 TGGGTGGGC AGGCCTGGG TGAAATRAGA AAGGCCAGA ACGTGCAGGT CTGCGGAGG 540  
GAAGTGCTT GAGTGAAGGA GGGGACCCC ATCCTGGGG ATGCTGGAG TGAGTGAGT 600  
AGATGGCTGA GTGAGGTTA TGGGAGCCT GAGGTTTAT GGGCCTGTG ATCCCTTCT 660  
30 CCGGCCCCA GCCTGCCTCC CTCCTGCCG CCTGGCCAC AGGTCTCCT CTGGTCCCTG 720  
TCCCTCTGGT GGTGGGGAT GGAGCGGAG CAAGGGGTG AATGGGCTG GGTCTGTCT 780  
35 TCTACAGGC ACCCCGAGT CCTCAGTGGT TGCCTGGGA GCCGACGGG GCTCCTGAGG 840  
GGTACAGTT GGTGGGCC TCCCTGAGG TCTGGGTCA GGCTTTGGCT CTGCTGCCTC 900  
TCAGTCACCA AGTCACCTCC CTCTGAAAT CCAGTCCCT CTTGGATGT CCTGTGAGT 960  
40 CACTCTGGC CTGGCTGTC TCCCTCCTCA GCTTCTGTT CCTGGACAA GGTCAAGCC 1020  
AGGATGGCC CAGGCCTGG ATCCCCACC CCAGGACCC CAGGCCCTT CCCCTGCTG 1080  
45 TTTGCGGGG GCAGGGCAGA AATGGACTC TTTTGGGTCC CCGAGGTGG GTCCCTCCC 1140  
AGCCCTGCAT CTCCTGTGCC STAGACCTG TCCCAGAGG AGGGGCTTG ACCACAGGA 1200  
CGTGTGGTGG CGCCTGGCAC TCAGGACCC CCAGCTGCC CAGCCCTGG CTCTGGGCA 1260  
50 TCTCTCCCT CTGTCCCGA AGATCTGCG CTCTAGTGC TTTGAGGG TTCCATCAT 1320  
CCCTCCCTGA TATTGTATTG AAAATATTAT GCACACTGTT CATGCTTCTA CTAATCAATA 1380  
55 AACGCTTTAT TTAAAGCCAA AAAAAAAAA AAAAAACTCG AGGGGGGGCC CGTACCCAAT 1440  
TCGCCA 1446

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## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1471 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CAAAAAATAA TAATGATAAT TTAAAATAAA TAAGTAACTA ATAAAAAGAT TTTATATCCC 60  
AGTCTTATGA TGTGGTGG CAAGGCTAGA TAAAAAGATG TTAGAATGAA AGAACATATT 120  
15 TTTAGTGATA TGTAAATGAA GGATTCTACA ATAGTCATAT ATTTTATAT GAATGAATGT 180  
TGGGTGGGC TGGAGAGGTA TGTGTGTGTA AATATAAAGG TCTCACATTC AGAGTATAGC 240  
20 TCTGAAATAA TGGAACTCAT GTCTACAATT CAACATGCAT CTGTATAGTT ACATCTCATG 300  
TAAATATACA CAGACATATT TTGCAGCCAG TAATTGACAG TTAATGTCCA AACAGGTGA 360  
TTGATAGGTA ACAGAAATTA GATAACCACC AATTTGCCC AAGAGAAAGA CTAGAAGGAC 420  
25 TAAAAGCAGT TGAATGTATG GTACTGACAT TGTCTAAGC AGTCTGATAA CCAGTTTATT 480  
GAAACGTGTG CATTAACAGA GAATTTAATT TTAAACCCAT AATTCTCCT ATCCATTAAA 540  
30 ATATTATAAT TGTTAGTAGT ATGAAACCAA CAGGAAATGT TTTTAATCA TTTAGTGAGG 600  
TGATTCATTT GTTTCATGGG CAAACACTAT CCAGGAAAAG CCTTGCTTGC CTGTTCCCA 660  
AAGAGCTCTA AGAAATAGAA TCAAGTGTA AATGGTTCAG ACCATTCAGG ATTTCTTGTC 720  
35 ACTCTTCTCA ACCCCGATCT TCCTGTTATT ACTGATGTTT GAAACCCTGT CATTAGCCCC 780  
GGCCTGGTTA AAGCCCCCTCA GAGTCACCTC TCATTCATAG CAATAGAATT CAACCCCAAG 840  
40 TGGTTGATGG TGTCCCGAGC ACAGCCGAGA GACCTGATCT CTGGATTGAG TGCTTTTAGC 900  
TCTTCGAGTT TACCCTAAGA TACCTTCGGG CAATATTTTT AACCAACCCA AAAGCTCTTC 960  
AGGTCATTTT TGAAGAGGAC AAGGGAATC TTGGCTTGA ACACCATTTT TGGGCTCTTG 1020  
45 CTACTGAATG AATCAGAAAG GAATTTTTC TGAAGAGCAT TAGAAAGTAA AGGAGATGTT 1080  
AAAATAAGTT CTTGAAGTAT GTTTTATATT TATCTAAAAC ACTGATTTTA AAAGTTTACA 1140  
50 TTCAAATGTG TATTCAAAG AAGTACTGAT TTGTAATTAT TATAGTTTGT GTGTATCATC 1200  
CCCTTTTAAC CGTGCCTAAC AACTGTACTT AAATTTTGT TTCTAGTGT AACAAATGTT 1260  
TCCCATAGA TTTCTAGAG CCAAATAATG GGAGTGAAAA ATTCCTTAAG TGTATATAA 1320  
55 GAAATATAT TAGAAATCA GCTTTGATT ATACGATTTT TAAATATAC TAATACAGAA 1380  
TCCTCAGTAA TATGTTTTGA ATTGGATTTT TTCTCAGAAC TGTACATAA TAAATAATAC 1440  
60 ATCAACCAGA AAAAAAAAAA AAAAAAATTN C 1471

## 5 (2) INFORMATION FOR SEQ ID NO: 22:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1402 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

15 AGGGACGTCT TGCCTGAGGA GATGCCCAT TCTGTCCTGG RTTACCCTCA CTGCGTGGTG 60  
CATGAGCTGC CAGAGCTGAC GCGGAGAGT TTGAAGCAG GTGACAGTAA CCAATTMTGC 120  
TGGAGGAACC TCTTTTCTTG TATCAATCTG CTTCGGATCT TGAACAAGCT GACAAAGTGG 180  
20 AAGCATTCAA GGACAATGAT GCTGGTGGTG TTCAAGTCAG CCCCATCTT GAAGCGGGCC 240  
CTAAAGGTGA AACAAGCCAT GATGCAGCTC TATGTGCTGA AGCTGCTCAA GGTACAGACC 300  
25 AAATACTTGG GCGGCAGTG GCGAAAGAGC AACATGAAGA CCATGTCTGC CATCTACCAG 360  
AAGGTGCGGC ATCGGCTGAA CGACGACTGG GCATACGGCA ATGATCTTGA TGCCCGGCCT 420  
TGGGACTTCC AGGCAGAGGA GTGTGCCCTT CGTGCCAACA TTGAACGCTT CAACGCCCCG 480  
30 CGCTATGACC GGGCCACAG CAACCCTGAC TTCCTGCCAG TGGACAAC TGCTGCAGAGT 540  
GTCCTGGGCC AACGGGTGGA CCTCCCTGAG GACTTTCAGA TGAACATGA CCTCTGGTTA 600  
35 GAAAGGGAGG TCTTCTCAA GCCCATTTCC TGGGAAGAGC TGCTGCAGTG AGGCTGTTGG 660  
TTAGGGGACT GAAATGGAGA GAAAGATGA TCTGAAGGTA CCTGTGGGAC TGTCCTAGTT 720  
CATTGCTGCA GTGCTCCCAT CCCCCACCAG GTGGCAGCAC AGCCCCACTG TGTCTTCCGC 780  
40 AGTCTGTCTT GGGCTTGGGT GAGCCCAGCT TGACCTCCCC TTGGTTCCCA GGGTCTTGCT 840  
COGAAGCAGT CATCTCTGCC TGAGATCCAT TCTTCCTTTA MTCCCCCAM CCTCCTCTCT 900  
45 TGGATATGGT TGGTTTGGC TCATTTTACA ATCAGCCCAA GGYTGGGAAA GCTGGAATGG 960  
GATGGGAACC CCTCCGCCGT GCATCTRAAT TTCAGGGGTC ATGCTGATGC CTCTCGAGAC 1020  
ATACAAATCC TTGCCTTTGT CAGCTTGCAA AGGAGGAGAG TTTAGGATTA GGGCCAGGGC 1080  
50 CAGAAAGTCG GTATCTTGGT TGTGCTCTGG GGTGGGGTG GGTGTTTCT GATGTTATTC 1140  
CAGCCTCTG CTACATTATA TCCAGAAGTA ATTGCGGAGG CTCCTTCAGC TGCCTCAGCA 1200  
55 CTTTGATTTT GGACAGGGAC AAGGTAGGAA GAGAAGCTTC CCTTAACCAG AGGGGCCATT 1260  
TTTCCTTTTG GCTTTCGAGG GCCTGTAAAT ATCTATATAT AATTCTGTGT GTATTCTGTG 1320  
TCATGTTGGG GTTTTTAATG TGATTGTGTA TTCTGTTTAC ATTAAAAAGA AGCAAAAATA 1380  
60

ATAAAAAAAAAA AAAAAAAAAA CT

1402

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(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1047 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

15

GGCACAGGGG ACTACAGGCA CCCACGACCA TACCCAGCTA ATTTTGTAT TTTTGTAG 60

AGATGGGGTT TCACGATGTC GCCCAGGCTG GTCTTGAAGT CCTGGGCTTG AGCGATCTTC 120

20 CCATCTTTCC ATCTTGGCCT CCTAAAGTGC TGGGACTGCA GGCATGAGCC ACCATGCCCA 180

GCCAAGATTG TTATTGATTA CCATGTTGCT TCAAGAAGCC AAGCCAGTTT CCAATATTCC 240

CCATTTGCTG GAGTCTTGGT ACTTTGGGTA GAAGCAACTG GTAAATTGTT AATTGGAACA 300

25

NTTGGTGGTG TAGATAACCA CGTATGGCCA AACCTAGAGC ATCTAGGCTC ACAATTACTA 360

TCCTGACTTG ATAACAAGTG TTCTGATATT AACCTGAAAA TGGGAATAAT GCCAAATCTG 420

30 TGTAACCTAA CATCTATATA CACAGTGGGG AGAACTGAAG TTATTAAACC TGGAACTCTT 480

GTGATCAAGG CTAACAGTAG TTATCTAAGA AGCAAAGGAC CTACAATTCT TAGACTTGGA 540

GTCATATTCT TTAAGGACGT GTTCTGAAAC TATATCAAGC ATCTGGTTTC CACGTATTTT 600

35

TCCCTCAGAA ATTATGAAGT ACAAGTAAAA ATGAAGGTAC AGGGTAAGAC ACATGCTGCT 660

TTCTTGCTCT TGAGTGGAGA CAGTTTTCCTA GCCATCTTAA CCCCTTWACA CAAAACAATT 720

40 TGTGTTTAT AGCAAATAAG TGAATCAACA TAATTTCAAT ATGATGTTTA TCCACCAGTA 780

CTTTCCTTTC AGCTTCTAGT CCCATAARTG GTTGTGAAG TCATCGGTTA CATTAGCCAA 840

GATAGGCCTA GACTTGAAGT CTAGAATGTT TTCCCACTA TATGCCAAAG TAGAATGTGG 900

45

GTATCTCAGG GTCATTTTGG TTGTTCAATT TCCACCTGT ACAGTTGTTA TGATTCACCT 960

TCCMTATGTG TCTAATAAAT CTTGTCCAT GAAATGATCA AAAAAAAAAA AAAAAAACT 1020

50 CGAGGGGGGG CCCGGTACCC AAATCGC 1047

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(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 990 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

5 TTGGAAGGG TCTAGCTCTT TCTCATTCAC CAACTATATT AGAAGCACTT GAGGGAAATT 60  
TACCACTCCA AATCCAAAGC AATGAACAGT CTTTCTGGA TGATTTTATT GCCTGTGTCC 120  
CAGGATCAAG TGGTGAAGG CTGCAAGGT GGCTTCAGCC AGATTCATAT GCGGATCCTC 180  
10 AGAAAACATC TTTGATCCTG GAATAAGGAT GATATTCGTT GTGGTTGGCC TACCACCATA 240  
ACTGTTCAAA CAAAAGACCA GTATGGGGAT GTGGTACATG TTCCAATAT GAAGGTAATT 300  
15 ATAATGGAT TAAATTAGCA GACATCTATA TACTGGCTGC AATGACTGAT AAAATTTTAG 360  
AAATGCCAAG TGCTGAGRGT CCATTTGTC TACCCTCTTT ATATAAAGG TGATGCTGAA 420  
AGTTTGTTTA AATGACTTGT TTATATTAAT TAGTCCCCAA GTGTCCAAGT TACACCTGTT 480  
20 TTTTGTGA GTTTGTTCTT TACATTTTGC TACCTGTAC GGGGACTCAA AGGAGGGATA 540  
AGAAAGTATC CATCTAAAGA GTGCTAGACA CATACAGTGA AGCCCTCAA TATGTATTGA 600  
25 TTGAATAAAT GCATGAAAGA ATACATTTT AAATTTTGTG TATAGTTTGT AAAGACTCAA 660  
GTACGTTCTG TGTTTGGTAT TACTGAAACC ACATTTTAAA AATAACACTC ATTAAGTTAG 720  
AAATATATGA GTTTAGATTG TAAAAGAATG AGGAATTGAA ATAGTTGTAT ACCATATTGA 780  
30 TGAATATAGA GTTTTATAGG TACCTCTTAC CTGAAATATT AATAATAATG TTTNCAGAGC 840  
ATATTATACA TAATTATTG TGATTAAATC TGTTAATATG AATATCTCAT TTAACCTTT 900  
35 TATTTCTGAA AAAATTATAT TGAATAAAT TTTATATAGG CAGTCCCAG CCCTTCTC 960  
CTTCAAAGTT GTCTTATAGA GTGATTGGTT 990

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(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 1208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TAATCGCTAC TATAGGGAAA GCTGGTCGCT GCAGGTACCG GTCCGGAATT CCGGGTCGAC 60  
CCACGCGTCC GAGCGAAATG GCGCCTCCGG CCCC CGGCC GGCCTCCGGC GGCTCCGGG 120  
55 AGGTAGACGA GCTGTTGAC GTAAAGAACG CCTTCTACAT CGGCAGCTAC CAGCAGTGCA 180  
TAAACGAGGC GCASGGGTGA AGCTRTCAAG CCCAGAGAGA GACGTGGAGA GGGACGTCTT 240  
60 CCTGTATAGA GCGTACCTGG CGCAGAGGAA GTTCGGTGTG GTCCTGGATG AGATCAAGCC 300

CTCCTCGGCC CCTGAGCTCC AGGCCGTGCG CATGTTTGCT GACTACCTCG CCCACGAGAG 360  
TCGGAGGGAC AGCATCGTGG CCGAGCTGGA CCGAGAGATG AGCAGGAGCK TGGACGTGAC 420  
5 CAACACCACC TTCCTGCTCA TGGCCGCCTC CATCTATCTC CACGACCAGA ACCCGGATGC 480  
CGCCCTGCGT GCGCTGCACC AGGGGGACAG CCTGGAGTGC ACAGCCATGA CAGTGCAGAT 540  
10 CCTGCTGAAG CTGGACCGCC TGGACCTCGC CCGGAAGGAG CTGAAGAGAA TGCAGGACCT 600  
GGACGAGGAT GCCACCCTCA CCCAGCTCGC CACTGCCTGG GTCAGCCTGG CCACGGGTGG 660  
TGAGAAGCTG CAGGATGCCT ACTACATCTT CCAGGAGATG GCTGACAAGT GCTCGCCCAC 720  
15 CCTGCTGCTG CTCAATGGGC AGGCGGCCTG CCACATGGCC CAGGGCCGCT GGGAGGCCGC 780  
TGAGGGCCTG CTGCAGGAGG CGCTAGACAA GGATAGTGGC TACCCRGAGA CGCTGGTCAA 840  
20 CCTCATCGTC CTGTCCCAGC ACCTKGGCAA GCCCCCTGAG GTGACAAACC GATACCTGTC 900  
CCAGCTGAAG GATGCCACCA GGTCCCATCC CTTTCATCAAG GAGTACCAGG CCAAGGAGAA 960  
CGACTTTGAC AGGCTGGTGC TACAGTACGC TCCCAGCGCT GAGGCTGGCC CAGAGCTGTC 1020  
25 AGGACCATGA AGCCAGGACA GAGGCCAGGA GCCAGCCCTG CAGCCCTCCC CACCCGGCAT 1080  
CCACCTGCAT CCTCTGGGG CAGGAGCCCA CCCCAGCAC CCCCATCTGT TAATAAATAT 1140  
30 CTCAACTCCA RGGTGTCCA CCTGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1200  
AAAAAAA 1208

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(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 1922 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTGCTGCGCT ACTGAGCAGC GGCATGGAGG ACTCTGAAGC ACTGGGCTTC GAACACATGG 60  
GCCTCGATCC CCGGCTCCTT CAGGCTGTCA CCGATCTGGG CTGGTCGCGA CCTACGCTGA 120  
50 TCCAGGAGAA GGCCATCCCA CTGGCCCTAG AAGGGAAGGA CCTCCTGGCT CGGGCCCGCA 180  
CGGGCTCCGG GAAGACGGCC GCTTATGCTA TTCCGATGCT GCAGCTGTTG CTCCATAGGA 240  
55 AGGCGACAGG TCCGGTGGTA GAACAGGCAG TGAGAGGCCT TGTTCCTGTT CCTACCAAGG 300  
AGCTGGCACG GCAAGCACAG TCCATGATTC AGCAGCTGGC TACCTACTGT GCTCGGGATG 360  
TCCGAGTGGC CAATGTCTCA GCTGCTGAAG ACTCAGTCTC TCAGAGAGCT GTGCTGATGG 420  
60



	AGAAGCCAGA TGTGGTAGTA GGGACCCCAT CTCGCATATT AAGCCACTTG CAGCAAGACA	480
	GCCTGAAACT TCGTGACTCC CTGGAGCTTT TGGTGGTGA CGAAGCTGAC CTTCTTTT	540
5	CCTTTGGCTT TGAAGAAGAG CTCAAGAGTC TCCTCTGTCA CTGCCCCGG ATTTACCAGG	600
	CTTTCTCAT GTCAGCTACT TTAAACGAGG ACGTACAAGC ACTCAAGGAG CTGATATTAC	660
	ATAACCCGGT TACCCTTAAG TTACAGGAGT CCCAGCTGCC TGGGCCAGAC CAGTTACAGC	720
10	AGTTTCAGGT GGTCTGTGAG ACTGAGGAAG ACAAAATTCCT CTGCTGTAT GCCCTGCTCA	780
	AGCTGTCAAT GATTCGGGGC AAGTCTCTGC TCTTTGTCAA CACTCTAGAA CGGAGTTACC	840
15	GGCTACGCCT GTTCTTGGA CAGTTCAGCA TCCCCACCTG TGTGCTCAAT GGAGAGCTTC	900
	CACTGCGCTC CAGGTGCCAC ATCATCTCAC AGTTCAACCA AGGCTTCTAC GACTGTGTCA	960
	TAGCAACTGA TGCTGAAGTC CTGGGGGCCC CAGTCAAGGG CAAGCGTCGG GGCCGAGGGC	1020
20	CNAAAGGGGA CAAGGCCTCT GATCCGGAAG CAGGTGTGGC CCGGGGCATA GACTTCCACC	1080
	ATGTGTCTGC TGTGCTCAAC TTTGATCTTC CCCCACCCC TGAGGCCTAC ATCCATCGAG	1140
25	CTGGCAGGAC AGCAGCGCT AACAACCCAG GCATAGTCTT AACCTTTGTG CTTCCACGG	1200
	AGCAGTTCCA CTTAGGCAAG ATTGAGGAGC TTCTCAGTGG AGAGAACAGG GGCCCCATTC	1260
	TGCTCCCCTA CCACTTCCGG ATGGAGGAGA TCGAGGGCTT CCGCTATCGC TGCAGGGATG	1320
30	CCATGCGCTC AGTGAATAAG CAGGCCATTC GGGAGGCAAG ATTGAAGGAG ATCAAGGAAG	1380
	AGCTTCTGCA TTCTGAGAAG CTTAAGACAT ACTTTGAAGA CAACCTAGG GACCTCCAGC	1440
35	TGCTGCGCA TGACCTACCT TTGCACCCCG CAGTGGTGAA GCCCCACCTG GGCCATGTC	1500
	CTGACTACCT GGTTCCTCCT GCTCTCCGTG GCCTGGTRCG CCCTCACAAG AAGCGGAAGA	1560
	AGCTGTCTTC CTCTGTAGG AAGGCCAAGA GAGCAAAGTC CCAGAACCCA CTGCGCAGCT	1620
40	TCAAGCACA AGGAAAGAAA TTCAGACCCA CAGCCAAGCC CTCCTGAGGT TGTGGGCCT	1680
	CTCTGGAGCT GAGCACATTG TGGAGCACAG GCTTACACCC TTCGTGGACA GGCGAGGCTC	1740
45	TGGTGTCTAC TGCACAGCCT GAACAGACAG TTCTGGGGCC GGCAGTGCTG GGCCCTTTAG	1800
	CTCCTTGGA CTTCCAAGCT GGCATCTTGC CCCTTGACAA CAGAATAAAA ATTTAGCTG	1860
	CCCCAAAAA AAAAAAAAAA AAAAAAATC GAGGGGGGC CCGTACCCAA TTCGCCCTAT	1920
50	AA	1922

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(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1951 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

5	TCGTCCCCAG AGCGGGCTGA GCCCCAGGCG SAGGGTGGCG GGGGAGCCTG GGGGAGCCGC	60
	CGCCACCTCC ACGGGCCTCT CTGAGCTCGG ACACCAGCGC CCTGTCTTAT GACTCTGTCA	120
10	AGTACACGCT GGTGGTAGAT GAGCATGCAC AGCTGGAGCT GGTGAGCCTG CGCCGTGCTT	180
	CGGAGACTAC AGTGACGAGA GTGACTCTGC CACCGTCTAT GACAACTGTG CCTCCGTCTC	240
	CTCGCCCTAT GAGTCGGCCA TCGGAGAGGA ATATGAGGAG GCCCCGCGGC CCCAGCCCCC	300
15	TGCCTGCCTC TCCGAGGAAC TCCACGCTG ATGAACCCGA CGTCCATTTC TCCAAGAAAT	360
	TCCTGAACGT YTTTCATGAGT GGCCGCTCCC GCTCCTCCAG TGCTGAGTCC TTCGGGCTGT	420
20	TCTCTGCAT CATCAACGGG GAGGAGCAGG AGCAGACCCA CCGGGCCATA TTCAGGTTTG	480
	TGCCTCGACA CGAAGACGAA CTTGAGCTGG AAGTGATGA CCTCTGCTA GTGGAGCTCC	540
	AGGCTGAAGA CTACTGGTAC GAGGCCTACA ACATGCGCAC TGGTGCCCGG GGTGTCTTTC	600
25	CTGCCTATTA CGCCATCGAG GTCACCAAGG AGCCCGAGCA CATGGCAGCC CTGGCCAAAA	660
	ACAGTGACTG GGTGGACCAG TTCCGGGTGA AGTTCTGGG CTCAGTCCAG GTTCCCTATC	720
30	ACAAGGGCAA TGACGTCTC TGTGCTGCTA TGCAAAGAT TGCCACCACC CGCCGGCTCA	780
	CCGTGCACAT TAACCCGCCC TCCAGCTGTG TCCTGGAGAT CAGCGTGCGG GGTGTGAAGA	840
	TAGGCGTCAA GGCCGATGAC TCCCAGGAGG CCAAGGGGAA TAAATGTAGC CACTTTTTC	900
35	AGTTAAAAA CATCTCTTTC TCGGATATC ATCCAAAGAA CAACAAGTAC TTTGGGTTC	960
	TCACCAAGCA CCCCCTGAC CACCGGTTTG CCTGCCAGT CTTGTGTCT GAAGACTCCA	1020
40	CCAAAGCCCT GGCAGAGTCC GTGGGAGAG CATTCCAGCA GTTCTACAAG CAGTTTGTGG	1080
	AGTACACCTG CCCCACAGAA GATATCTACC TGGAGTAGCT GTGCAGCCCC GCCCTCTGCG	1140
	TCCCCCAGCC CTCAGGCCAG TGCCAGGACA GCTGGCTGCT GACAGGATGT GGCAGTCTT	1200
45	GAGGAGGGGC ACCTGCCACC GCCAGAGGAC AAGGAAGTGG GGCGCTGGCC CAGGGTAGGG	1260
	GAGGGTGGGG CAATGGGAG AGGCAAATGC AGTTTATGT AATATATGGG ATTAGATTCA	1320
50	TCTATGGAGG GCAGAGTGGG CTGCCTGGG ATTGGGAGG ACAGGGCTTG GGGAGCAGGT	1380
	CTCTGGCAGA GAAGGATGTC CGTCCAGGA GCACACGGC CTGCCCCATC CTGGGCCTTA	1440
	CCTCCCCTGC CAGGGCTCGG GCGCTGTGGC TCCTGCCTTG ATGAAGCCCG TGTCTGCCT	1500
55	TGATGAAGCC TGTGCCACCT GCAAGTGCCC GCCCTGCCCC TGCCCCAACC CCCACCGAAG	1560
	AGCCCTGAGC TCAGGCTGAG CCCAGCCACC TCCCAAGGAC TTTCCAGTGA GGAAATGGCA	1620
60	ACACGTGGAG GTGAAGTCCC TGTCTCAGC TCCGTCTCT CCGGGGCTTC TGGGTGGCTC	1680

CTGCCACTGA CCTCACCAGC ATGCTGGCCT GTGGCAGGCC TAGGACCTCA GCGGGGAGG 1740  
 AGGAGCTGCC GCAAGGCCCT GTCCCAGCAG AAGAGGGAGG CTTCTGACT GACACAGGCC 1800  
 5 AGCCCCATCT TGGTCTGTC ACCCTGGCCC CAACTATTAA AGTGCCATT TCTGTCAAAA 1860  
 AAAAAAAAAA AAAATCGGGG GGGGCCCGGA ANCCAATTTC CCCCAAAAG GGGGTTATA 1920  
 10 AAAATCCCN GGCNGTGT TTAATAATTC G 1951

15 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3989 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

25 GGCACAGGCC GCAGGNACC TATGGCGCA TATAGGTTGT AATGAACTG TAGTCTCAGT 60  
 TGAAGCCTA GACATGAAAT GGGTCAGTGA GCAAGGCTCT ATTCCTAGTC TCCAGCCATG 120  
 CCTGTGGAAC CTGARCCRC TCTCAGCACA TTGGACCCAG GCAGATGYAA AAAATTCACA 180  
 30 GAACTATGAT TTGACTCAA GGGTTGTAG ATTCTCCTCT TCATTCTAAT TTCAGTGTCT 240  
 AAAATCTTG CATCCRTGAA CGAGCTGGGC ATTTGATGAG ACAGGGCYGA ATACTGCAGT 300  
 35 TTCTCTCTA GAAATCATCT GGGGCATTTT CTTTGAAGT ATGGGAACAA TAGGCATAA 360  
 CTGTTTGAC AAACCTGGGA TAARTGATTT TGGGATAACG ATCTACCAGA ATGGGGATAT 420  
 TTCACCCTTG GTTCTGAGAT GCAAACCAA GAATATCATG ACCAGCTTTC AGGCCTCCTG 480  
 40 AAGTATATCT CTCACATTGT CCTGTCTCA TGCTGAGGAG CCTGAGATCC CTGTGTGGG 540  
 ATTAGACAGT GGAAGTTAT GGGTGTAGGT GAATTGGCTT ATTTGTCTG TCCCTGTCTG 600  
 45 AATGTATTGC AGGAAYTAA AAGGACCAAG AAGAGGAAGA AGACCAAGGC CCACCATGCC 660  
 CCAGGCTCAG CAGGGAGCTG CTGGAGGTAG TAGAGCCTGA AGTCTTGCAG GACTCACTGG 720  
 ATAGATGTTA TTCAACTCCT TCCAGTTGTC TTGAACAGCC TGAATCCTGC CAGCCCTATG 780  
 50 GAAGTTCTT TTATGCATTG GAGGAAAAAC ATGTTGGCTT TTCTCTTGAC GTGGGAGAAA 840  
 TTGAAAAGAA GGGGAAGGGG AAGAAAAGAA GGGGAAGAAG ATCAAAGAAG GAAAGAAGAA 900  
 GGGGAAGAAA AGAAGGGGAA GAAGATCAAA ACCCACCATG CCCAGGCTC AGCAGGGAGC 960  
 TGCTGGATGA GAAAGRCCT GAAGTCTTGC AGGACTCACT GGATAGATGT TATTCAACTC 1020  
 60 CTTCAAGTGT GTTGAAGTGT GTGACTCATG CCAGCCCTAC AGAAGTGCCT TTTATGTATT 1080

	GGAGCAACAG CATGTTGGCT TGGCTGTTGA CATGGATGAA ATTGAAAAGT ACCAAGAAGT	1140
	GGAAGAAGAC CAAGACCCAT CATGCCCCAG GCTCAGCAGG GAGCTGCTGG ATGAGAAAGA	1200
5	GCCTGAAGTC TTGCAGGACT CACTGGATAG ATGTTATTCG ACTCCTTCAG GTTATCTTGA	1260
	ACTGCCTGAC TTAGGCCAGC CCTACAGCAG TGCKGTTTAC TCATTGGAGG AMCAKTACCT	1320
	TGGCTTKKCT CTTGACGTGG ASAAATTGAA AAGAAGGGGA AGGGGAARAA AAGAAGGGGA	1380
10	AGAAGATCAA AGAAGGAAAG AAGAAGGGGA AGAAAAGAAG GGAAGAAGA TCAAAACCCA	1440
	CCATGCCCCA GGCTCAGCAG GGAGCTGCTG GATGAGAAAAG GGCCTGAAGT CTTGCAGGAC	1500
15	TCACTGGATA GATGTTATTTC AACTCCTTCA GGTGTCTTTG AACTGACTGA CTCATGCCAG	1560
	CCCTACAGAA GTGCCTTTTA YRTATTGGAG CAACAGYGTG TTGGCTTGGC TGTTGACATG	1620
	GATGAAATTG AAAAGTACCA AGAAGTGGAA GAAGACCAAG ACCCATCATG CCCCAGGCTC	1680
20	AGCAGGGAGC TGCTGGATGA GAAAGAGCCT GAAGTCTTGC AGGACTCACT GGATAGATGT	1740
	TATTCGACTC CTTTCAGGTTA TCTTGAAGT CCGTACTTAG GCCAGCCCTA CAGCAGTGCT	1800
25	GTTTACTCAT TGGAGGAACA GTACCTTGGC TTGGCTCTTG ACGTGGACAG AATTAAAAAG	1860
	GACCAAGAAG AGGAAGAAGA CCAAGGCCCA CCATGCCCCA GGCTCAGCAG GGAGCTGCTG	1920
	GAGGTAGTAG AGCCTGAAGT CTTGCAGGAC TCACTGGATA GATGTTATTTC AACTCCTTCC	1980
30	AGTTGTCTTG AACAGCCTGA CTCCTGCCAG CCCTATGGAA GTTCCTTTTA TGCATTGGAG	2040
	GAAAAACATG TTGGCTTTTC TCTTGACGTG GGAGAAATTG AAAAGAAGGG GAAGGGGAAG	2100
35	AAAAGAAGGG GAAGAAGATC AAMGAAGRAA AGAAGAAGGG GAAGAAAAGA AGGGGAAGAA	2160
	GATCAAAACC CACCATGCCC CAGGCTCAAC GCGTGTCTGA TGAAGTGA AGAGCSTGAA	2220
	GTCTTACAGG ACTCACTGGA TAGATGTTAT TCGACTCCGT CAATGTACTT TGAACCTCT	2280
40	GACTCATTCC AGCACTACAG AAGTGTGTTT TACTCATTG AGGAACAGCA CATCAGCTTC	2340
	GCCCTTTACG TGGACAATAG GTTTTTTACT TTGACGGTGA CAAGTCTCCA CCTGGTGTTC	2400
45	CAGATGGGAG TCATATTCCC ACAATAAGCA GCCCTTASTA AKCCGAGAGA TGTCATTCTC	2460
	GCAGGCAGGA CCIATAGGCA MGTGAAGATT TGAATGAAAG TACAGTTCCA TTTGGAAGCC	2520
	CAGACATAGG ATGGGTCACT GGGCATGGCT CTATTCCTAT TCTCAAACCA TGCCAGTGGC	2580
50	AACCTGTGCT CAGTCTGAAG ACAATGGACC CACGTTAGGT GTGACACGTT CACATAACTG	2640
	TGCAGCACAT GCCGGGAGT ATCAGTCRGA CATTTTAATT TGAACCACGT ATCTCTGGGT	2700
55	AGCTACAAAA TTCCTCAGG ATTTCATTTT GCAGGCATGT CTCTGAGCTT CTATACCTGC	2760
	TCAAGGTCAK TGTCACTTTT GTGTTTAGCT CATCCAAAGG TGTACCCTG GTTTCAATGA	2820
60	ACCTAACCTC ATTCTTTGTG TCTTCAGTGT TGGCTTGTTT TAGCTGATCC ATCTGTAACA	2880

	CAGGAGGGAT CCTTGGCTGA GGATTGTATT TCAGAACCAC CAACTGCTCT TGACAATTGT	2940
	TAACCCGCTA GRCTCCTTTG GTTAGAGAAG CCACAGTCCT TCAGCCTCCA ATTGGTGTCA	3000
5	GTACTTAGGA AGACCACAGC TAGATGGACA AACAGCATTG GGAGGCCTTA GCCCTGCTCC	3060
	TCTCRATTCC ATCCTGTAGA GAACAGGAGT CAGGAGCCGC TGGCAGGAGA CAGCATGTCA	3120
10	CCCAGGACTC TGCCGGTGCA GAATATGAAC AAYGCCATGT TCTTGAGAA AACGCTTAGC	3180
	CTGAGTTTCA TAGGAGGTAA TCACCAGACA ACTGCAGAAT GTRGARCACT GAGCAGGACA	3240
	GCTGACCTGT CTCCTTCACA TAGTCCATRT CACCACAAAT CACACAACAA AAAGGAGARG	3300
15	AGATATTTTG GGTTCAAAAA AAGTAAAAAG ATAATGTAGC TGCATTTCTT TAGTTATTTT	3360
	GARCCCCAAA TATTTCTCTA TCTTTTGTGTT GTTGTCATKG ATGGTGGTGA CATGGACTTG	3420
20	TTTATAGAGG ACAGGTCAGC TGTCTGGCTC AGTGATCTAC ATTCTGAAGT TGTCTGAAAA	3480
	TGTCTTCATG ATTAAATTC A GCCTAAACGT TTTGCCGGGA AACTGCAGA GACAATGCTG	3540
	TGAGTTTCCA ACCTYAGCCC ATCTGCGGGC AGAGAAGGTC TAGTTTGTCC ATCASCATTA	3600
25	TCATGATATC AGGACTGGTT ACTTGGTTAA GGAGGGTCT AGGAGATCTG TCCCTTTTAG	3660
	AGACACCTTA CTTATAATGA AGTATTTGGG AGGGTGGTTT TCAAAATTAG AAATGTCCTG	3720
30	TATTCRATG ATCATCCTGT AAACATTTTA TCATTTATTA ATCATCCCTG CCTGTGTCTA	3780
	TTATATATAT CATATCTCTA CGCTGGAAAC TTTCTGCCTC AATGTTTACT GTGCCTTTGT	3840
	TTTTGCTAGT GTGTGTTGTT GAAAAAAAAA ACATTCTCTG CCTGAGTTT AATTTTTGTC	3900
35	CAAAGTTATT TTAATCTATA CAATTAAG CTTTTCCTA TCAAAAAAAAA AAAAAAAAAA	3960
	AAAAAAAAA AAAAAGCGGA CGCGTGGGC	3989

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(2) INFORMATION FOR SEQ ID NO: 29:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3735 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

	CTGCTGTCG CTGGCTGGGC TCCGCAGCAG GCTTGGCCAG CSGCTGACGG GTCGGCGGGC	60
	GGGTTTGTGT GAACAGGCAC GCAGCTGCAG ATTTTATTCT GGTAGTGCAN CCCTCTCAAA	120
55	GGTTGAAGGA ACTGATGTAA CAGGGATTGA AGAAGTAGTA ATTCCAAAAA AGAAAACTTG	180
	GGATAAAGTA GCCGTTCTTC AGGCACTTGC ATCCACAGTA AACAGGGATA CCACAGCTGT	240
60	GCCTTATGTG TTTCAAGATG ATCCTTACCT TATGCCAGCA TCATCTTTGG AATCTCGTTC	300

	ATTTTACTG GCAAAGAAAT CCGGGAGAA TGTGGCCAAG TTTATTATTA ATTCATACCC	360
	CAAATATTTT CAGAAGGACA TAGCTGAACC TCATATACCG TGTTTAATGC CTGAGTACTT	420
5	TGAACCTCAG ATCAAAGACA TAAGTGAAGC CGCCTGAAG GAACGAATTG AGCTCAGAAA	480
	AGTCAAAGCC TCTGTGGACA TGTTTGATCA GCTTTTGCAA GCAGGAACCA CTGTGTCTCT	540
10	TGAAACAACA AATAGTCTCT TGGATTWTT GTGTTACTAT GGTGACCAGG AGCCCTCAAC	600
	TGATTACCAT TTTCAACAAA CTGGACAGTC AGAAGCATTG GAAGAGGAAA ATGATGAGAC	660
	ATCTAGGAGG AAAGCTGGTC ATCAGTTTGG AGTTACATGG CGAGCAAAAA ACAACGCTGA	720
15	GAGAATCTTT TCTCTAATGC CAGAGAAAA TGAACATTCC TATTGCACAA TGATCCGAGG	780
	AATGGTGAAG CACCGAGCTT ATGAGCAGGC ATTAAACTTG TACACTGAGT TACTAAACAA	840
20	CAGACTCCAT GCTGATGTAT ACACATTTAA TGCATTGATT GAAGCAACAG TATGTGCGAT	900
	AAATGAGAAA TTTGAGGAAA AATGGAGTAA AATACTGGAG CTGCTAAGAC ACATGGTTGC	960
	ACAGAAGGTG AAACCAAATC TTCAGACTTT TAATACCATT CTGAAATGTC TCCGAAGATT	1020
25	TCATGTGTTT GCAAGATCGC CAGCCTTACA GGTTTTACGT GAAATGAAAG CCATTGGAAT	1080
	AGAACCCTCG CTTGCAACAT ATCACCATAT TATTCGCCTG TTTGATCAAC CTGGAGACCC	1140
30	TTTAAAGAGA TCATCCTTCA TCATTTATGA TATAATGAAT GAATTAATGG GAAAGAGATT	1200
	TTCTCCAAAG GACCCGGATG ATGATAAGTT TTTTCAGTCA GCCATGAGCA TATGCTCATC	1260
	TCTCAGAGAT CTAGAACTTG CCTACCAAGT ACATGGCCTT TTAAAAACCG GAGACAACTG	1320
35	GAAATTCATT GGACCTGATC AACATCGTAA TTTCTATTAT TCCAAGTTCT TCGATTTGAT	1380
	TTGTCTAATG GAACAAATTG ATGTTACCTT GAAGTGGTAT GAGGACCTGA TACCTTCAGC	1440
40	CTACTTTCCC CACTCCCAA CAATGATACA TCTTCTCAA GCATTGGATG TGGCCAATCG	1500
	GCTAGAAGTG ATTCTAAAA TTTGAAAGA TAGTAAAGAA TATGGTCATA CTTTCCGAG	1560
	TGACCTGAGA GAAGAGATCC TGATGCTCAT GGCAAGGGAC AAGCACCCAC CAGAGCTTCA	1620
45	GGTGGCATTT GCTGACTGTG CTGCTGATAT CAAATCTGCG TATGAAAGCC AACCCATCAG	1680
	ACAGACTGCT CAGGATTGGC CAGCCACCTC TCTCAACTGT ATAGCTATCC TCTTTTAAAG	1740
50	GGCTGGGAGA ACTCAGGAAG CCTGGAAAAT GTTGGGGCTT TTCAGGAAGC ATAATAAGAT	1800
	TCCTAGAAGT GAGTTGCTGA ATGAGCTTAT GGACAGTGCA AAAGTGCTA ACAGCCCTTC	1860
	CCAGGCCATT GAAGTAGTAG AGCTGGCAAG TGCCTTCAGC TTACCTATTT GTGAGGGCCT	1920
55	CACCCAGAGA GTAATGAGTG ATTTTGCAAT CAACCAGGAA CAAAAGGAAG CCCTAAGTAA	1980
	TCTAACTGCA TTGACCAAGT ACAGTGATAC TGACAGCAGC AGTGACAGCG ACAGTGACAC	2040
60	CAGTGAAGGC AAATGAAAGT GGAGATTCAG GAGCAGCAAT GGTCTCACCA TAGCTGCTGG	2100

	AATCACACCT GAGAACTGAG ATATACCAAT ATTTAACATT GTTACAAAGA AGAAAAGATA	2160
	CAGATTTGGT GAATTTGTTA CTGTGAGGTA CAGTCAGTAC ACAGCTGACT TATGTAGATT	2220
5	TAAGCTGCTA ATATGCTACT TAACCATCTA TTAATGCACC ATTAAAGGCT TAGCATTTAA	2280
	GTAGCAACAT TCGGGTTTTTC AGACACATGG TGAGGTCCAT GGCTCTTGTC ATCAGGATAA	2340
10	GCCTGCACAC CTAGAGTGTC GGTGAGCTGA CCTCACCATG CTGTCCCTCGT GCGATTGCCC	2400
	TCTCCTGCTG CTGGACTTCT GCCTTTGTTG GCCTGATGTG CTGCTGTGAT GCTGGTCCTT	2460
	CATCTTAGGT GTTCATGCAG TTCTAACACA GTTGGGGTTG GGTCAATAGT TTCCCAATTT	2520
15	CAGGATATTT CGATGTCAGA AATAACGCAT CTTAGGAATG ACTAAACAAG ATAATGGCAG	2580
	TTTAGGCTGC ACAACTGGTA AAATGACTGT AGATAAATGT TGTAATTAGT GTACACGTTT	2640
20	GTATTTTTGT TAATATAGCC GCTGCCATAG TTTTCTAACT TGAACAGCCA TGAATGTTTC	2700
	ATGTCTCCCT TTTTTTTTTG TCTATAGCTG TTACCTATTT TAGTGGTTGA AATGAGAGCT	2760
	AGTGATGACA GAAGGATGTG GAATGTCTTC TTGACATCAT TGTGTATTGC TGGTAATCAA	2820
25	GTGGTAACG ACTACTTCTA GCAGCTCTTA CCACTATGAC TTAAGTGGTC CTGGAAGGCA	2880
	GTAAGTGAG GTTTGCAGCA TTCCTGCCTT CATGAGGGCT TCTACCACTG ACCACTTTGC	2940
30	ACGTACCTGG CTCCCAGATT TACTTAGGTA CCCCACGAGT CGTCCACATA AGCAGCTTCA	3000
	TCTTTACCTT GCCAGAGTTG ACAATTATGG GATACTCTAG TCTACTTATA CTTGTGTTCC	3060
	CATCTGTCTG CCATCCTCTG AAGGCCAGGA CCCAGTCATA CATCCTTAGA AACCAAAGTA	3120
35	TGGTTTTTGT TTTCTCTTGG AATGTCAGGT CTTAAGGCAT TTAATTGAGG GACAAAAAAA	3180
	AAAAAAGCC GATATAGTAG CTAGCTACTT AAGCATCCAT GGGTATTGCT CCATATCAAA	3240
40	GCAGATTTGC AGGACAGAAA GAGTAAATTA GCCTTCAGTC TTGGTTTACA GCTTCCAAGG	3300
	AGAGCCTTGG CCACCTGAAA TGTAACTCG GTCCCTTCCT GTCTCTAGTT CATCAGCACC	3360
	TGCAGATGCC TGACTCTTGT TAGCCTTACT ATTCAATACA GTCCTTAGAT TCACGGTATG	3420
45	CCTCTTCCTA TCCAGGCACC TATTCTGAAT CACCATGTTG CTCTGCAGCT AGAGTTGATA	3480
	GGAGAAAATC CATTTGGGTA GATGGCCTAT GAATTTGTAG TAGACTTTCA AAATGAGTGA	3540
50	TTTGTAGCT TGGTACTTTT AAGTTTGTGG TACAGATCCT CCAAACCCAT ACTCTGAGCA	3600
	ATTAAGTCC TTGAACATAG AGAAAATTAA GGCCTCACAG GATGAGTCTC CATCTCTGT	3660
	AAATGCTTAT TTTATCATAG TCTTTAGCCN CTAATATGAG TAAATGTTC TCTTCNGCCG	3720
55	GGTGTGGTGA CTCAC	3735

## (2) INFORMATION FOR SEQ ID NO: 30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1667 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

5 TAGTAATTCA TTAACTCCT CTTACATGAG TAGCGACAAT GAGTCAGATA TCGAAGATGA 60  
AGACTTAAAG TTAGAGCTGC GACGACTACG AGATAAACAT CTCAAAGAGA TTCAGGACCT 120  
15 GCAGAGTCGC CAGAAGCATG AAATTGAATC TTTGTATACC AAAGTGGGCA AGGTGCCCCC 180  
TGCTGTTATT ATTCCCCCAG CTGCTCCCTT TTCAGGGAGA AGACGACGAC CCACTAAAAG 240  
CAAAGGCAGC AAATCTAGTC GAAGCAGTTC CTTGGGGAAT AAAAGCCCCC AGCTTTCAGG 300  
20 TAACCTGTCT GGTGAGAGTG CAGCTTCAGT CTGACACCCC CAGCAGACCC TCCACCCTCC 360  
TGGCAACATC CCAGAGTCCG GGCAGAAATCA GCTGTTACAG CCCCTTAAGC CATCTCCCTC 420  
25 CAGTGACAAC CTCTATTTCAG CCTTCACCAG TGATGGTGCC ATTTTCAGTAC CAAGCCTTTC 480  
TGCTCCAGGT CAAGGAACCA GCAGCACAAA CACTGTTGGG GCAACAGTGA ACAGCCAAGC 540  
CGCCCAAGCT CAGCCTCCTG CCATGACGTC CAGCAGGAAG GGCACATTCA CAGATGACTT 600  
30 GCACAAGTTG GTAGACAATT GGGCCCGAGA TGCCATGAAT CTCTCAGGCA GGAGAGGAAG 660  
CAAAGGGCAC ATGAATTATG AGGGCCCTGG AATGGCAAGG AAGTTCTCTG CACCTGGGCA 720  
35 ACTGTGCATC TCCATGACCT CGAACCTGGG TGGCTCTGCC CCCATCTCTG CAGCATCAGC 780  
TACCTCTCTA GGTCACTTCA CCAAGTCTAT GTGCCCCCA CAGCAGTATG GCTTTCAGC 840  
TACCCCATTT GCGCTCAAT GGAGTGGGAC GGGTGGCCCA GCACCACAGC CACTTGGCCA 900  
40 GTTCCAACCT GTGGGAACCT CCTCCTTGCA GAATTTCAC ATCAGCAATT TGCAGAAATC 960  
CATCAGCAAC CCCCAGGCT CCAACCTGCG GACCACTTAG ACCTAGAGAC ATTAAGTAA 1020  
45 TAGATCTGGG GGCAGGAGAT GGAATGCTGA GGGGTGGGT GGGGTGGGA AGTAGCCTAT 1080  
ATACTAACTA CTAGTGCTGC ATTAACTGG TTATTCTTG CCAGAGGGGA ATGTTTTTAA 1140  
TACTGCATTG AGCCCTCAGA ATGGAGAGTC TCCCCGCTC CAGTTATTGG AATGGGAGAG 1200  
50 GAAGGAAAGA ACAGCTTTTT TGTCAGGGG CAGCTTCAGA CCATGCTTTC CTGTTTATCT 1260  
ATACTCAGTA ATGAGGATGA GGGCTAGGAA AGTCTGTTC ATAAGGAAGC TGGAGAACTC 1320  
55 AATGTAAAT CAAACCCATC TGTAATTTCG AGTGGGTGGA GCTCTGCTT TTGGTACATG 1380  
CCCTGAATCC CTCCTCCCT CAAGAATCCG AACCACAGGA CAAAACCCAC CTACTGGGCT 1440  
CTCTCCTACC CTGCCCTCCT CCCTTTTTTT TACCCCTCTC TTTTATTAT TTTCTTTGCT 1500  
60



	CTTTAGAACC CAGTGAAAAA TACCAGGGTA CTGGGGTGCA ACTCTTTCTT ATGATAGGTC	1560
	ATTAGTGCTT TAAGCAAAAG ATATTAGCAG CTTTGACTGC AGCATTAGCA ATTAGGRAAA	1620
5	AAAAAANWA AAAACTCGAG GGGGGGCCCG GTTACCCAAT TCGCCCT	1667
10	(2) INFORMATION FOR SEQ ID NO: 31:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1408 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:	
20	ATTACACACC TGAGCACTGT GCCTGGCAAG ACCTGTCTTA ATAGATTAGA GAACCACTGA	60
	TAGATGGTCA GCTTTCTGTA GCAGTGAGAA CCCTACATTT CAAATGTGGA TAGCACCTTT	120
	GCGGGGAAAC ATCACTTGGC ACATCTGCAT TCTTTTTTGA CACAGGGTCT CACTCTGTTG	180
25	CCCAGGCTAG AGTGCATGGC ACGATCTTAG CTCACTGCAA CCTCCACCTC CCAAGTTCAA	240
	GCGATTCTTC TGCTTCAGCC TCCTGAGCAG CTGGGATCAC AGACATGCGC TACCATGCCC	300
30	AGCTAATTTT TTGTATTTT TGTKTGTGTT TTTTGTGTTK TAAGTAGAGA CGGGCTTTCA	360
	CCACGTTGGS CAGGCAGGTC TCGAACTCCT GAMCTCAGGT GATCCACCCA CATCTGCGTT	420
	CCAATATCTT TCTCAACATA ATGATAGCCG TAATTAATAT TTTCCAGTAC ATTTTATGTC	480
35	CTTTACACAC GAGAGTGGTA GACAGACACA AACCCAGATC TGTCTGACTC CAAAGCCCGT	540
	TTGTCAATCAT TCCTTTTACG GTATCCTATA GTGGTATCCT TTACAGAAAG ACAGCTTTTA	600
40	CCCAACAAAG ACTTAACTTC CCAGGATGCC AGAAGGACAA AGCGGGATTG CTTTAAAGRA	660
	GRAAGTTATC AAGAMCTTAT TTTATAAATG AGATTAGATA GGGAAAGGCA ATTTATCTTT	720
	ATTAAAAACT GAAAAGGCCA GCATAGGGAA GGAGGTCCTT CGGTGGTCTT TTTCAGGGAA	780
45	ATACTTCAGT TGCTTTTATT AGAAACAGAT AGTACCTAAG GTTTTGAGGT AGGWACAGCT	840
	TAAGGCATGC TAATGKTCAT GGGTCCTTCC ATAGTCATTT TKGTATTTTG GTTWACATTT	900
50	GAGCAATAGG CAGCCCTTCA CTGCTGCTGG AYTCATTCCT GCCAYTATTA CAGGTGACAG	960
	AGGAGACAGG AGGTATGTCT TTTCTATTTT TAWACATGCT TTATATTTAA CACAAGCTCT	1020
	TGGGTATCTT AGATAAACAG AAGTTGCCTA GCACTCCTTT TAGTGCAATTG AACCCTTTAA	1080
55	CATTAAAGCA AAATAATAAA CAGTCTTTTG AGGTTCTTCA ACAATGAAAC GTGTTGAGT	1140
	GGCAGCAGCG GAATCCATGC YTCTTCTCCT GGAGTGTGCA AKAGTCCGTG GTCCTGAGTA	1200
60	TCTCACACAG ATGTGGCATT TTATGTGTGA TGCTCTAATT AAGGCCATTG GTACAGAACC	1260

AGATTCAGAC GTCTCTCAG AATAATGCA TTCTTTTGCA AAGGTGAATA TTTTCTCTT 1320  
 AAAAAATATG TATPAGGTGG TATGTTCATT TATTAGTCTT GCTAAAAAAA AAAAAAAAAA 1380  
 5 ACTINGAGGG GGGGNCGGT ACCCAATT 1408

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(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

20

AGGATATGCA TGATTCCTAA CCAGGCTATA TGTTAAAAA AAATTGGAAA ATGCAATACA 60  
 TTTTCTATTA TACAACTAC AGAATGAGTA TGCAAGTTTT ATTTATCAAA ATGTAATGGA 120  
 25 TTTTAAAGG CTGAGAAATT TTCCTTATAC CTACCTTTTC AGTTATTTTA ATTATACCAA 180  
 ATTTTCARCT AGLATAGCTT CATCCATATG AAATATAAAA TGAAGAGACA CCTAGGCTCT 240  
 ATCAGGCTTA GGATTCCTTG ACTTATTTTC CACTTTAATT TCTCAGTGGA AGTTAAGAGG 300  
 30 GGTGAGAAA CAPAGAGGG GAAAACTGA CAACTAACAA AACCAGCACC ACATCGCTAG 360  
 GTGGTGCTTA CTAAATACCT TCTCAGGATT TTCCTCAGAT TGAAAAGCTT ATGAGGATTT 420  
 35 CTGGGAGTC TTATAACCT GCCTGTTAGT ACAGAGCTTT CCTGATGATA TTTACTCTTG 480  
 AGCACATGTG GTTGTAACAC CTTAACTTTC TTTCTCCAGG AGGGTGGTGA TAGAAACAGA 540  
 TGGTAGTATT TATGAAGTGA TGTCTCGTG AAATGTTGAG GGTGGGAGGA AAAGACTTTA 600  
 40 AGGGAGGAGA GCCATCTATT TGTTCCTAA AGCCACCTCT CAGCAGAATC GTCATGTTTT 660  
 TCTGATGCAC CGCTCTGCTT CATGCCAAG ATGACTTGCG AGGCAATCTC AGGAGCTGTG 720  
 45 GACTTAACCR TTGCAAGCA CACTGTCTTT CTCAGCGTTC TCTGCAAGTC AGTAGGTGTT 780  
 AGTATGGTTC CAAAGTTCAC TGTCTCAGCA AAGTTGAAC TGGCTACCTC TCTACAGCTG 840  
 TTTCTCAGA GGGAAAATC TTGAGACCAG ATGGTGGAGC TCTGGAGTCA GAGGAAATGG 900  
 50 GTGTCTTCAG CACAAAGCTG CTGCTTTTAC TTCAGCCACT TCTGACATTT TTACATACCG 960  
 AGCCTGAGAT TRGTGATTA TCTCAAATCA AATCACTTTG ATGGAGATAA ATAATCAAAA 1020  
 55 CTGTTTTATA GTCATTGATT TGGTGAGAAC AGTAATGGAA AATGGTGTG AAGGACTTCT 1080  
 CATTTTTGGA GCTTTCCTTC CAGAGTCTG GCTGATTGGT GTTCGCTGTT CATCTGAGCC 1140  
 CCAAAAAGCA TTATTACTGA TACTTGACA CAGTCAAAAG CGCAGACTGG ATGGATGGTC 1200  
 60

TTTTATAAGG CATTTAAGGG TACACTACTG TGTTCACCTG ACCATACATT TTTCTTAGCC 1260  
 CCTCAAGTAA TATAGCACAG AGTTATGAAT GACAATTCCC CTAACCATTC CTCTTCATAT 1320  
 5 CTGCCTCTTC CCCTTACCAT CGTAATTCTC CAAACTGGTC ATAAAGGCAC TCTGTGAAGA 1380  
 TATTGGGGAC TGACATCTTA AGCTCTCACC TGGCTGCAGT AGGAAAGGCC AAAGTACGA 1440  
 CAAAAAAAAA ATTCTTTTATA AAGATGATAT GGTAACATGT ATCTTTGCCC TGGGTCTGGG 1500  
 10 TGGGTCCAGT CAGTCTCAGA TTTACAAGCA TTTAGGAGCC TAGGTAAAAG CTGCTAGTAT 1560  
 TCTTTTAAAA GTTACATTTA TGACTTGCAA TGATAGAAAA CTCCTTCCAA TTAAATGGCA 1620  
 15 TTTTATAATA TTATGTGTGT ACTTCACAGT GTTAAAAATA CCCTCATACG TTATGCATT 1680  
 TGATCTTCAC AGAAAGTGCA TTTTAACCAG TACTCTGGGT GCAATAAATA ATATGTAGAA 1740  
 ATTTAAGTCC TCCAATTCCA GCATATCCAG TGAGTTTGA CAGTGTGTTT ATGTGGAATG 1800  
 20 TTTAAGGATA TACAATTGTA CTTTATATAA ATTGGTTCTT GTTCTTCTTA AATGTGACAT 1860  
 GAAATAATTG TGCTGCTACA TTATACTGGA AATTAACAGG GGAAAAGGGA AGAGCTCTTG 1920  
 25 GCTCCCTTGA GGTCTGCTA GTGGTGTAG GAGTGGTTAC AACTGAGCTT TTAGTAACCA 1980  
 TTTAACCGTA TGTAAGCTTG GTTTCTAATT AAAAAAAAAA TTCTTTTTC A 2031

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(2) INFORMATION FOR SEQ ID NO: 33:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 971 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CGCGTCGGAA CTCGCCCGCG GGACATCCAC GGGGCCGAG TGACACGCGG GAGGGAGAGC 60  
 AGTGTCTCTG TGGAGCCGAT GCCAAAAACC ATGCATTTCT TATTCAGATT CATGTGTTTC 120  
 45 TTTTATCTGT GGGGCCTTTT TACTGCTCAG AGACAAAAGA AAGAGGAGAG CACCGAAGAA 180  
 GTGAAATAG AAGTTTTCGA TCCTCCAGAA AACTGCTCTA AGACAAGCAA GAAGGGAGAC 240  
 50 CTACTAAATG CCCATTATGA CGGTACCTG GCTAAAGACG GCTCGAAATT CTACTGCAGC 300  
 CGGACACAAA ATGAAGGCCA CCCCAATGG TTTGTTCTTG GTGTGGGCA AGTCATAAAA 360  
 GGCCTAGACA TTGCTATGAC AGATATGTGC CCTGGAGAAA AGCGAAAAGT AGTTATACCC 420  
 55 CCTTCATTG CATACGGAAA GGAAGGCTAT GCAGAAGCA AGATTCCACC GGATGCTACA 480  
 TTGATTTTTC AGATTGAACT TTATGCTGTG ACCAAAGGAC CACGGAGCAT TGAGACATTT 540  
 60 AAACAAATAG ACATGGACAA TGACAGGCAG CTCTCTAAAG CCGAGATAAA CCTCTACTTG 600

CAAAGGGAAT TTGAAAAAGA TGAGAAGCCA CGTGACAAGT CATATCAGGA TGCAGTTTTA 660  
 GAAGATATTT TTAAGAAGAA TGACCATGAT GGTGATGGCT TCATTTCTCC CAAGGAATAC 720  
 5 AATGTATACC AACACGATGA ACTATAGCAT ATTTGTATTT CTACTTTTMT TTTTAGCTA 780  
 TTTACTGTAC TTTATGTATA AAACAAAGTC ACTTTTCTCC AAGTTGTATT TGCTATTTT 840  
 10 CCCCTATGAG AAGATATTTT GATCTCCCA ATACATTGAT TTGGTATAA TAAATGTGAG 900  
 GCTGTTTTGC AAACCTAAAA AAAAWWAAA AAACTSGAG GGGGGCCCGT ACCCAANTCG 960  
 CCGNATATGA T 971  
 15

## (2) INFORMATION FOR SEQ ID NO: 34:

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## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GAACCCCTT TCTCCTGGTA AAGGTAAGG GGGGGATAA TGTTTACCAC AGGTACGAAA 60  
 30 TAGTCACTTT AACATTGAGA CCTCTGCCTC ATTGAATTCA GGTTTTTTAA GTACTTGAAA 120  
 CTCTTCAGAT TCTCCTTATT TTAGTTTCTT TTTACATTTA TGAAGTAGAA AGCATTGTTT 180  
 35 TGTAAGTGT TTTGAAAATA AATAGCCTAG TCTCTTATCC TCTTTAGCGT GGATTAAAGG 240  
 TGAAGTTCTG CAAATGGGAG AGTGTTCACA GTAGATAGCT CAGATTGATT GAACACATTT 300  
 GAGGAAGAGA CTCCTGCATG AGATACCAGC ATTTTTACAA ATACTTTTAA TGTACATTCT 360  
 40 TTATTTTGTG ATTTTGTCAA CCTCTCCCC AAGCACATCT TCTTCCCTT TACTATGTCT 420  
 ATGTAGGGAA AAACAAAACA AAAAATTGCA CTTACGTTAC ACTCCCAAAA TGTGGGTAAT 480  
 45 CCGTGTCTTT CAAAAACAT TTCTGTTTTT TGTTTTGTG TGGTCAGTCC ATTGCATAAG 540  
 TGACAAGTTT GGGTGCTTGT GGCACGTATG TATGAAGCGG GAGGGGGATG ASAATTGCCT 600  
 GTCCTTCAGT ARGCTGTAAA AGTAATTTAC ATGTAAGTAA AAAGGGAAAA TAGAATAGAT 660  
 50 GCCAAAGTCA TTTATTCAGT CCTTAGTTTT CTTATGTGGC ATTACTGCAT CTGCTAGTTA 720  
 GTGAGAAAGC ACCCTCAGCT TTTACTGCTC CCTCCCTGC CTGCCAACAC ACTTGATGTG 780  
 55 TGCAAACAGC CCTCAAGTAT CTGTCAGATG ACCTATATAA GGTATTGAAT AAGGTATTCT 840  
 TGTCAGTTTA GAAATGGACT GGATAAACT TACTTGGTGT TCATTATTTT ATCTCATTTG 900  
 TCCTGTTACA TGCCCTATGT TAAGATAATT ATATTGCCAC TAATAATCAA GATGCTAAAT 960  
 60

GAGTATTACA ACTGGCTAAT ATCATTTTTT ATATACAAGG GTATGTGTAT ATTGGGAATT 1020  
 GRTATGAGAA ACTCATTTGT ACCCATTTGA GTGATATTGC ACAACAAACA CAGATAYCTA 1080  
 5 CAGACTCCGT TTTCATTTTC TCGTGTCTT TATGATAATG ATCTTTGTAG ATTGGTTATT 1140  
 TCTGTACTTT ATCTGTAATA AACTTTGTAG ATCCTGTGAA CCATTACTTT GCCTAAATCA 1200  
 CTTGAGACTT GAGTCTTTAA TAACAAAGCA TCAATATTCA CTAAAGTCAA TCTCTTTTGA 1260  
 10 GTTCTGTGA CTGGCTAGA AGCTCTTGAC ACTAAGGGAT TAGTGTTAAT TTTCCCTGGG 1320  
 GGTGTTCCAC TAGGGCAITA CTGTATAATG ACTTGATGTT GCCACATAGA CTTCAAGATA 1380  
 15 TATAATATTT TGAGGATTTT GTTGATTGGC CTATGTTTTA TTGCATAGTG TGAAACGTGT 1440  
 AAAGCTTGGT TAACCTGTAT ATAGATAGCT TATTGTTGAC TAGTTATAGT GTATTAGGG 1500  
 TTGCCTGTAA TATTTAAGCT TCTTTACTGA TGTGTGTGCT GGTAGGAACA TATAATTTTT 1560  
 20 GTACATTATA TTTACTGAGA TGTGCTTTT TTTATTTTAC AAATACTTTG GAATTCCAAT 1620  
 GTGTTTTTTG CTTCCTGTAG GATTAATTTG GAAAGGTTTT TAATGACATT CCACTGATTT 1680  
 25 CAGATTTTGC TTGAGATTGA CTTCAATAAA TTGCTCTGTA TGTTCACAAA AAAAATTAAA 1740  
 AAACCTGAGG GGGGCCCCGT ACCCAANNCG CCGGATATGA TCGTAAACAA TC 1792

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(2) INFORMATION FOR SEQ ID NO: 35:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 896 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AGTTGNANAC AACAGGACCT GAGTCTTGG GCAGCACCAG TAGGTTGCC CYTGCYTCYT 60  
 GCCAGCYTCA CYTGCCACYT TYTGCCCTY TCGGGATGCC TTCGCAGACA GAGYTYTTG 120  
 45 CTGCCGTGG TGGCCAYTCT TTGCTTTTGG TTYTCTTGCC CCTTGGCCTC CCTTTTTGTC 180  
 CCGGGGCAGC CTTGTGTGAC CTGCCCTTTT CCCTCCCTTC CTTTCCAGGA CAAGCACGCC 240  
 50 GAGGAGGTGC GGAAAAACAA GGAGCTGAAG GAAGAGGCCT CCAGGTAAAG CCTAGAGGCC 300  
 AAAGAAGTTT CCAGGTCAGC CGGACAGCTC CAGCAGCTCC ACGTTCAGG CAGCCTCGMC 360  
 CGCCGGCTGC GCTCCACGA CTGGGGTTTG GGGGGAGGG GGTGGCCAAG GGGCGTTTCC 420  
 55 TCTGCTTTG GTGTTGTAC ATGTTAAGAA TTGACCAAGT AAGCCATCCT ATTTGTTTCC 480  
 GGGGAACAAT GACGGGTGG GARAGGGGAG AGGAGAGAGT TTGGGAAAGG GAGATGGAGA 540  
 60 AGAACTCAAG GACATTGCAA CCCTGCCCGG CGCAGATCTG ATTTTCACAT CTCTACCTGG 600

ACATTGAGCC TCCCAGGCAC CATGTTGAGG AGAGATGAAA ACCAGGGCGG TAGAACTTCA 660  
 GGGTGAAGGA CAGAGTCCTG GGTGGGGCAG CGGCTGCAGG GCGCACCAGA GAACCCAGCC 720  
 5 AGAGGGGGTG TGAGTACCAG TGGTGTGCT TCCACCCTGC AGCAGGTGGG ATGAGGTCTG 780  
 TGTGTGTGTG TGAACCATCA TTTTGTGATC ATCATGACCA ATGAAACATT GAAAAAAAAA 840  
 10 AAAAAAAGTG GAGGGGGGCC CGTACCCAAN TCGCCGNATA GTGATCGTAA ACAATC 896

15 (2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

25 TCGACCCACG CGTCCGGTCA GCCAGTCGCA TCCAGCCATG ACAGCCTTCT GCTCCCTGCT 60  
 CCTGCAAGCG CAGAGCCTCC TACCCAGGAC CATGGCAGCC CCCCAGGACA GCCTCAGACC 120  
 AGGGGAGGAA GACGAAGGGA TGCAGCTGCT ACAGACAAAG GACTCCATGG CCAAGGGAGC 180  
 30 TAGGCCCCGGG GCCAKCCGCG GCAGGGCTCG CTGGGGTCTG GCCTACACGC TGCTGCACAA 240  
 CCCAACCCCTG CAGGTCTTCC GCAAGACGGC CCTGTTGGGT GCCAATGGTG CCCAGCCCTG 300  
 35 ARGGCAGGGA AKGTCAACCC ACCTGCCCAT CTGTGCTGAG GCATGTTCTT GCCTACCATC 360  
 CTCCTCCCTC CCCGGCTCTC CTCCTCAGCAT CACACCAGCC ATGCAGCCAG CAGGTCTCTC 420  
 GGATCACYGT GGTTKGGTGG AGGTCTGTCT GCACTGGGAG CCTCARGARG GCTCTGCTCC 480  
 40 ACCCACTTGG CTATGGGAGA GCCAGCAGGG GTTCTGGAGA AAAAAAGTGG TGGGTTAGGG 540  
 CCTTGGTCCA GGAGCCAGTT GAGCCAGGGC AGCCACATCC AGGCGTCTCC CTACCCTGGC 600  
 45 TCTGCCATCA GCCTTGAAGG GCCTCGATGA AGCCTTCTCT GGAACCACTC CAGCCCAGCT 660  
 CCACCTCAGC CTGGGCTTTC ACGCTGTGGA AGCAGCCAAG GCACTTCCTC ACCCCYTCAG 720  
 CGCCACGGAC CTYTYTGGGG AGTGGCCGGA AAGTCCCSG GCCTYTGGCC TGCAGGGCAG 780  
 50 CCCAAGTCAT GACTCAGACC AGGTCCACCA CTGAGCTGCC CACACTCGAG AGCCAGATAT 840  
 TTTTGTAGTT TTTATKCTT TGGCTATTAT GAAAGAGGTT AGTGTGTTCC CTGCAATAAA 900  
 55 CTTGTTCTCG AG 912

60 (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

10	AATTCGGCAC GAGCGGAGGC GAGGGAACT RAGGGCGAAA GTTGTGTGTC GTGTGGCAG	60
	GAGGGCCTAG AAGGGAAAGA CTGTCTAGTG GGACAATGTC ATATTATAAA TTTGGAATGC	120
	TGAATAGAAA ATTATAGATT TTGATATTGA AGGAAATGAA GCGAAGCYTA AATGAAAATT	180
15	CAGCTCGAAG TACAGCAGGC TGTTCGCTG TTCCGTTGTT CAATCAGAAA AAGAGGAACA	240
	GACAGCCATT AACTTCTAAT CCACCTAAAG ATGATTCAGG TATCAGTACC CCTTCTGACA	300
20	ATTATGATTT TCCTCCTCTA CCTACAGATT GGGCCTGGGA AGCTGTGAAT CCAGAGTTKG	360
	CTCCTGTAAT GAAAACAGTG GACACCGGGC AAATACCACA TTCAGTTTCT CGTCCTCTGA	420
	GAAGTCAAGA TTCTGTCTTT AACTCTATTC AATCAAATAC TGAAGAAGC CAGGGTGGTT	480
25	GGAGCTACAG AGATGGTAAC AAAAATACCA GCTTGAAAAC TTGGRATAAA AATGATTTTA	540
	AGCCTCAATG TAAACGAACA AACTTAGTGG CAAATGATGG AAAAAATTCT TGTCCAATGA	600
30	GTTCCGGAGC TCAACAACAA AAACAATTAA GAACACCTGA ACCTCCTAAC TTATCTCGCA	660
	ACAAAGAAAC CGAGCTACTC AGACAAACAC ATTCATCAAA AATATCTGGC TGCACAATGA	720
	GAGGGCTAGA CAAAACAGT GCACTACAGA CACTTAAGCC CAATTTTCAA CAAAATCAAT	780
35	ATAAGANACA AATGTTGGAT GATATTCCAG AAGACAACAC CCTGAAGGAA ACCTCATTGT	840
	ATCAGTTACA GTTTAAGGAA AAAGCTAGTT CTTTAAGAAT TATTCTGCA GTTATTGAAA	900
40	GCATGAAGTA TTGGCGTGAA CATGCACAGA AAAGTGTACT TCTTTTGTAA GTATTAGCTG	960
	TTCTTGATTG AGCTGTTACA CCTGGCCCAT ATTATTCGAA GACTTTTCTT ATGAGGGATG	1020
	GGAAAAATAC TCTGCCTTGT GTCCTTTATG AAATCGATCG TGAACCTCCG AGACTGATTA	1080
45	GAGGCCGAGT TCATAGATGT GTTGGCAACT ATGACCAGAA AAAGAACATT TTCCAATGTG	1140
	TTTCTGTGAG ACCGCGTCT GTTCTGAGC AAAAACTTT CCAGGCATTT GTCAAAATTG	1200
50	CAGATGTTGA GATGCAGTAT TATATTAATG TGATGAATGA AACTTAAGTA GTGATAAAG	1260
	GAAGTTTAGC ATAAATTATA GCAGTTTCTT GTTATTGCTT AATTTACCAT CTCCATAGTT	1320
	TTATAGCTAC TATTGTATTT CACTTGTTGA ATTAAAGTAT TTGAATTCCTT TTAACAAAAA	1380
55	AA	1382

## (2) INFORMATION FOR SEQ ID NO: 38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GGGCTACTTC AAAGCCCTGG GCCTTATTC TTCAGGTAAA AAAATATAAA GTCAGATCTC 60  
ATCCCGGCTG GCCATGCTGT TAGACCCTTT CATCCTCTC TTCTGCCTCT TCTCAACAGC 120  
TGCCCACTCC TGTTCGAAT TCATATACAT ACAGTTCTAA TACTGATGTA TTTACCCCTCA 180  
TAAGCCACTC AACCCAGAAT CTTATTTGAA TTATAATCCA GAAACATCAG GTGACGTGTG 240  
AGACTACTGT ATGAGAAAGA GACAGTTTAA GGGTCAGTCC AATGGAAAAA AGAGTTCTCA 300  
GAGCTTTCTT TAGCTTATTC TCATCAAAGA GCTTTCTCTG CAGAAGGAAC CTACTGGTTC 360  
CTCCTTTCCA GTCCTAGAAA TCCTGACCTA GAGTGGCTTA ATCCTGCTAG CACCTCTCTC 420  
TCGCACTCTG GTGCCAAATG ACTCCAGGAA CTGGGCCATG ATGTGGTGGG AATGACCTTA 480  
CCCTGAGCAT GTCACTCATG CATGAACAA CAGCTAAGAG CAGAGCTTAG AGCTTAGAGC 540  
TGGGCCCTGT AAGGTGAGAG GAATCACATC CTGCAGAAGT CTGTCCTGAG AAGCAGGTAC 600  
TCCTGTCA CA GCAGAGACAC AGTGGATACC TGAGTAACAA TAATAACAAGA CAGGACGTGG 660  
GMAACAGCAA AGATTTGGGT GTCAGAAGAR GCCGAGAACA CTTYCAGGCA GGAACATTCA 720  
RARTTGTCT TGGAGGAART AGGCMCSAAG GCTGGGCAGG ATTTTCMCGG GCAGAGATGG 780  
AGCAAGCAAT TGAAATGAAA GCCATGGCAT GGGAAAAGGA GCACTGGCCA CAGGGAGTGC 840  
AACGTTGTGA TGCAAGGCCA CTGTGGAGCC AT 872

## (2) INFORMATION FOR SEQ ID NO: 39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GGCAGAGGCT CACCCAGCA GAGATTGAGG GGAACCGTG ATGAAATTTT TAAGTATTCT 60  
GCTTGATGAT AATAATTTTY CTCTTATGTT AATGTTGGCT CCGTTTGGGT GTTTAGCTTT 120  
TGAAAGGAGT ATGAAATGC GGAATGGGGC TTGGGGCTT GAGGAGGTGT GATCTCTAGT 180  
GTTTAAAAAA TTTAATTGCA CAAATAGAAA TAATTCACCC ACATTATTGA ACCCCACTAA 240



AGCATATCCT TTTTGTCCAT ATTCCCTTCC TGCTGCCCTC GTGTGTACCA TTATTACTCA 300  
GTGTGATTT GAGCTCGTTC CACTTAAAGT CATTATAGA TACTTTTGCG TCGTGTTKGA 360  
5 ATATTTATTG AATTTCTATT CTGTGTTTTC CTTAATTACT TTATTATGGA ACCTTTACAC 420  
AGGTCTGGTG TACTTGTCTT TTGAAAAGTC TTATGTTGAC CACCATCACT GAGCATATAG 480  
10 CTTTTTCCTT ATTTCCCTGG GATAATTACC CGAAGTGGA ATACCGAATC AAACCTCTGT 540  
TTTCTTTCTT TGGCACTATT ATATAAATTG TTTTCCAAAC AAGGCATGTT TACAATAGAC 600  
ATTTTTCAAA ATCTGGGTAT TTGTCTTATT TTGCTCTCTG TATGCAGAAT TCAGCGGGGT 660  
15 GCCAAGTCGT TTTCTGTGTG GGTGAGAGA CAGGCTGTGC AGCCCACTGT TGCATAGGAC 720  
TAATACTAC AAATCATGCT GAGACCGAGC TATTTTTGCT GCTTAGARGC TTTGCAGCCT 780  
20 TGAGTAAGTT TCGNCATCTG GAAACNTTGN AA 812

25 (2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1515 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

35 AATTCGGCAC GAGGGAAATT CAAGCACTTT TCCTAAAAGA AGGGGGAATG GATGCTGAAA 60  
CAACACGTNT CCCACAAAGG GAGCAGACAC TGGGCTGTG AAGCTGCCCC ATACCTTCCC 120  
CACAGAACTG GGGTCCGGCC TCCCTGACAT GCAGATTTCC ACCCAGAAGA CAGAGAAGGA 180  
40 GCCAGTGGTC ATGGAATGGG CTGGGGTCAA AGACTGGGTG CCTGGGAGCT GAGGCAGCCA 240  
COGTTTCAGC CTGGCCAGCC CTCTGGACCC CGAGGTGGA CCCTACTGTG ACACACCTAC 300  
45 CATGCGGACA CTCTTCAACC TCCTCTGGCT TGCCCTGGCC TGCAGCCCTG TTCACACTAC 360  
CCTGTCAAAG TCAGATGCCA AAAAAGCCGC CTCAAAGACG CTGCTGGAGA AGAGTCAGTT 420  
TTCAGATAAG CCGGTGCAAG ACCGGGGTTT GGTGGTGACG GACCTCAAAG CTGAGAGTGT 480  
50 GGTTCCTGAG CATCGCAGCT ACTGCTCGGC AAAGGCCCGG GACAGACACT TTGCTGGGGA 540  
TGTACTGGGC TATGTCACTC CATGGAACAG CCATGGCTAC GATGTCACCA AGGTCTTTGG 600  
55 GAGCAAGTTC ACACAGATCT CACCGTCTG GCTGCAGCTG AAGAGACGTG GCCGTGAGAT 660  
GTTTGAGTTC ACGGGCCTCC ACGACGTGGA CCAAGGGTGG ATGCGAGCTG TCAGGAAGCA 720  
TGCCAAGGGC CTGCACATAG TGCCTCGGCT CCTGTTTGAG GACTGGACTT ACGATGATTT 780  
60

CCGGAACGTC TTAGACAGTG AGGATGAGAT AGAGGAGCTG AGCAAGACCG TGGTCCAGGT 840  
 GGCAAAGAAC CAGCATTTTCG ATGGCTTCGT GGTGGAGGTC TGGAACCAGC TGCTAAGCCA 900  
 5 GAAGCGCGTG ACCGACCAGC TGGGCATGTT CACGCACAAG GAGTTTGAGC AGCTGGCCCC 960  
 CGTGCTGGAT GGTTCAGCC TCATGACCTA CGACTACTCT ACAGCGCATC AGCCTGGCCC 1020  
 TAATGCACCC CTGTCTGGG TTCGAGCCTG CGTCCAGGTC CTGGACCCGA AGTCCAAGTG 1080  
 10 GCGAAGCAAA ATCCTCCTGG GGCTCAACTT CTATGGTATG GACTACGCGA CCTCCAAGGA 1140  
 TGCCCGTGAG CCTGTTGTCG GGGCCAGGTA CATCCAGACA CTGAAGGACC ACAGGCCCCG 1200  
 15 GATGGTGTGG GACAGCCAGG YCTCAGAGCA CTCTTCGAG TACAAGAAGA GCCGCACTGG 1260  
 GAGGCACGTC GTCTTCTACC CAACCCTGAA GTCCCTGCAG GTGCGGCTGG AGCTGGCCCCG 1320  
 GGAGCTGGGC GTTGGGGTCT CTATCTGGA GCTGGGCCAG GGCCTGGACT ACTTCTACGA 1380  
 20 CCTGCTCTAG GTGGGCATTG CGGCCTCCGC GGTGGACGTG TTCITTTCTA AGCCATGGAG 1440  
 TGAGTGAGCA GGTGTGAAAT ACAGGCCTTC ACTCCGTAA AAAAAAAAAA AAAAAAAAAA 1500  
 25 AAAAAAAAAA AAAAA 1515

30 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

40 AAGATGGTGG CGCCAGAGC TTCGCTCTAT GCTGCTCCCC TGAGAGAGGC GTTTCATCA 60  
 ACCAGTTTTC CAAGGAGTTC AATGAGAGGA CAAAGGACAT CAAGGAAGGC ATTCTCTGC 120  
 CTACCAAGAT TTTAGTGAAG CCTGACAGGA CATTTGAAAT TAAGATTGGA CAGCCCACTG 180  
 45 TTTCCTACTT CCTGAAGGCA GCAGCTGGGA TTGAAAAGGG GGCCCGGCAA ACAGGAAAG 240  
 AGGTGGCAGG CCTGGTGACC TTGAAGCATG TGTATGAGAT TGCCCGCATC AAAGCTCAGG 300  
 50 ATGAGGCATT TGCCCTGCAG GATGTACCCC TGTCGTCTGT TGTCCGCTCC ATCATCGGGT 360  
 CTGCCCCTTC TCTGGGCATT CGCGTGGTGA AGGACCTCAG TTCAGAAGAG CTGCGAGCTT 420  
 TCCAGAAGGA ACGAGCCATC TTCCTGGCTG CTCAGAAGGA GGCAGATTTC GCTGCCCAAG 480  
 55 AAGAAGCTGC CAAGAAGTGA CCCTTGCCCC ACCAACTCCC AGATTTCAAA GGAGGTAGTT 540  
 GCAAAAGCTG TGCCCAAGGG GAGGAAGGAG GTCACACCAA TATGATGATG GTTTTCATGA 600  
 60 CTTTGAATGA TATATTTTTC TACATCTAGC TGTATCGAGG CATCAGGCCT GAATAAACAT 660

CCTTCTCTTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA

704

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(2) INFORMATION FOR SEQ ID NO: 42:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1094 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

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GGCAGCTTTC TTACAAACCC ATCCTTCTGA AATGTTGCTT CAAATTCATC CTCTGCTCCC 60  
CAGTCCCCTACT ATTCCACACA TACTGTTACT GTTTCCTTAT CCTACTTCTT CAATTTTGGA 120  
ACATAGTTGC AGTTACTGCA TTGAATACCT GTGGGTTTGC CTGTTGTTCT GTCTGTCTCT 180  
GTGGTTCTTG TAATANIGGA TCCCAGAGAT AAAATGGACA GTGTGNATGC ACAGTTAATT 240  
CAGAACTAG ACCTTACTTG CTGTGTGAAA TACCACTAA ATTCTCAGTG AACTCAGCTG 300  
ANCTTTATCT CCTTTTGTTC CCCCAATTTA TAATTTTCAGT TCAGGCCCTG AAAGATGGAA 360  
TCCCAGCTAA GAAATACAAG TTACACCTTG TACTAGCAGC CCATGTGTGC ATGTTCTTTA 420  
AGTGCTCTTG CAGCTATGTC ATTTATATTG ATTTCCCTGT ATTATTATAA GCAAAGCAAA 480  
TTTGAGGAAA AAAACCCATA ATACCACACC TCATTTTTTT CAAGTAATAG GGTGATAAGT 540  
CTCATYCTYC ATATAATATG TTGAGTATGC AGTATATTAT GTGTTAGGCT CTGGANAGGC 600  
AGAGGTTAGA TCATGTWACA GATCATATCK GATTAGGCAG ATAAACAGTA TTTTAACCTT 660  
TTCCTTATTA TATGTAACCT GCTTTCAGGT TTTTAAATGT TACTATTATG TCTTTAATAT 720  
ATTATCTTTA TTGTACTTT TGTATACAGA GTGATTTTCC TTTTTTAAAA AAAATGTGT 780  
CTTTAGGATG GATTCCAAAG ATGTGGAATC AGTAGGTTTA AGGAATATGG ATATTTTGGC 840  
TGGAAGGTG GCTCACACCT GTAATCCAG CACTTTGGGA GGCTGAGGTG GGTGGATCAC 900  
CTGAAGTCAG GAGTTCGAGA CCAGCCTGAC CAACATGGCG AAACCCTGTT TTTACTAAAG 960  
ACACACWAA AATTRGCCAG TGGTGGTGGC ATGTGCTTGT AGTCCCACTT AGCTACTCGA 1020  
GAGGCTGAGG CAGGAGAATC GCTTGAACCC GGGAGGCAGA GGTGTCAGTG AGGCAAGATG 1080  
GCACCTCTAC ACTC 1094

(2) INFORMATION FOR SEQ ID NO: 43:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

	TGGCTTAGGC CATCACCCCTT CCCTTGGCTG GAACTACTGG ACAGACCCCTT TTGAGATGTG	60
10	CCTGTGGTGC TGTGAGATG TGTGTAGTGG TCTTAGCTCT TTGTTGAGCT TGTGTGTGTG	120
	TTGTGTAGTC TTAGCTGTAT GCTGAAATTG GCGGTGTGTT GGAGGGCTTC TTAGCTCTTT	180
15	GGTGAGATTG TATTTCATG TGTGTGTATC ASCTGAATGT TGCTGGAAAT AAAACCTTGG	240
	TTGTGTAAGG CTCATTTTTC TGGGAAGTAA GTAGGGGAAA AGGTCTTTGA GGGTTCCTAG	300
	GCTCCTTTGT ACACAGGAA AATGCCTCAA AGCCTTGCTT CCCAGCAACC TGGGGCTGGT	360
20	TCCAGTGGC TGGTCTGCC CCTTCTGGT TCTTATCTCA AGGCAGAGCT TCTGAATTC	420
	AGGCCTTCAT TCCAGAGCCC TCTGTGGCC AGGCCTTCCT TTGCTGGAGG AAGGTACACA	480
25	GGGTGAAGCT GATGCTGTAC TTGGGGGATC TCCTTGGCCT GTTCCACCAA GTGAGAGAAG	540
	GTACTTACTC TTGTACCTCC TGTTCAGCCA GGTGCATTAA CAGACCTCCC TACAGCTGTA	600
	GGAACTACTG TCCAGAGCT GAGGCAAGGG GATTTCTCAG GTCATTGGA GAACAAGTGC	660
30	TTTAGTAGTA GTTCAAAGTA GTAACGCTA CTGTATTAG TGGGGTGAA TTCAGAAGAA	720
	ATTGAAGAC CAGATCATGG GTGCTCTGCA TGTGAATGAA CAGGAATGAG CCGGACAGCC	780
35	TGGCTGTGAT TGCTTCTTC CTCCCATTT GGACCTTCT CTGCCCTTAC ATTTTGTTT	840
	CTCCATCTAC CACCATCCAC CAGTCTATTT ATTAACCTAG CAAGAGGACA AGTAAAGGGC	900
	CCTCTTGGCT TGAATTTGCT TCTTCTTTC TGTGGAGGAT ATACTAAGTG CGACTTTGCC	960
40	CTATCCTATT TGGAAATCCC TAACAGAATT GAGTTTCTA TTAAGGATCC AAAAAGAAAA	1020
	ACAAATGCT AATGAAGCCA TCAGTCAAGG GTCACATGCC AATAACAAT AAATTTCCA	1080
45	GAAGAAATGA AATCCAATA GACAAATAAA GTAGAGCTTA TGAAATGGTT CAGTAAGGAT	1140
	GAGTTGTG TGTTTGTGTT TGTTTGTGTT TGKTTTMTA AAGACGGAGT CTCGCTCTGT	1200
	CACTCAGGCT GGAGTGCAGT GGTATGATCT TGGCTCACTG TAACCTCCGC CTCCCGGGTT	1260
50	CAAGCCATTC TCCTGCCTCA GTCTCTGAG TAGCTGGGAT TACAGGTGCG TGCCACCATG	1320
	CCTGGCTAAT TTTGTGTTT TTAGTAGAGA CAGGGTTTCA CCATGTTGGT CGGGCTGGTC	1380
55	TCAAACCTCT GACCTCTTGA TCCGCTGCC TTGGCTCCC AAAGTGATGG GATTACAGAT	1440
	GTGAGCCACC CGTGCCTAG CCAAGGATGA GATTTTAAA GTATGTTTCA GTTCTGTGTC	1500
	ATGGTTGGAA GACAGAGTAG GAAGGATATG GAAAAGTCA TGGGAAGCA GAGGTGATTC	1560
60	ATGGCTCTGT GAATTTGAGG TGAATGGTTC CTTATTGTCT AGGCCACTTG TGAAGAATAT	1620

GAGTCAGTTA TTGCCAGCCT TGGAAATTAC TTCTCTAGCT TACAATGGAC CTTTTGAACT 1680  
GGAAACACC TTGTCTGCAT TCACTTTAAA ATGTCAAAAC TAATTTTAT AATAAATGTT 1740  
TATTTTCACA TTGAAAAAAA AAAAAATTT AAAAACYCGG GGGGGGCCCS G/ACCCCAT 1800  
NGCCCCTAAG GGGGGGGTT T 1821

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1024 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GGGCGCAGT TGAAGAAGCG ACCGAGGGAC TGGGAGTCGT TAGTGAGGAT GACGCGGCAT 60  
GGCAAGAACT GCACCGCAGG GCCGTCTACA CCTACCAGA GAAGAAGAAG GACACAGCGG 120  
CCTCGGGCTA TGGGACCCAG AACATTCGAC TGAGCCGGGA TGCCGTGAAG GACTTCGACT 180  
GCTGTTGTCT CTCCCTGCAG CCTTGCCACG ATCCTGTTGT CACCCAGAT GGCTACCTGT 240  
ATGAGCGTGA GGCCATCCTG GAGTACATTC TGCACCAGAA GAAGGAGATT GCCCGGCAGA 300  
TGAAGGCCTA CGAGAAGCAG CGGGGCACCC GGCAGGAGGA GCAGAAGGAG CTTACGCGGG 360  
CGGCTCGCA GGACCATGTG CGGGGCTTCC TGGAGAAGGA GTCGGCTATC GTGAGCCGGC 420  
CCCTCAACCC TTTCACAGCC AAGGCCCTCT CGGGCACCAG CCCAGATGAT GTCCAACCTG 480  
GGCCAGTGT GGGTCCTCCA AGTAAGGACA AGGACAAAGT GCTGCCCAGC TTCTGGATCC 540  
CGTCGCTGAC GCCGAAGCC AAGGCCACCA AGCTGGAGAA GCCGTCCCGC ACGGTGACCT 600  
GCCCCATGTC AGGAAGCCC CTGCGCATGT CGGACCTGAC GCCCGTGAC TTCACACCGC 660  
TAGACAGCTC CGTGGACCGC GTGGGCTCA TCACCCGAG CGAGCGCTAC GTGTGTGCCG 720  
TGACCCGCGA CAGCTGAGC AACGCCACCC CCTGCGCTGT GCTGCGGCC TCTGGGCTG 780  
TGGTCACCCT CGAATGCGTG GAGAAGCTGA TTCGGAAGGA CATGGTGGAC CCTGTGACTG 840  
GAGACAACT CACAGACCGC GACATCATCG TGCTGCAGCG GGGCGGTACC GSTTCGCGGG 900  
CTCCGAGTG AAGCTGCAAG CGGAGAAATC ACGGCCGGT ATGCAGGCCT GAGTGTGTGC 960  
GGGAGACCAA ATAAACCGGC TTGGGTGCGC AAAAAAAAA AAAAAAAAA AAAAAAAAA 1020  
AAAA 1024

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 983 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CGACACGGCT GCGAGAAGAC GACAGAAGGG CCCGACCGCG AGCGTCCAG GTCTCAGTGC 60  
TGTGCCCCC CCAGAGCCTA GAGGATGTTT CATGGGATCC CAGCCACGCC GGGCATAGGA 120  
GCCCCTGGGA ACAAGCCGGA GCTGTATGAG GAAGTGAAGT TGTACAAGAA CGCCCGGGAG 180  
AGGGAGAAGT ACGACAACAT GGCAGAGCTG TTTGCGGTGG TGAAGACAAT GCAAGCCCTG 240  
GAGAAGGCCT ACATCAAGGA CTGTGTCTCC CCCAGCGAGT AACTGCAGC CTGCTCCCGG 300  
CTCCTGGTCC AATACAAAGC TGCCTTCAGG CAGGTCCAGG GCTCAGAAAT CAGCTCTATT 360  
GACGAATTCT GCCGCAAGTT CCGCCTGGAC TGCCCGCTGG CCATGGAGCG GATCAAGGAG 420  
GACCGGCCCA TCACCATCAA GGACGACAAG GGCAACCTCA ACCGCTGCAT CGCAGACGTG 480  
GTCTCGCTCT TCATCACGGT CATGGACAAG CTGCGCCTGG AGATCCGCGC CATGGATGAG 540  
ATCCAGCCCC ACCTGCGAGA GCTGATGGAG ACCATGCACC GCATGAGCCA CCTCCCACCC 600  
GACTTTGAGG GCCGCCAGAC GGTGAGCCAG TGGCTGCAGA CCCTGAGCGG CATGTCGGCG 660  
TCAGATGAGC TGGACGACTC ACAGGTGCGT CAGATGCTGT TCGACCTGGA GTCAGCCTAC 720  
AAGCCTTCA ACCGCTTCCT GCATGCCTGA GCGCGGGCA CTAGCCCTTG CACAGAAGGG 780  
CAGAGTCTGA GCGGATGGCT CTTGGTCCCC TGTCCGCCAC ACAGGCCGTG GTCATCCACA 840  
CAACTCACTG TCTGCAGCTG CTTGTCTGGT GTCTGTCTTT GGTGTCAGAA CTTTGGGCC 900  
GGGCCCCCTC CCACAATAAA GATGCTCTCC GACCTTCAA AAAAAAAAAA AAAAAAAGR 960  
KSGGGCCGGT CCCANTCCC CCC 983

## (2) INFORMATION FOR SEQ ID NO: 46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2421 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

CCGGCTGATC GCTGCCGCTC CGCCAATACA ATAGAGCCAK CCACTACCAG CAGCCTGGCC 60

	CTCTTCCTCC TTCTCCAGAG AGACCAATCC AGCCGAATC GGGTTTGCC TGAGGAGAAG	120
	GAGGAAGTGA CCATGGACAC AAGTGAAAAC AGACCTGAAA ATGATGTTCC AGAACCTCCC	180
5	ATGCCTATTG CAGACCAAGT CAGCAATGAT GACCGCCCGG AGGGCAGTGT TGAAGATGAG	240
	GAGAAGAAAG AGAGCTCGCT GCCCAAATCA TTCAAGAGGA AGATCTCCGT TGTCTCAGCT	300
10	ACCAAGGGGG TGCCAGCTGG AAACAGTGAC ACAGAGGGGG GCCAGCCTGG TCGGAAACGA	360
	CGCTGGGGAG CCAGCACAGC CACCACACAG AAGAAACCTT CCATCAGTAT CACCACTGAA	420
	TCACTAAAGA GCCTCATCCC CGACATCAAA CCCCTGGCGG GGCAGGAGGC TGTGTGGAT	480
15	CTTCATGCTG ATGACTCTCG CATCTCTGAG GATGAGACAG AGCGTAATGG CGATGATGGG	540
	ACCCATGACA AGGGGCTGAA AATATGCCGG ACAGTCACTC AGGTAGTACC TGCAGAGGGC	600
20	CAGGAGAATG GGCAGAGGGA AGAAGAGGAA GAAGAGAAGG AACCTGAAGC AGAACCTCCT	660
	GTACCTCCCC AGGTGTCACT AGAGGTGGCC TTGCCCCCAC CTGCAGAGCA TGAAGTAAAG	720
	AAAGTGACTT TAGGAGATAC CTTAACTCGA CGTTCCATTA GCCAGCAGAA GTCCGGAGTT	780
25	TCCATTACCA TTGATGACCC AGTCCGAACT GCCCAGGTGC CCTCCCCACC CCGGGGCAAG	840
	ATTAGCAACA TTGTCCATAT CTCCAATTTG GTCCGTCCTT TCACTTTAGG CCAGCTAAAG	900
30	GAGTTGTTGG GCGCACAGG AACCTTGGTG GAAGAGGCCT TCTGGATTGA CAAGATCAAA	960
	TCTCATTTGCT TTGTAACGTA CTCAACAGTA GAGGAAGCTG TTGCCACCCG CACAGCTCTG	1020
	CACGGGGTCA AATGGCCCCA GTCCAATCCC AAATTCCTTT GTGCTGACTA TGCCGAGCAA	1080
35	GATGAGCTGG ATTATCACCG AGGCCTCTTG GTGGACCGTC CCTCTGAAAC TAAGACAGAG	1140
	GAGCAGGGAA TACCACGGCC CTGCACCCC CCACCCCCAC CCCCGGTCCA GCCACCACAG	1200
40	CACCCCGGG CAGAGCAGCG GGAGCAGGAA CGGGCAGTGC GGGAACAGTG GGCAGAACGG	1260
	GAACGGGAAA TGGAGCGCGG GGAGCGGACT CGATCAGAGC GTGAATGGGA TCGGGACAAA	1320
	GTTCGAGAAG GGCCCCGTC CCGATCAAGG TCCCGTRACC GCCGCCGCAA GGAACGTGCG	1380
45	AAGTCTAAAG AAAAGAAGAG TGAGAAGAAA GAGAAAGCCC AGGAGGAACC ACCTGCCAAG	1440
	CTGCTGGATG ACCTTTTCCG AAAGACCAAG GCAGCTCCCT GCATCTATTG GCTCCCACTG	1500
50	ACTGACAGCC AGATCGTTCA GAAAGAGGCA GAGCGGCGG AACGGGCCAA GGAGCGGGAG	1560
	AAGCGGCGAA AGGAGCAAGA AGAAGAAGAG CAAAGGAGC GGGAGAAGGA AGCCGAGCGG	1620
	GAACGGAACC GACAGCTGGA GCGAGAGAAA CGTCGGGAGC ACAGTCGGGA GAGGGACAGG	1680
55	GAGAGAGAGA GAGAAAGGGA GCGGGACAGG GGGGACCGAG ATCGGGATAG GGAAAGGGAC	1740
	CGAGAACGAG GCAGGGAAG GGATCGCAGG GACACCAAGC GCCACAGCAG AAGCCGAGT	1800
60	CGGAGCACAC CTGTGCGGGA CCGGGGTGGG CGCCGCTAGC TGGGAAAACA CTAGAGCTGC	1860

AGGTACCAGC CACTCGGCCC CAGGGGGTTA TGGCCACAGA GGGATAGGCA CAGTCTCCAC 1920  
 CACCCTGGAG CCAAGGTCTT TTCACATCAC CTATCCCTAC ATACATACCA AATGGAAAAG 1930  
 5 TGGCCATCCT TTTCCCCCCA AACACACCCC CTTAACCTAT CTCTTGGGAC TTAGCCCGAC 2040  
 CCTCCCTCTC ATTTCCCAT T AAGTCTGAGA GGCAAGAGCT AGGTTAGGCA AGGAGGTGGT 2100  
 TGGCCAGAGA TGGGGAACAG CCAGGTGCCC CAGTCTCTG ATTTTTCCTC CATCCTGCTT 2160  
 10 ACCACCTCCC TGGGTACTTA CAGCCTTCTC TTGGGAACAG CCGGGGCCAG GACTGGGTCA 2220  
 CCTATGAGCT GAATCAGCAT CTCCTCCTGA GTCCAGGGC CCCTGCAGTT CCCAGTCTCT 2280  
 15 TCTGTCCTGC AGCCCTTGCC TCTTTCCAC AGGTTCCTACT TTATATCCAC CTTTTCCTTT 2340  
 TGTTCATTTT TTATTTTAT TTTTITATT ATTAAATGAT GTGGTCTATG GAAAAAATA 2400  
 TAAAAATCTG ACTTAGTTTT A 2421  
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(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CTCAAACTCC TGAGCTGAAG CGATCTACCT GCCTCAGCTA GGATTACAGG TGTGAGCCAC 50  
 35 CGCACCCAAC CTCAATAAGC KTATTTGATA AAKATATGC AAGCTCCCTT TATKCACTTT 120  
 TCATTCAGAA TGTTAGTAA TTGTATGT TTTTCAGATT TTCAGCCCA TATATCTCTT 180  
 40 TGCCCACTGT GTCACGTAT TCTACCTAWA CATCATCAG TGTTCCTGCT ATGGCTGTA 240  
 TGATGGAACA CTGCGGCTCA TTTCTGAA AACTGCCGAT AGTGCATAGA RTGCTGGGAT 300  
 GGAAACCAGA ARCTTTGAAT TCAAGCCTTG GTTCTGCCTT GTTTTGTCTT GGGTGGCCTT 360  
 45 GAGTCAGCCA CATACCTTTT AAAATCTCAA TTTATTAGAA ATTATTCCTA ATCAAAATCA 420  
 AATGAGAAGG TATATACAAA AGTGCTTTAT CCCACAATAA ACTATTCAG AGAGAGCAA 480  
 50 GGAGAGGACA TTTACTCAAC ACCTCTAAA AGGCAGCCAG TGAAATTAGG CATTTTATTT 540  
 AATCCTCTG GCAACTCTGA GAGTAAAGCA TTATTAATCC CATTTTGGCT GTTTAAAGAA 500  
 ATTATTGCA CTAGATTCCA GCTGTAGTTT AGYTTGAGAA AAAAAATCC TGAGATGTGA 560  
 55 ATTCACAGCT TTCTGGGTTT AAAGCCCAAG CTCTATCACA TCATGCTATT ATTGTTACAT 720  
 TACTGCTAGT TCTATGAAA GAAATACTAA TTTATGAAAT ACATCTTATC CAAAAAATA 780  
 60 AAAAAAATC TGGGAGGGGG GGCCGTACC CAAATCGCCG GATAGTGATC GTAAACAATC 840



## 5 (2) INFORMATION FOR SEQ ID NO: 48:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2432 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

15 GGCACGAGGC CCGGAACGCT GAGGAAGGGC CCGTCCCGCC TTCCCCGGCG CGCCATGGAG 60  
CCCCGGGCGG TTGCAGAAGC CGTGGAGACG GGTGAGGAGG ATGTGATTAT GGAAGCTCTG 120  
CGGTCATACA ACCAGGAGCA CTCCAGAGC TTCACGTTTG ATGATGCCCA ACAGGAGGAC 180  
20 CGGAAGAGAC TGGCGGASTG CTGGTCTCCG TCCTGGAACA GGGCTTGCCA CCTCCACC 240  
GTGTCATCTG GCTGCAGAGT GTCCGAATCC TGTCCCGGA CCGCAACTGC CTGGACCCGT 300  
25 TCACCAGCCG CCAGAGCCTG CAGGCAYTAG CCTGYTATGY TGACATCTCT GTCTCTGAGG 360  
GGTCCGTCCC AGAGTCGCA GACATGGATG TTGTA CTGGA GTCCCTCAAG TGCCTGTGCA 420  
ACCTCGTGCT CAGCAGCCCT GTGGCACAGA TGCTGGCAGC AGAGGCCCGC CTAGTGGTGA 480  
30 AGCTCACAGA GCGTGTGGG CTGTACCGTG AGAGGAGCTT CCCCCACGAT GTCCAGTTCT 540  
TTGACTTGCG GCTCCTCTTC CTGCTAACGG CACTCCGCAC CGATGTGCGC CANAGCTGTT 600  
35 TCAGGAGCTG AAAGGAGTGC GCCTGCTAAC TGACACACTG GAGCTGACGC TGGGGGTGAC 660  
TCCTGAAGGG AACCCCCAC CCACGCTCCT TCCTTCCCAA GAGACTGAGC GGGCCATGGA 720  
GATCCTCAAA GTGCTCTTCA ACATCACCTT GGA CTCCATC AAGGGGGAGG TGGACGAGGA 780  
40 AGACGCTGCC CTTTACCGAC ACCTGGGGAC CCTTCTCCGG CACTGTGTGA TGATCGCTAC 840  
TGCTGGAGAC CGCACAGAGG AGTTCCACGG CCACGCAGTA ASCCTCCTGG GGA ACTTGCC 900  
45 CCTCAAGTGT CTGGATGTTT TCCTCACCTT GGAGCCACAT GGAGACTCCA CGGAGTTCAT 960  
GGGAGTGAAT ATGGATGTGA TTCGTGCCCT CCTCATCTTC CTAGAGAAGC GTTGTGCACAA 1020  
GACACACAGG CTGAAGGAGA GTGTAGCTCC CGTGCTGAGC GTGCTGACTG AATGTGCCCCG 1080  
50 GATGCACCGC CCAGCCAGGA AGTTCTTGAA GGCCAGGTG CTGCCCCCTC TCGGGGATGT 1140  
GAGGACACGG CCTGAGGTTG GGGAGATGCT GCGGAACAAG CTGTCCGCC TCATGACACA 1200  
55 CCTGGACACA GATGTGAAGA GGGTGGCTGC CGAGTTCTTG TTGTCTCTGT GCTCTGAGAG 1260  
TGTGCCCCGA TTCATCAAGT ACACAGGCTA TGGGAATGCT GCTGGCCTTC TGGCTGCCAG 1320  
GGGCCTCATG GCAGGAGGCG GCCCGAGGGC AGTACTCAGA GGATGAGGAC ACAGACACAG 1380  
60

ATGAGTACAA GGAAGCCAAA GCCAGCATAA ACCCTGTGAC CGGGAGGGTG GAGGAGAAGC 1440  
 CGCCTAACC TATGGAGGGC ATGACAGAGG AGCAGAAGGA GCACGAGGCC ATGAAGCTGG 1500  
 5 TGACCATGTT TGACAAGCTC TCCAGGAACA GAGTCATCCA GCCAATGGGG ATGAGTCCCC 1560  
 GGGGTCATCT TACGTCCCTG CAGGATGCCA TGTGCGAGAC TATGGAGCAG CAGCTCTCCT 1620  
 CGGACCCTGA CTCGGACCCT GACTGAGGAT GGCAGCTCTT CTGCTCCCC ATCAGGACTG 1680  
 10 GTGCTGCTTC CAGAGACTTC CTTGGGGTTG CAACCTGGGG AAGCCACATC CCACTGGATC 1740  
 CACACCCGCC CCACTTCTC CATCTTAGAA ACCCCTTCTC TTGACTCCCG TTCTGTTCAT 1800  
 15 GATTTGCCTC TGGTCCAGTT TCTCATCTCT GGA CTGCAAC GGTCTTCTTG TGCTAGAACT 1860  
 CAGGCTCAGC CTCGAATTCC ACAGACGAAG TACTTTCTTT TGTCTGCGCC AAGAGGAATG 1920  
 TGTTCAGAAG CTGCTGCCCTG AGGGCAGGGC CTACCTGGGC ACACAGAAGA GCATATGGGA 1980  
 20 GGCAGGGGT TTGGGTGTGG GTGCACACAA AGCAAGCACC ATCTGGGATT GGCACACTGG 2040  
 CAGAGCMANT GTKTTGGGT ATGTGCTGCA CTTCCAGGG AGAAAACCTG TCAGAACTTT 2100  
 25 CCATACGAGT ATATCAGAAC ACACCTTCC AAGGTATGTA TGCTCTGTTG TTCCTGTCTT 2160  
 GTCTTCACTG AGCGCAGGGC TGGAGGCTC TTAGACATTC TCCTTGGTCC TCGTTCAGCT 2220  
 GCCCACTGTA GTATCCACAG TGCCCGAGTT CTCGCTGGTT TTGGCAATTA AACCTCCTTC 2280  
 30 CTACTGGTTT AGACTACACT TACAACAAGG AAAATGCCCC TCGTGTGACC ATAGATTGAG 2340  
 ATTTATACCA CATACCACAC ATAGCCACAG AACATCATC TTGAAATAAA GAAGAGTTT 2400  
 35 GGACAAAAA AAAAAAAAAA AAAAAAAAAA AA 2432

40 (2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

50 GTCCTGCAGG AGCTGCACGC GGCCGAGGTG CGCANGAACA AGGAGCAGCG AGAAGAGATG 60  
 TCGGGCTAAG GGCCCGGSAC GRSGGGCGCC CATCCTGCGA CGGAACACGT TCGGGTTTGG 120  
 GTTTTGTTC GTTCACTCT GTCTAGATGC AACTTTTGTT CCTCCTCCCC CACCCAGCC 180  
 55 CCCAGCTTCA TGCTTCTCTT CCGCACTCAG CCGCCCTGCC CTGTCTCTGT GGTGAGTCGC 240  
 TGACCACGGC TTCCCTGCA GGAGCGCGCG GCGGTGRAGA CCGGTCCCT CCGTGCAGAC 300  
 60 ACCAGGCCGG GCGCGGCTGG GTCCCCGGG GGCCTGTGA GAGAGGTGGY GGTGACCGT 360

GTAAACCCAG GCGGCTGGCG TGGATCRCG GGTCTTACG CTGGGCTGTC TGGTCAGCAC 420  
GTGCAGGTCA GGCAGGTCC TCTGAGCCGG CGCCCTGGC CAGCAGGCGA GGCTACAGTA 480  
5 CCTGCTGTCT TTCCAGGGGG AAGGGGCTCC CCATGAGGRA GGGGCGACGG GGGAGGGGGG 540  
TGATGGTGCC TGGGAAGCCT GCKTGTGCAN CCGGTGCTTG TTGAACTGGC AGGCGGGTGG 600  
10 GTGGGGGCTG CAGCTTTCCT TAATGTGGTT GCACAGGGGT CCTCTRAGAC CACCTGGCGT 660  
GAGGTGGACA CCCTGGGCCT TCCTGGAAGC CTGCAGTTGG GGGCCTGCCC TGAGTCTGCT 720  
GGGGAGTGGG CATCTCTGTC CAGGGACCCA TGAGCAGGCT GCATGGTCTA GAGGTTGTGG 780  
15 GCAGCATGGA CAGTCCCCCA CTCAGAAAGT CAAGAGTTCC AAAGAGCCTC TGGCCCAGGC 840  
CCCTCCGTGG GACAGCCCCG CCGCCCCCTCC CCACCAGGGC TTTGCAGATG TCCTTGAAAG 900  
20 ACCCACCCTA GAGCCCTTTG GAGTGTCTGGC CCCTCCTGTG CCCTCTGCCC TGGTGGAAAGC 960  
GGCASCACAA GTCCTCTCTA GGGAGCCCCA AGGGGGATTT TKTGGGACCG CTGCCCACAG 1020  
ATCCAGGTGT TGAAGGGCA GCGGTAAGG TTCCCAAGCC AGCCCCAACA CCCTTCCCAC 1080  
25 TTGGCACCCA GAGGGGGCTG TGGGTGGAGG CCTGACTCCA GGCCTCTCCT GCCCACACCC 1140  
TCTGGGCTGA GTTCTTCTT TCCCTTGGAC GCCCAGTGCT GGCCTTGGAG GACGGTCAGC 1200  
30 TGGAGGATGG CCGTGGGGGA GGCTGTCTTT GTACCACTGC AGCATCCCC ACTTCTCCAC 1260  
GGAAGCCCCA TCCCAAAGCT GCTGCCTGGC CCCTTGCTGT AAAGTGTGAA GGGGGCGGCT 1320  
GAGTTCTCTT AGGACCCAGA GCCAGGGCCC TCAACTTCCA TCCTGCGGGA GGCCTTGGCC 1380  
35 GGGCACTGCC AGTGTCTTCC AGAGCCACAC CCAGGGACCA CGGGAGGATC CTGACCCCTG 1440  
CAGGGCTCAG GGGTCAGCAG GGACCCACTG CCCCATCTCC CTCTCCCCAC CAAGACAGCC 1500  
40 CCAGAAGGAG CAGCCAGCTG GGATGGGAAC CCAAGGCTGT CCACATCTGG CTTTGTGGG 1560  
ACTCAGAAAG GGAAGCAGAA CTGAGGGCTG GGATATTCTT CATGGTGGCA GCGCTCATAG 1620  
CGAAAGCCTA CTGTAATATG CACCCATCTC ATCCACGTAG TAAAGTGAAC TAAAAAATTC 1680  
45 AATCAAATGA ACAATTAAAT AAACACCTGT GTGTTTAAGA AAAAAAAAAA AAAAAAATG 1740  
CG 1742

50

(2) INFORMATION FOR SEQ ID NO: 50:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

	GGCACGAGCC TCCGCGAACT GTGAGTCCG CGAGGGCTG GAATCAGCGT GGGCTCCAGG	60
5	TCGCTGGCAG CCGGGTGGCA GAACTCTTCC GAGGCTCCTT GGGAAGAAGC TACACCCGAG	120
	GGAGCCGAT GGGCCTCGAA AACCTGGCCC GCTCTGGTTC TGTACCATTG CAAGGGGAAC	180
	CGTAAACTGA GCTTTTCTAA CGTGGGTTC TGCCAAGTAC TTTTCCAGCT GGGCCCTTCC	240
10	CCCCAGCACA CAGGAGAGCC TCTGTGTAGC CAGCGCTTGA CAGTCGTTAG GTAGGTTGTA	300
	CTGTGTAGGG AGGAGCTCAA GATCATGAAT GGTGTGCACA GGAGAAAGCG GTTGCATCTT	360
15	TGCAAACTA TATACCTGCT GTGGTTTGTG TTTTCTTTC TGCTGAGTAA TGAAGTTGTA	420
	AGTTCACACT GGCACATTCT CAGGGCTGTG CAGATTATTT GCACTTTATT TCATAGGTGR	480
	ATAAGTGCTT TTTAGCTTTC TTTGTATATT GAGTTGCTTT TGAATGCTT CCCATATTTT	540
20	TATTTCATAC AAACTGAACA ATTGTGGCCC CTCTATTTTA TTTATAAAGG TTCAGTGTAT	600
	CTTTGCCTGC CTACATCAAT CTGCAAGGGA GTTGCAGAAA GCCTCATGTT CATCGAGCCG	660
25	TGAGTCACAA CCAATTTCTA AGCTGTTATA ACAAAAAAGT GTTTGCTTTT TTTTACAAGT	720
	AACTTTAAAA GTGTAGTTTA GAAAGAAAAC ATTTTCAATA AAAAGACACT ACATTAATCC	780
	TGGATGCTTG CAAATCCTAA AATMTATTCC TCCTCTAGCG TTGCACAGCT CTGTGTTGTA	840
30	TACACAGACT AGCTTTAAAA TTTGTCACAT ACCACTTTAC CTTTACTTTT ATGTATCATT	900
	CCCCCGACTT CCTTACTGCA GGTGTGGGCA AGAAAACTTT TCCTTTAACA CTTTCAACA	960
35	GCGGGCATAA AATTCTGCAG CTGAGGTCTT GAAGAATGCA GATGGGTACA GTATGTGTTG	1020
	GAGCTCACAG TGTGTATTGA CTAACCTAGT TCCTTTTTTG CTTTTTTTGG TATTGTCTTG	1080
	TTAAAAGTGA CTCCCAGGTA GCAACTCTCT TTTTAAAGG TGGGAACGAA AGGGACGTAG	1140
40	GAAGAATAGA TCTAGATTAT TTAACAGTCT TCGATAGAGT TTGAAAGCTT TCTTCTTCAT	1200
	TCAATTTTGG GCAAAATACT GCCTCTGCAT TTGTTCATAA CAAAAGATT AGATTAATAA	1260
45	GTAGCTTTTG TTGGTGGAAA TTACCAGCTC TATAAGTCAC CCTTGGTGGT TCATGGACCT	1320
	CTGATTAGCT TGGGTTTTGC AGTCTCATTG CCACATGTAT ATGTGGAGCC AATGGCCTTT	1380
	TGGTGCTCAG CTGTTTACGT CTGACTCCTT GACTTCTTTG GTACAGTGAT GGAGTCAGAT	1440
50	CTCATTAAGT GTGATTCTCC ATGGATATAA CCAGCCCCAA AAAAANG	1487

55

## (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1328 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

5 GGCACGAGCT CGTGCCGAAT TCGGCACGAG AGAAGATTG AAGAAGCCAG ATCCAGCTTC 60  
CCTGCGGGCT GCTTCTGTG GGAAGGGAA AAAGAGGAAG GCCTGTAAGA ACTGCACCTG 120  
10 TGGCCTTGCC GAAGAACTGG AAAAAGAGAA GTCAAGGGAA CAGATGAGCT CCCAACCCAA 180  
GTCAGCTTGT GGAAACTGCT ACCTGGGCGA TGCCTTCCGC TGTGCCAGCT GCCCCTACCT 240  
TGGGATGCCA GCCTTCAAAC CTGGGGAAA GGTGCTTCTG AGTGATAGCA ATCTTCATGA 300  
15 TGCTTAGGAG GTTCCTGACA TGGGACCCAT CTGCTCCTCC AGCCAACTCC TGTCCCTCAC 360  
ATCCCACCAT GGTGGCTCCT CCCACCTCCT CTGGATTTGT TCACTCTGAG ATCTGTTTGC 420  
20 AGAGTGGGTG CTTAGCAGAC AGAGTGAAGC TGGCTGGGGG GCACAGTGGT GTGTAGTGCT 480  
GCTGTGTATC AAAAGACCAA GGTATTATGG GACCTGGTTT CAGAATGGGA TGGGTTTCTT 540  
CACCTCATGT TAAGAGAAGG GAGTGTGTCC TGAAGAAGCC CTTCTTCTGA TGTAAAATG 600  
25 CTGACCAGAA CGCTCTTGAG CCCAGGCATC GTTGAGCATT AACACTCTGT GACAGAGCTG 660  
CAGACCCCTG CCTTGAGTCT CATCTCAGCA ATGCTGCCAC CCTCTTGTCT TTCAGAGTTG 720  
30 TTAGTTTACT CCATTCTTTG TGACACGAGT CAAGTGGCTC ACAACCTCCT CAGGGCACCA 780  
GAGGACTCAC TCACTGGTGT CTGTGATGAT ATCCAGTGTC CCTCTGCCCC CTTCATCCC 840  
CAACCACATT TGA CTGTAGC ATGCACTG TGCTCTGTTG TCATTTATGT TAACCTTCAG 900  
35 GTATTAAACT TGCTGCATAT CTTGACATAT CTTGAGATTC TGCATGTCTT GTAAAGAGAG 960  
GGGATGTGCA TTTGTGTGTG ATGTTGGATA GTCATCCACG CTCAGTTTGG ACCATTGGAG 1020  
40 GAACTTAGTG TCACGCACAA ATGGGGCTAT TCCTACGCTT AGAATAGGGC TTGTCTGCCC 1080  
ACTTTAGAAG AGTCCCAGGT TGGTGAGCAT TTAGAGGGAA GCAGGGCAGA ACTCTGAACG 1140  
ACAATACGTC TCTCTGAGCA GAGACCCCTT TGTTCTTGTT ATCCACCCAT ATGGACTTGG 1200  
45 AATCAATCTT GCCAAATATT TGGAGAGATT GTGTGGATTT AAGAGACCTG GATTTTTATA 1260  
TTTTACCAGT AAATAAAAGT TTTCATTGAT ATCTGTCCTT GAAAAAAAAA AAAAAAAAAA 1320  
50 AAACTCGA 1328

55 (2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1856 base pairs

(B) TYPE: nucleic acid

60 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

5	GAATTCGGCA CGAGCTCTGC AACATTGCAA ATGAATTTGT AGCCGAGGGT TCCGCTGCCC	60
	CCTAGATTAA ATTCCCGGGG CTGAATTTGA GTTCAGATT TACATATCA TATTTTAAAT	120
	TGCTGTCTTC AATTAAACCA TTTATGACCA TAATTAATTT TCAAGATGTC GATGCATGCT	180
10	TTTCCAGGCC TTCCCTCTTT GTACAAAGT AAATGTGCAT AAGCGTTTC ACTTATAATC	240
	TTCAAACATG ATGCTAATTT AAATTAATA CTTCCTATGA TATGTTATTA TTCCTATGAT	300
15	TTTGCCACTG TTATTAGTTC TCTCAAAAT ACATCTAGGG AAGAGGATTA TTTTAAGTRA	360
	TTTGATTATC TTCTATCTC TTTTATTTAT TTCTCAATTA CTTACGAAAT TCGTTCCATT	420
	GGTGGCATT GATACAGTAA ATTTGTAAAT GAGGAGACCA TAAAAAAAT CTAAATTACT	480
20	TGTGCTTAAT GACTGTAGCA GAATSCCTTT TCTCTAAATC AGATTGTCTT TCTTGCAGTT	540
	TAGTTTGATA GATTTCGAAG CTATGCTGCT TCCATGAAGT TACCTGCGCT GGTAGGAACG	600
25	CAGGCTTCTT TGTCTCTGGT TGTAGCTTGC ATGATGCGCT CATTAGGCGG ACAACGTAGC	660
	CGGAGATCAC AAATCAGGCC CTGGGTGTAG TTGCTAGTGT GTGGAGGTGC AGAGAGGTTC	720
	GCAGAACTG ACCTCACTGG GCAAGGCTGG CCAAGGACCT GATTCTTTTA TGCACCTCTAT	780
30	GTGTTTCAGGA AGCCACAGGC CATATTTCAC TCTGAGAAAG AAAACAAGAG GAAAAACCCC	840
	ACAAAGTATA ACAACCCCTT AAGATACATC TATTTTAAAG TGAATTAAT TTTTCAGTTT	900
35	ATACCATTGG CCAATTACAA GATAAAATG TTCAATTTCT TTAAGATCC TTTGTTGACT	960
	TGCTTTTTCA TCTCTTGCTA TTATATTTTG TCACTGTTAG TCAACAAAGT CTTATTGCT	1020
	GAGGAAGGAC TTTGCTGCAC TTAAGTACG ACATCAACCA CTGGGGAGGG TGGTGTTTAA	1080
40	CTTTTAAAAA AATGTTATTC TGATTATTAAC AATAAATTC GCTTTTTCAT TGAAAAGAGC	1140
	GCCACCTTGC AAGGTTTAGT GAGATTTCAG GAGTTGAAI ACCTAGCGG GAATTGCTGC	1200
45	TAGCTCCAAA AATTGCGGAA GCAAAACCTA GCCCCATTG GTTTGGAAGT TTGAAACTGA	1260
	TTAACAGATT TGCATTTGAA GTGACTCGG ACATTAGGTC CAGACATTAG TTAAAAATAG	1320
	AAAGAGGAAT AAAGACATCT YTTCTCTCTA GAAAAGATAA CACCTCAATT AATAATCCTT	1380
50	CCCACCTTCA TTGAGATCAG CTTGTCTGAT AACCTGATAI GAGTGTGACA ATGATAAACA	1440
	TGATAATAGT GGTACTTTTG TAATTTTGCT GGTGCATTIA ABAAGATAGT AAKGATGAG	1500
55	TTCACTTTT CTYCGAACAT YCCTATTCCT AGATGTAGTT TACCTCAAAT TGGGAATTAT	1560
	AACTGTCTTA ATTTTGTGTG TGTACCTTGA TGCCCTTTT GCTTTAATAC CCACAGTGTA	1620
60	ACAATTAAAT ATCACACTAT GACATAAGAT TTAGTAGGA TATTTTAAAG ATAAATTTTA	1680

	GGGGTAAATG TTTACTTCAA AATGACTCCA TATTTCAAAT ATCTGTTTAG ACTGTGAAGG	1740
	CCAAATAATT TTTAAGAAAA CATTGAAGA GTAGTGTGTT TGCATTTGTG AATAATCTTA	1800
5	CTCACAGCAA GTAAACGTAA TAAAGCCAA CATTTAAGCC AAAAAAAAAA AAAAAA	1856
10	(2) INFORMATION FOR SEQ ID NO: 53:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1558 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:	
20	TGGGTATCCA TTCCTGNAAT TACTTTACTT AGGATAATGG CCTCCAGCTC CGTCCAAGTT	60
	GCTGCAAAG GTATTATTTC GTTCCTTTTT GTGGCTGAGT AGTATTCCAT GGTGTATATA	120
	TACCACATTT TCTTTATCCA CTCATTGCCT GATGGGCAGT TAGGTTGGTT CCACATCTTT	180
25	GCAATGTGA GTTGTGCTGC TCCAGATATC ATCTTTAACT CCTTTGCCTT CTCCACATAC	240
	ATTTCCAAGT CCTGTTCAAT CTACCTCCAA AATGTATCTT GTATCCATTC ATCTCTCTCC	300
30	ATCTTCAATC TATTTCAATG CCCCATCATC TCTTGCATGG AGGAGTGTA TAATGGCTA	360
	ACTGGCCTGT TCTTACATTT TAAATCAAA AGATGTGACA GGTGAAATGC CTATTTTCAGT	420
	GTCCATTGAT GGTTCCTGCTT ACACACCACC TGGCTGCCTG GTGTGCGAGT GGCAGAGTTG	480
35	AGCAGTGTGA AAAAGACTGC TTGGCCCTTT ACAGGGAAAG CAGGTCCACT GTGGCCTGTG	540
	AGGACGAGAG CTCTGGGCAG GCTCGGACAC TGGCAGACCC TGGTCCTGGC TGGCCAAGGC	600
40	AGCAGGGTAT GTGTTTCGGG TCACTCACAG GGCTCAGCAC CACTCCTCAT GGCTTCCTTA	660
	CTGTTTCGGC AGAGGCTGAC CCGCGGCTGA TTGAGTCCCT CTCCCAGATG CTGTCCATGG	720
	GCTTCTCTGA TGAAGCGGC TGGCTCACCA GGCTCCTGCA GACCAAGAAC TATGACATCG	780
45	GAGCGGCTCT GGACACCATC CAGTATTCAA AGCATCCCC GCCGTGTGA CCACTTTTCG	840
	CCACCTCTTC TGGTGCCCC TCTTCTGTCT CATAGTTGTG TTAAGCTTGC GTAGAATTGC	900
50	AGGTCTCTGT ACGGGCCAGT TTCTCTGCCT TCTTCCAGGA TCAGGGGTTA GGTGCAAGA	960
	AGCCATTTAG GGCAGCAAAA CAAGTGACAT GAAGGGAGGG TCCCTGTGTG TGTGTGTGCT	1020
	GATGTTTCCT GGGTGCCCTG GCTCCTTGCA GCAGGGCTGG GCCTGCGAGA CCCAAGGCTC	1080
55	ACTGCAGCGC GCTCCTGACC CCTCCCTGCA GGGGCTACGT TAGCAGCCCA GCACATAGCT	1140
	TGCCTAATGG CTTTCACTTT CTCTTTTGTT TTAAATGACT CATAGGTCCC TGACATTTAG	1200
60	TTGATTATTT TCTGCTACAG ACCTGGTACA CTCTGATTTT AGATAAAGTA AGCCTAGGTG	1260

TTGTCAGCAG GCAGGCTGGG GAGGCCAGTG TTGTGGGCTT CCTGCTGGGA CTGAGAAGGC 1320  
 TCACGAAGGG CATCCGCAAT GTTGGTTTCA CTGAGAGCTG CCTCCTGGTC TCTTCACCAC 1380  
 5 TGTAGTTCTC TCATTTCCTAA ACCATCAGCT GCTTTTAAAA TAAGATCTCT TTGTAGCCAT 1440  
 CCTGTAAAT TTGTAAACAA TCTAATTAAA TGGCATCAGC ACTTTAACCA AAAAAAAAAA 1500  
 10 AAAAAAAAAA AAANAAAAAA AAAAGGGGGC CGCTCTAGAG GTCCAAGTTA NGACGNGG 1558

15 (2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 948 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

25 TAAAAATCAT GCTCTGTACC ATCCTCACCG TAGTCATCAT CATCGCCGCG CAGACCACGA 60  
 GAACTACTGG GATCCCTAAA AACGCCCTG GTCCGGCCCC ACTCTGGGCC CCTCGATCTC 120  
 CCAGGCTCTT TCTGCAGWCA TACCGCGGAC CCAATGGGCG CCCTGCACAC CCGTTTCTGG 180  
 30 GGCCGTCAGA CTTGGATACA TCGTAAACTC CGCCTCCACG GAACGTCTCG CCTKGCGAGC 240  
 AAGMTCGGAA TCCAGTTCCT CAGGAACCCC TCCAAAACCC ACACCCCAG GGACGCCGCT 300  
 35 TTCCGGGATC CCGGSCAAAC GCCGACCCT CAGTCGCTCC AGGCCCCCTC ACCCTCAAAG 360  
 TGTAGCGCCC CCAACCGAGC AACCTCGGTT TGGTCCCTAA AACCCCGCCT CCTCTATAAG 420  
 CACCGCCCCA GCTCTGACAA AACCCCGCCT CCAGGTCGGC AGGCTCCGCT TCTTTTCTTC 480  
 40 TCCGCGGGGT GATTCACTCC AGTGATTGGG TTTGTGGCTC CAGGCCTCGC CCACAGACGG 540  
 ACAGACCCTT CCCTTTCTTC CGGCAAAAGG ACCGAGCCCT GGGGTAGTAA GGSCCCACA 600  
 45 CTCTGTMTT TTGCAAGTAC ATTTTGTGCC YTCCTCCACC CAGGTATCTG CCTATTTTCT 660  
 TGCTAATCCC AGAACCTTC CTTTGTCTTT TTTTAAGGAC ATTTGGAAG TTCCTGGTGT 720  
 AGGACCCTTC TCCCTGGGAT AAGAAACCTG CCTGTAAACG CTCTGTAAAT ACTCCCTTCC 780  
 50 ACCCATCCCA GCCCCTGGGC AGCCGGGCAG AAGGGAATCC AGGCTATGGA CCTCCCAAGT 840  
 CCCCCTCCCG CGCTCCCTTC GCGGCCCCCG CCTGTGTTCTG ATCTGTGTGT GAGTGTGTGT 900  
 55 GAACTTCTGA AAGACAATAT TAAAGAGACT TAGTTGAAAA AAAAAAAA 948

60 (2) INFORMATION FOR SEQ ID NO: 55:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

10 GGGGAAGTGC AGTGACAGCA GGAGTAAGAG TGGGAGGCAG GACAGAGCTG GGACACAGGT 60  
ATGGAGAGGG GGTTCAGCGA GCCTAGAGAG GGCAGACTAT CAGGGTGCCG GCGGTGAGAA 120  
TCCAGGGAGA GGAGCGGAAA CAGAAGAGGG GCAGAAGACC GGGGCACTTG TGGGTTGCAG 180  
15 AGCCCTCAG CCATGTTGGG AGCCAAGCCA CACTGGCTAC CAGGTCCCCT ACACAGTCCC 240  
GGGCTGCCCT TGGTTCGGT GCTTCTGGCC CTGGGGGCCG GGTGGGCCCA GGAGGGGTCA 300  
20 GAGCCCGTCC TGCTGGAGGG GGAGTGCCCTG GTGGTCTGTG AGCCTGGCCG AGCTGCTGCA 360  
GGGGGGCCCG GGGGAGCAGC CCTGGGAGAG GCACCCCTTG GCGAGTGGC ATTGTGTCG 420  
GTCCGAAGCC ACCACCATGA GCCAGCAGGG GAAACCGCA ATGGCACCAG TGGGGCCATC 480  
25 TACTTCGACC AGGTCTGGT GAACGAGGGC GGTGGCTTTG ACCGGGCCTC TGGCTCCTTC 540  
GTAGCCCTG TCCGGGGTGT CTACAGCTTC CGGTTCATG TGGTGAAGGT GTACAACCGC 600  
30 CAACTGTCC AGGTGAGCCT GATGCTGAAC ACGTGGCCTG TCATCTCAGC CTTTGCCAAT 660  
GATCCTGACG TGACCCGGA GGCAGCCACC AGCTCTGTGC TACTGCCCTT GGACCTGGG 720  
GACCGAGTGT CTCTGCGCCT GCGTCGGGGG NAATCTACTG GGTGGTTGGA AATACTCAAG 780  
35 TTTCTCTGGC TTCCTCATCT TCCCTCTCTG AAGGACCCAA GTCTTTCAAG CACAAGAATC 840  
CAGCCCTGA CAACTTCTTT CTGCCCTCTC TTGCCCCANA AACAGCANAA GCAGGANANA 900  
40 NACTCCCTCT GGTCTCTATC CCACCTCTTT GCATGGGAAC CTGTGCCAAA CACCCAAGTT 960  
TAAGAAAAAA ATAAACTGT GGCATCTCCA 990

45

## (2) INFORMATION FOR SEQ ID NO: 56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1603 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

50 GGTCGACCCA CGCGTCCGGC CCGCCGGCTC CGGAGCGGCT CTGCCTTCCC GAGCGCGGGA 60  
CCGCGCCCTG GGGGAGGAGG GCGAACGACG CGGCGATGGC TCCGCGGCA CTCCCGGGT 120  
60

	CCGCCGTCCT AGCCGCTGCT GTCTTCGTGG GAGGCGCCGT GAGTTCGCCG CTGGTGGCTC	180
	CGGACAATGG GAGCAGCCGC ACATTGCACT CCAGAACAGA GACGACCCCG TCGCCCAGCA	240
5	ACGATACTGG GAATGGACAC CCAGAATATA TTGCATACGC GCTTGTCCTT GTGTTCCTTA	300
	TCATGGGTCT CTTTGGCGTC CTCATTTNGC CAMCTNGCTT NAAGAAGAAA GGCTATCGTT	360
	GTACAACAGA AGCAGAGCAA GATATCGAAG AAGAAAAAGG TTGAAAAGWT AGRATTGAAT	420
10	GACAGTGTGA ATGAAAACAG TGACACTGTT GGGCAAATCG TCCACTACAT CATGAAAAAT	480
	GAAGCGAATG CTGATGTYTT AAAGGCGATG GTAGCAGATA ACAGCCTGTA TGATCCTGAA	540
15	AGCCCCGTGA CCCCCAGCAC ACCAGGGAGC CCGCCAGTGA GTCCTGGGCT TTGTCACCAG	600
	GGGGGACGCC AGGGAAGCAC GTCTGTGGCC ATCATCTGCA TACGGTGGGC GGTGTWGTCC	660
	AGAGGGATGT GTGTCATCGG TGTAGGCACA AGCGGTGGCA CTTTATAAAG CCCACTAACA	720
20	AGTCCAGAGA GAGCAGACCA CGGCGCCAAG GCGAGGTCAC GGTCTTTTCT GTTGGCAGAT	780
	TTAGAGTNAC AAAAGTGGAG CACAAGTCAA ACCAGAAGGA ACGGAGAAGC CTGATGTCTG	840
25	TTAGTGGGCG TGAAACCGTC AATGGGGAGG TGCCGGCAAC ACCTGTGAAG AGAGAACGCA	900
	GTGGCACAGA GTAGCAGGTG AGCCGTGGTT TTGGTGACAT TGGGGGCAGA GTGGTGCAGG	960
	GTGAGGAGAA GGTACTTTGA GCCTCCCAGG TGCTGTGGCA GCATAGGAAT GGTATTTGAC	1020
30	AGGGAAGTGG GAGAGCTTTC CTTGACCCAG GAAGACTGAG GGGGACTGAA CATGATTACT	1080
	TGTCTGCCTA GAGCTTCTTG TAAAGAAGTC ACAAACTTAG TGCCTCCAGG GGCTTGGCTG	1140
35	TGTGATAATG AGGATAGAGG ATTACTTGTG AGGCAATGTG GCATGGTGGG GATTGTGGCA	1200
	AACTAGAATT CACATCACCC ACCATATAGG GCTTGCATTA CCACGAGGCA GAAAGCACCT	1260
	AGTGTGCTG CATCTTCTTA CGCAAAAAG ACAAAATCCA GACTTCTAAA ATGTAAATC	1320
40	ACTGATTTTC GATATTGGCA GCTTACTTTT TTTTTTTAAA CAACCATGCA GGCCAAATGA	1380
	CTTGTAATCT TGTACCACTT TTTAGGTAAA CTGTGACTTG AAAAAGTCTG GAGCAAACAA	1440
45	ACCAATGCTT TTTCCTTTTA TTCTGTGGR AACCAGTTTT CTTGTGTGCA CAGTTYTGAA	1500
	ACCTCAATAC GAATATTTCT CTTCCACCA AATATTTTGA GGCAATTGAA AAGCCACAGT	1560
50	GATTTATTTT TTGATTGGC AATTTTAATT TTGCAAGACA ATT	1603

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1052 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

5 TACAGCTCAG GATGCCTGTA ACATTGTCAT CTCTGGGCTT CTGGGTCCTG CTTAGCCTGC 60  
 TTTTCCCTG GAGGACTGAC CAGGGATGCG GCCCAGCAAC ATGTTACTAA ATCATACTCT 120  
 CCTCCCTACC TTTCCAGAC CTCTCACTCC TGCCTGGTGT TCCAAACCGT TCTGTGGCCA 180  
 10 GAGTATACAT TTTGGAACCT CTTGAGGCC ATCCTGCAGT TCCAGATGAA CCATAGCGTG 240  
 CTTCAGCAGN AAGGCCCCGAG ACATGTATGC AGAGGAGCGG AAGAGGCAGC AGCTGGAGAG 300  
 GGACCAGGCT ACAGTGACAG AGCAGCTGCT GCGAGAGGGG CTCCAAGCCA GTGGGGACGC 360  
 15 CCAGCTCCGA AGGACACGCT TGCACAACT CTCGGCCAGA CGGGAAGAGC GAGTCCAAGG 420  
 CTTCTGCAG GCCTTGGAAC TCAAGCGAGC TGA CTGGCTG GCCCGTCTGG GCACTGCATC 480  
 20 AGCCTGAATG AGGCTGGCCA CTTGCCACTT TGCCCTGCCC TCTGCCTCCA GGGCTCCMCT 540  
 MYCCTTCCTT TTCTTGGTGA AAGGCACCTC CTTTCTGAT AATGAATGGT GTTCCCTTTG 600  
 CTTGGCTGGG GAGCCCCCA GGCCAGGTTT GCTGGCCATA GATACCTTTG GGCTGCCTGR 660  
 25 GACAGGCTCC TGAGGAGGAT TGAGGGTGAA AGTCTCCAC GAGTACACTA AACCTAGGTC 720  
 TGGTCACCAA TAGGGTTTGG AGAGCAAAGG GCCACAATC ATCAGCTGCC TGTCTCTTAG 780  
 30 ATGCACTTT TTTTCCACC AGCACATCCT TCAACACACA GAATTTTCAGG GAAGAGTTCT 840  
 CCCCAAAACC CTAGCTCTTT ACCCTTCCAT TTTAGCCTTC CACCCAGCTT CCACAAAAGA 900  
 TTTGGCTCTA CTTGGATCT GCTAGTAAAT AACTAATAGG CAGGCAGTTA TTTGGGTAAG 960  
 35 GAAAAAAGGG GTGGGAGAGA CAGAAAATT GCCCACTGCT GCTCCTCCCC TTGGSTYTCC 1020  
 ACCTGGGATT TGCTATTGAA TCTCTACCCT NN 1052  
 40

## (2) INFORMATION FOR SEQ ID NO: 58:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 814 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

ACNCGNTGGC GGCCGCTCTA GAACTAGGGG ANCCCCCGG CTGCAGGAAT TCGGCACGAG 60  
 55 CATAGACTTT TAAACTGGTA CGGTCTTAG AGATGGTCCT TGGCCTCTG TTGTGTGTGT 120  
 KGTMTTTC TTTTCTTCT TCTCCTCTC CTTCTCTTC TCTCTCCTT CTTCTCTCTT 180  
 TTTTTCAT GAGTCTGCT CTGTACCAA GACTGGAGTG AAGTGATGTG ATCTCGGCTT 240  
 60

ACTGCAACCT GGGAGGCAGA GGTTCAGTG AGTCGAGATG GTGCCATTGC TCTCGTTTGG 300  
 GCAACAAGAG TGAAACTCTT GTCTCAAAAA AAAAAAAAAA ATGAGGTTTA AGACAGTTTT 360  
 5 GTCAATTACTG GTGGGATCTG GTCACACAAG ATAGCATTAA ACGTGACATG GCACATAAAA 420  
 TTGGTTAAAA AATTTTGT TTAAATTACG TAATGTAAAA GCCCAACAAA CACTTTATGC 480  
 AAGATTGGA TGTATCTTCA AATTCAGATT TAATAACAT GTAAAGATCC TCTGTATATA 540  
 10 AAAGTTGTAT TTAATCCCTT GTGCCCCAAG AATGCTATAA AAGATCCCAA GAATGTTATC 600  
 TATGAAAAGA TAGCAATAGG GAATGGTGAA CAAATAATTT AATTGCCAA TTCTAAAAAA 660  
 15 CATGGACTTA AACCCCATGA AAACCTGGTT CCATAGTTTT AACTGTTTTA TGGTTCCAAT 720  
 ACAAACCAG AGTGGTTTAC ATTCCACAAT NACCAAATTT GCATCCAATN TTGGGGTAAT 780  
 TTTNGGTATT TGCCATGGGA TACTATTTCAT TTTT 814  
 20

25 (2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

35 AGAGGAAGTC TTTTGCCAAG CCTGTTCTCT GGAATAACGC CATCCAGGCT GGGAGGGGAA 60  
 GAGTGCTCTG CTACACTCGT CCCCCTCCTG CCTCATCTTC CTTCTCAGCC TTGGTTCTCTG 120  
 ATGGGAACAG AATGGAGGCG CTGAGAACAT ACTTTCTAAA TGCCTTTGAC CCAGGAACCG 180  
 40 ATTATCTATA TTTGTTCCCA TTTTCTCTCA CCGTGACATT CCAGCATTGT CTGACTGTGA 240  
 GGTGGGCCTT TGAGAGCCTC CAGGTTCTCT AAAACAGGCC TGAGCGATGG GCATCACACC 300  
 CTCTGCCTAC CCACRTGCCT GCTTACCTGC CAGATAACCA AGTGNAGATG TCTGCGAGTG 360  
 45 GCTAGTTTTT ACATTCTTAC TAGTGTTTGG YTCACCTTTG GGCAAAGGCC CCTCTAGGC 420  
 CTTGCCCCAC CTCCATCAAA CGCAGACACT GTAGTCAGAC CTCAGYAATA TAGGAGGCAA 480  
 50 TAATCTTTTA ACAGTGTTTT GCAAACAAAC AAAAAGAGAA AAATCCCAGC CAGGGGAACT 540  
 CGCCACCTGC CCACGCTAGT TCCATCCACG CTCAAGACCC GCCCTTAGAC CAGGCAGGCA 600  
 AAGGCCCCCA TCACACTCGG CCACTAGTGG GGTCTGAGG CCAAGAAAGA AACCAGACCC 660  
 55 TGTATGACAA GTTGGGKTCT TTCCAGAACA CGACAGAAAC AGGGGGGGCC CCTTGTTAAT 720  
 GCCACTCCAT ACTCCAGAAG CATTATTCCT TATTTGGGAC AGCCAAGGGC AGATTACAG 780  
 60 GTTATTGTAG GAATAAGAC TAGTTTACAA AGGARAAGA GSCCCTGGAC TTCCCMAGGA 840

AAGGTCAGGT TAGGGCTCCT GTACCCATTC TGTTCACCA CTGTTTGATC TCTCTGGCCT 900  
 CCCACCAGGA ATGCCGTTTC CTTTTTATGG ATCTGTTGGG AACCAGAGAG AATCAACAGA 960  
 5 TCAATGACAT AGGATCCGAA GTGCAATGAT AGTCACTTCT AGTTTGGCAT TTCACAAACT 1020  
 CTGNACAGCA AGGTATTGGT AGGTTACTCA ATTTCAAAAG GGCCCCATGG CCAAATATGT 1080  
 10 TTAGGAACCG CTGTTTGNAT TTCTTTT TTTT GGAGACGCAT TGTATATAAT ATATGTCAAA 1140  
 GGCTTTCGGA ATTCCTGCAG GAAAGAAATC AGCTTTGTGA AATCCNAAAA AAAAAAAAAA 1200  
 AAAAAAATAG ACTCG 1215  
 15

20 (2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 478 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

30 ATTTCTTATG ACATGGGGGT TTGAATTGGT TGGCAAATGT TTAATTTTAA TATCCATAAT 60  
 CAGTGAGGTC CTGCTGGCTG TAATCATTAA TTGTGAAATC TAAGGAGCTT AGTTCATGGC 120  
 TCTAGAATTT CACAGAAAAR TGYGMTATGA TACGAGCATT AAGTTTATTT CTTCTGATCT 180  
 35 TTGATGCAGC TTTGTTCACT TTATCTGTTT TTGTATTTAT TGGTCATCTA CTTCCCATGC 240  
 CAAAAGGGAC TGGTCTACAT AGCTGCGCTA AACACCTGAT CAAATCACTA AAAGAAAATG 300  
 TGTACCTCT AATGAATTAT CCTGATTGTA AGTTAAAAAT CAATATTTCC CCGTAGTGAG 360  
 40 GTTTGCTTTT TAAAAGAAK KCTTAAAAAA AAAAAAAAAA AAACGAGTTN AAGAAAAGGA 420  
 AGCAAGCTCA GGTAAGGTGC ACACATTGGG CTAAGGAAGC TAGAGCCTGT GGAGANGC 478  
 45

50 (2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 618 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TATGACCTTG ATAACCCCAA GTTNGAAATT AACCTTCANT AAAGGGAACA AAAGCTGGAG 60  
 60 TTCCGCGCCT TGCAGTTGCA CACTAGTGGA TCCCAAAGAA TTCGGCACGA GTCATAATGA 120

5 GCTACTAGGT AAGCCTTCTG GGACTTTCAG ATATTTTGGG GAAGATTGAT TTTTGTCTTT 180  
 ACATGCTGTG GACCCCTGGC CATCAAATGG TATGGGGAAG CTCATCCGTC TGTCTGTGAT 240  
 GGTCAATGTC GTCAGGCGTC TTTTGTAGTAT TTACTGGGTG CTCAGTACTG TGCCAGATGC 300  
 TGTGCGGAGC CGTGGTGGTA TGGAGGAGGA GTGCTCCAGA GGACTCTGCT GTGTGGCAGG 360  
 10 CCAGCATAAA CAAGCCAAGG GGAAAAGGCA GGCATGGAAT AAAGGGGGAG AATACCAAGT 420  
 TGTGACTTAC TGCTGACTGT GTGGATTAGC CTATCAGCAG TAATCAAGCA GGGCGGAGGG 480  
 15 CATTATCTTT GAGCCAGAAG AGTGAGCACT GGSCCGAGGG TGGAGCATCA AGAGGGGGTG 540  
 TAGGACCNCA AGGCTTCTTN CNGGGGAGAC AACGTCAATA AGCNGTCAGT AGTCACCGAC 600  
 AGTTTGGGA AGCAAGG 618

## (2) INFORMATION FOR SEQ ID NO: 62:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 751 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCGACCCACG CGTCCGAGGA GCTGGACTTC TGAGACAGCC ATTCTCCTTG CATAGCACTG 60  
 35 TCTGCTGCTA CAGCTCATAG AAGTCAACAA TTTTCTTCAA CACTGGTAGG CAGCCTCTAA 120  
 ATGGCCCTGA TCACCCCTCAC CTCCTGCCAT TCACACCMNT GTAAAATTCC ACCCCTGGAC 180  
 40 CTAGTGACTC ACTTCTAACA ANGAGAATAC AGCAAAAGTA ACATCGCTTC TGAGGTGAGG 240  
 CTACAAGGAG ACTACGATGC CTGCCTTGGT CACCCCTTCTC CTGCTCTTTC CATTGCTCCC 300  
 TCTGATGGAA GCCAGTTGCC ATGTGATGAG GTGCCCTATG GAGAGGCCCA CGTGACAAGG 360  
 45 TATTGTAAAA AGCCTCTGAC CAATAGCCAT CTAGAAACGG AGGCCAGTC CAGCAGCCTC 420  
 TGAGATGAAT CCTGCCAACC TGAGCTTGA GACAGATTCT CTCCCTATCC TGCCTTGGGA 480  
 50 TGATCACAGC CACCACCAAC ACCTTCACTG CCTGGTGAGA GGCCAAGCCA GTGAACCCAA 540  
 GGTAACTGG ACAGAATCCT GACCCACAGA AACTGAGATA ATGTTTGTTA TTTTAAGCTG 600  
 CTCAGTTTGT TACAGAGCAA TAGATACTA ACTCAAACAC CATAAAATTC TAATATTTTA 660  
 55 TTCTATCACA CAAACCAGGT AATACCAAGT AAATGCCATT ACTATACACA TATTTTGTGA 720  
 ACACAATTAC ATGTGATTTT TTAAGAAGGC T 751

## (2) INFORMATION FOR SEQ ID NO: 63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CNGXCACTCA CXTGCCCGA TCCCCGGTC GACCCACGCG TCCGGGTGG CAACTCCTGA 60  
GGCCTGCATG GGTGACTTCA CATTTTCCTA CCTCTCCTTC TAATCTCTTC TAGAGCACCT 120  
GCTATCCCCA ACTTCTAGAC CTGCTCCAA CTAGTACTA GGATAGAATT TGATCCCCTA 180  
ACTCACTGTC TCCGGTGCTC ATTGCTGCTA ACAGCATTGC CTGTGCTCTC CTCTCAGGG 240  
CAGCATGCTA ACGGGGCGAC GTCCTAATCC AACTGGGAGA AGCCTCAGTG GTGGAATTCC 300  
AGGCACTGTG ACTGTCAAGC TGGCAAGGGC CAGGATTGGG GGAATGGAGC TGGGGCTTAG 360  
CTGGGAGGTG GTCTGAAGCA GACAGGGAAT GGGAGAGGAG GATGGGAAGT AGACAGTGGC 420  
TGATGATTTG GGGGCTTGGG AGTCCCTTTG TCCTCATCTG AGACTGAAAT GTGGGGATCC 540  
AGGATGGCCT TCCTTCCTCT TACCCCTTCT CCCTCAGCCT GCAACCTCTA TCCTGGAACC 600  
TGCTCTCCCT TTCTCCCCAA CTATGCACT GTTGTCTGCT CCTCTGCAA GGCCAGCCAG 660  
CTTGGGAGCA GCAGAGAAAT AACAGCATT TCTGATGCCA AAAAAAAAAA AAAAAAACC 720  
GCGGCCGAAA GCTTATTNCC CTMTAAGTAA GGGTTAATT TTTAGCTTGG GCACTNGGCC 780

## (2) INFORMATION FOR SEQ ID NO: 64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

TTCCGAATTA ATCGACTCAC TATAGGAAT GCCGTGCCA TGACCCGCGG TAACCAGCGT 60  
GAGCTCGCCC GCCAGAAGAA TATGAAAAG CAGAGCGACT CGGTTAAGGG AAAGCGCCGA 120  
GATGADGGGC TTTCTCTGCT CCCCCGAAG CAGAGGGACT CGGAGATCAT GCAGCAGAAG 180  
CAGAAAAAGG CAAACGAGAA GAAGGAGGAA CCAAGTAGC TTTGTGGCTT CGTGTCCAAC 240  
CCTCTTGCCC TTCCGCTGTG TGCCTGGAGC CAGTCCCACC ACGCTCGCGT TTCTCCTGT 300

322

AGTGCTCACA GGTCCCAGCA CCGATGGCAT TCCCTTTGCC CTGAGTCTGC AGCGGGTCCC 360  
TTTTGTGCTT CCTTCCCTC AGGTAGCCTC TCTCCCCCTG GGCCACTCCC GGGGGTGAGG 420  
5 GGGTTACCCC TTCCCACTGT TTTTATTCC TGTGGGGCTC ACCCCAAAGT ATTAAGTA 480  
GCTTTGTAAT TCCAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 540  
AAAAAAAAA AAAAAAAAAA AAAANNCGGG GGGGGGCCCC CCCCCCCC 588

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTTAAAGATG AAGAAATGAC AAGGGAGGGA GATGAGATGG AAAGGTGTTT GGAAGAGATA 60  
AGGGGTCTRA GAAAGAAATT TAGGGCTCTG CATTCTAACC ATAGGCATTC TCGGGACCGT 120  
CCTTATCCCA TTTAATTAAT TTCTCTGACA ATTCAATTAT TTTCTGTTAT TAATGTTGCC 180  
30 ACTGCTTTCT GTTTGTCTGC ACTTTCTTGA TAAATATTG CTATCGTTTT ACTCCAGTCA 240  
TTCGATGTTG CTGAGATTTA CATATGACTC TTGTCAACAT CTCATCTTTT GACCCAATCT 300  
TATTCATTTA ATAAGAGGTC TCATTCATTT GCATGGAAAA ATGCTCATTG TATATTGCAA 360  
35 AGTGAAAATA ACGAGTTGCA AACAGTGTA TACATATATG TGTGTATATA TGTACACTTT 420  
ATTTGTACAT TTCTATGTGA CATAATGCAA AGGAAAGTGT CTGATTTTAT TATACACCAA 480  
40 AGGTAAACAG TGAATCTCTG TGTGATCTCT TTTTTTTCT TTTTGCCTAT CTGCATCTTC 540  
TCACTTGCCA AAAAATGAAT ATATGTTTAT GTGTGTATAT TACTTGTGTC ACAAAAACC 600  
CTAAAGTAGA CAGTAAAAGA ACTTGTCAAT CGCCTTTGGA AGGCAATGAA ACACTTAATA 660  
45 AACTCTCAAT AACAGAAGCG TAAAAATGAA ATGTAAACCT CCAATTACCT CTGGATCTCT 720  
TAGCCAGAGT AATAAAGTGG TAATTATTAC AGATAAAAAA AAAAAAAAAA AANA 774

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1866 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

	ACCCACGCGT CCGGTCCTCT TCTTCAGCAC ATGCCAAAGC TGTTCCTCAC GGCCTGTGAG	60
5	ACAAGAGCAT CTTGGATGTA GGACAATGGA AGAGTTAGAT GCCTTATTGG AGGAACTGGA	120
	ACGCTCCACC CTTCAGGACA GTGATGAATA TTCCAACCCA GCTCCTCTTC CCCTGGATCA	180
10	GCATTCCAGA AAGGAGACTA ACCTTGATGA GACTTCGGAG ATCCTTCTTA TTCAGGATAA	240
	CACAAGTCCC TTGCCGGCGC ATTCGTGTAT ACTACCAATA TCCAGGAGCT CAATGTCTAC	300
	AGTGAAGCCC AAGAGCCAAA GGAATCACCA CCACCTTCTA AAACGTCAGC AGCTGCTCAG	360
15	TTGGATGAGC TCATGGCTCA CTGACTGAG ATGCAGGCCA AGGTTGCAGT GAGAGCAGAT	420
	GCTGGCAAGA AGCACTTACC AGACAAGCAG GATCACAAGG CCTCCCTGGA CTCAATGCTT	480
	GGGGGTCTSG AGCAGGAATT GCAGGACCTT GGCATTGCCA CAGTGCCCAA GGGCCATTGT	540
20	GCATCCTGCC AGAAACCGAT TGCTGGGAAG GTGATCCATG CTCTAGGGCA ATCATGGCAT	600
	CCTGAGCATT TTGTCTGTAC TCATTGCAAA GAAGAGATTG GCTCCAGTCC CTTCTTTGAG	660
25	CGGAGTGGCT TGGNCTACTG CCCCAACGAC TACCACCAAC TTTTCTCTCC ACGCTGTGCT	720
	TACTGCGCTG CTCCCATCCT GGATAAAGTG CTGACAGCAA TGAACCAGAC CTGGCACCCA	780
	GAGCACTTCT TCTGCTCTCA CTGCGGAGAG GTGTTTGGTG CAGAAGGCTT TCATGAGAAG	840
30	GACAAGAAGC CATATTGCCG AAAGGATTTC TTAGCCATGT TCTACCCAA GTGTGGTGGC	900
	TGCAATCGCC CAGTGTGGA AAACCTACCTT TCAGCCATGG AACTGTCTG GCACCCAGAG	960
35	TGCTTTGTTT GTGGGGACTG CTTCAACAGT TTTTCTACTG GCTCCTTCTT TGAAGTGGAT	1020
	GGACGTCCAT TCTGTGAGCT CCATTACCAT CACCGCCGGG GAACGCTCTG CCATGGGTGT	1080
	GGGCAGCCCA TCACTGGCCG TTGTATCAGT GCCATGGGGT ACAAGTTCCA TCCTGAGCAC	1140
40	TTTGTGTGTG CTTTCTGCCT GACACAGTTG TCGAAGGGCA TTTTCAGGGA GCAGAATGAC	1200
	AAGACCTATT GTCAACCTTG CTTCAATAAG CTCTTCCAC TGTAAATGCCA ACTGATCCAT	1260
45	AGCCTCTTCA GATTCTTTAT AAAATTAAAA CCAAGAGAGG AGAGGAAAGG GTAAATTTTC	1320
	TGTTACTGAC CTTCTGCTTA ATAGTCTTAT AGAAAAAGGA AAGGTGATGA GCAAATAAAG	1380
	GAACCTCTAG ACTTTACATG ACTAGGCTGA TAATCTTATT TTTTAGGCTT CTATACAGTT	1440
50	AATCTATAA ATTCTCTTTC TCCCTCTCTT CTCCAATCAA GCACTTGGAG TTAGATCTAG	1500
	GTCTTCTAT CTGCTCCCTC TACAGATGTA TTTTCCACTT GCATAATCA TGCCAACACT	1560
55	GGTTTCTTA GGTTTCTCCA TTTTCACCTC TAGTGATGGC CCTACTCATA TCTTCTCTAA	1620
	TTTGGTCCTG ATACTTGTTT CTTTTCACGT TTTCCCATTT CCCTGTGGCT CACTGTCTTA	1680
60	CAATCACTGC TGTGGAATCA TGATACCACT TTTAGCTCTT TGCATCTTCC TTCAGTGTAT	1740

TTTTGTTTTT CAAGAGGAAG TAGATTTTAA CTGGACAACT TTGAGTACTG ACATCATTGA 1800  
TAAATAAACT GGCTTGTGGT TTCAATAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1860  
5 AAAAAA 1866

10 (2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1152 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

20 CTCAAGGATG TAAAGGCTCT GCAGATTTTCG GGAGGCCTGT CTCCCAGCAC CTGATGGGAC 60  
ACTTTTGGCC CCACTGTAAA TTCTGGGTGT ATCCTCCACT GTATGCTGTC ACCCCAAGGG 120  
CAAGCACTGC ATCTGCTTAG TGAAGGATTT ATTGTTCCGA AGATACATTT TCCCCTTKAG 180  
25 CAGAGAGTGG CGTATCCTGG CAGTCTTCGG TGAGCCAGTT GTACCAGGAT TATGAAATGC 240  
AGATGTTTAC TGTGTCAATTG TTGCTGTCAT TGCTACTGAG GAGTACTGAC CAGAATCATC 300  
30 TGCAACTYTT AGTTGGCAGA GAGGACCACT ATGCGGGTA GCTCTTTTCT TTCCTGCCAT 360  
TGTGGGGATG ATTCCAGGCC AAAGATGATG GARAAGTATG GAAATCATCT GAAAGGTTGA 420  
AGCTTGCCAC GTGAAGCCAT TCATGACTTT GTAAGGCAGT TTTGCTGAAG GCCAGTTCTG 480  
35 CCCTGGGAGG GACGGAGGTG AATCCTCCTG AGTACCTGTG GPTTCTTAC TTCCTGCTGA 540  
ATTTACCTAA GTGCCTGTTG TTTGCTTGCT GTGGAGGCTT TCTGGTATTT CATTTCAGGT 600  
40 GCAGATGCCT TCACTTTCCC ACCRAAAAAA CCCCMACCAA ACCTAAGACC TTA CTGCAAC 660  
TAAGTYTNCC AAGTACTTTT TAACCAATG GGATGAACAG CCTGTGGTCT GCTCAGATCA 720  
CCCTGAGTGC GTGTGAGAAG GCMINGGCTT TGCCAGGAAA TCCAGGAAGG CAGGGCCGGG 780  
45 CTGTGTTGGA AGCTGGCTTA GCTGGTGGGG CAGCCTTATT TCAATTAAAA GGGCATTGAC 840  
TGGGAGCAGC AGTCCTGGAG TTTGTTGCAT TTCCTATTGC CCTCAAAATG AGAAACCAGG 900  
50 AAAATAGCAG ATTGGAGCCT TCGAGAAGGC AGTAAATGGC TGTTTTATT GACAAAAGGA 960  
AAACATTTTA CTGCCATCTC ACTGATGGCA TCTCACTGAC TTAAATGAA GGCANGTTGT 1020  
AGTAAAAAAA AAAGTCTACA TTTTCCACC GCCACGTTCT TATATCCTGT TTGTCAGCCA 1080  
55 CTGCTCANAA GGGCATGTTG TCTTCCGAN TANAGGCGCT CTCCTCCCT CGTTTCCCT 1140  
ATAGGTTGGG TG 1152

## (2) INFORMATION FOR SEQ ID NO: 68:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2483 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

AGCAGGCGGT GCGCTGGGGG CGGGAGCAGC GCGKAGCCCG GCTCGGCCAC ACCGATCGCC 60  
15 CGCCGCCATG GGCTCCTCGC AAAGCGTCGA GATCCCGGGC GGGGGCACCAG AGGGCTACCA 120  
CGTTCTGCGG GTACAAGAAA ATTCCCCAGG ACACAGAGCT GGTTTGAGC CTTTCTTTGA 180  
TTTTATTGTT TCTATTAATG GTTCAAGATT AAATAAAGAC AATGACACTC TTAAGGATCT 240  
20 GCTGAAASCA AACGTTGAAA AGCCTGTAAA GATGCTTATC TATAGCAGCA AAACATTGGA 300  
ACTGCGAGAG ACCTCAGTCA CACCAAGTAA CCTGTGGGGC GGCCAGGGCT TATTGGGAGT 360  
25 GAGCATTCGT TTCTGCAGCT TTGATGGGGC AAATGAAAT GTTTGGCATG TGCTGGAGGT 420  
GGAATCAAAT TCTCCTGCAG CACTGGCAGG TCTTAGACCA CACAGTGATT ATATAATTGG 480  
AGCAGATACA GTCATGAATG AGTCTGAAGA TCTATTCAGC CTTATCGAAA CACATGAAGC 540  
30 AAAACCATTG AAAGTGTATG TGTACAACAC AGACACTGAT AACTGTGAG AAGTGATTAT 600  
TACACCAAAT TCTGCATGGG GTGGAGAAGG CAGCCTAGGA TGTGGCATTG GATATGGTTA 660  
35 TTGTCATCGA ATACCTACAC GCCCATTGGA GGAAGGAAAG AAAATTCTC TTCCAGGACA 720  
AATGGCTGGT ACACCTATTA CACCTCTTAA AGATGGGTTT ACAGAGGTCC AGCTGTCCTC 780  
AGTTAATCCC CCGTCTTTGT CACCACCAGG AACTACAGGA ATTGAACAGA GTCTGACTGG 840  
40 ACTTTCTATT AGCTCAACTC CACCAGCTGT CAGTAGTGTT CTCAGTACAG GTGTACCAAC 900  
AGTACCGTTA TTGCCACCAC AAGTAAACCA GTCCCTCACT TCTGTGCCAC CAATGAATCC 960  
45 AGCTACTACA TTACCAGGTC TGATGCCTTT ACCAGCAGGA CTGCCCAACC TCCCCAACCT 1020  
CAACCTCAAC CTCCCAGCAC CACACATCAT GCCAGGGGTT GGCTTACCAG AACTTGTAAG 1080  
CCCAGGTCTG CCACCTCTTC CTTCCATGCC TCCCCGAAAC TTACCTGGCA TTGCACCTCT 1140  
50 CCCCCTGCCA TCCGAGTTCC TCCCGTCATT CCCCTTGGTT CCAGAGAGCT CTTCTGCAGC 1200  
AAGCTCAGGA GAGCTGCTGT CTTCCCTCCC GCCCACCAGC AACGCACCCT CTGACCCTGC 1260  
55 CACAACACT GCAAAGGCAG ACGCTGCCTC CTCACTCACT GTGGATGTGA CGCCCCCAC 1320  
TGCCAAGGCC CCCACCACCG TTGAGGACAG AGTCGGCGAC TCCACCCAG TCAGCGAGAA 1380  
GCCTGTTTCT GCGGCTGTGG ATGCCAATGC TTCTGAGTCA CCTTAACCTT GAACCATTTCT 1440  
60

326

	TTGGAATTGG CGTGGTATAT TTAACCACGG GAGCGTGTCT GGAAACGCAA ACTATCATTA	1500
	ATTTTCATACT AGTTTGTACC GTATCTGTAG GCATCCTGTA AATAATTCCTA AGGGGAAAAC	1560
5	TAAACGAGGA CGTGGGTTGT ATCCTGCCAG GTTGAGTGGG GCTCACACGC TAGGGTGAGA	1620
	TGTCAGAAAG CGCTTGTATT TTAACAACCC AAAAAGAATT GTAAGGGTGG CTTGCTGCCA	1680
	GGCTTGCACT GCCGTCCTG GGGGTGTGCA TCTTCGGGAA AGGTGGTGGC GGGGCGTCCA	1740
10	CTAGGTTTCC TGTCCCTGCG TGCTCCTTCC GTAAGAAAAT GAAATATTCT ATGCCTAATA	1800
	CTCACACGCA ACATTCTTG TACTTGTAA GTCGTTTGGC AGAATGCAGA CCACCTCACT	1860
15	AAACTGTAAA CGGTAAAGAG ATTTTACTTT TGGTCTCCG TGAGTCGCAT CTCTACTAAG	1920
	GTTTACACAG GAATTCACCC TGAAGACTTG TGTAAAGTT CTACAGCGCG CACTGTTAAC	1980
	TGAACGTCCT TTTCTTCAGC CTATACGCGG ATCCTTGTTT TGAGCTCTCA GAATCACTCA	2040
20	GACAACATTT TGTAAGTCT GCTGTTGCTT TCTACATACA CCTTATAAAG TGACATTTCA	2100
	AAAGAAATAA GGTGCCACAG TTTTAAACCA GAAGGTGGCA CTCTGTGGCT CCTTGTAGTA	2160
25	TTATAGCTAT ACTGGGAAAG CATAGATACA GCAATAAAGT ACAGTAATTT TACTTTTTTT	2220
	CTTGTGTAC ATCTAAATTA CAACCTTAA TTGCCACGTG TGCACCTACT ACTCTCCAGT	2280
	ATGTCTTATT ACTCTCCAGT ATGTCACGCA TCTTTAACTT TTCACGTCCT ATGTTTGCTT	2340
30	TCTCCCATTT TTAAGAGATG GTAAGTTAAC TGGAAATGAT TTACTGAATG AAATTAAATG	2400
	CAGATATCCC TGTTTTTGAA ATAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2460
35	AAAAAAAAAA AAAAAAAAAA AAA	2483

40 (2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

50	GAGAAATGGA GCTTTGTTAG ATAAAAATTT TTTCAACGCA AACAGTCATT TTCCAGTGAA	60
	AGGAGAGCGT ATCCGCCGTA GGATGGACTT AGATCGTGTA AAAGCTGAGG CCACCGAGGA	120
	TATAACCTCC GGGGTCCTTT GCCTCCTTTT CCTTAGACTC CCTCCAACT CGTGATCTT	180
55	TCCTTCAGCA GTACTGGGCT CCACGCGAAC CTAGTCCTTT GTCTTTACCC TATTACCTTT	240
	CATAACATCC TAGTTGAAAA GTATTATTTC AACCGCGTTT GAAAATGAGA ACAGGTTTAC	300
60	AGARGCTAGG TTACTTGCGA AGGTCGTTCA ATTAGTAACC AGTAACGCCA GGACTGCCAG	360

TTTCTTGCTT CGGAATCTC ATGGTAGCTT TCACCARGCT CCCCGTCMAA TGCTAACGTC 420  
AACTACTGAA CTAGATTAGC AAAAAGGTCT TTAAACAGAA TTCCTGGTTT TCAGAGAGAG 480  
5 TTTCTTTTCAT GAAGCGCCCC ATTTCTACAG AGGAAAATAA ACTCCAAGCA GCCAGT 536

10

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

25

CCACGCGTCC GGCTTTCTT GGCCAGAGGC GCCGGTTGGA CTCACGGGCG GGGCATGATG 60  
GGTAACAGGA CCGGTGGGGT CCCAGGAAG TCCTAGAGGG GGTGGGGTT TGGGTGGACA 120  
AGCTTTCCTC GTCTCTCCC GACAGAGCTG ACGTGTCTTG GGTCCACCG GGAGCGGGCA 180  
TTTCCACCGG ACGGGAGGGT TCGGGGTGTC CGGGGCTGGG GAATACGTAG GGGTTGCCGC 240  
GCGGTGTGGG GAGTTGGGGC GTGTGGCTGC AGTCCCGGA GTTCTTGGAG GGGGTCGGCC 300  
30 CACCGAGCTT CCGGACCGGC TGATCTGCCC GTAGCTTGCC GGANGGARGG CGGAGCTGAC 360  
TCTCCGTCCC TTCTCCCATC CCTCCAGTG GTGGGTACGG GCACCTCGCT GGCCTCTCC 420  
TCCCTCTGT CCTGTCTGT CTTGTCTGGG ATGCAGATGT ACAGCCGTCA GCTGGCCTCC 480  
ACCGAGTGGC TCACCATCCA GGGCGGCTG CTTGGTTCGG GTCTCTTCGT GTTCTCGCTC 540  
ACTGCCTTCA ATAATCTGGA GAATCTTGTC TTTGGCAAAG GATTCCAAGC AAAGATCTTC 600  
40 CCTGAGATTC TCCTGTGCCT CTTGTGGCT CTCTTTGCAT CTGGCCTCAT CCACCGAGTC 660  
TGTGTACCA CCTGCTTCAT CTTCTCCATG GTTGGTCTGT ACTACATCAA CAAGATCTCC 720  
45 TCCACCCTGT ACCAGGCAGC AGCTCCAGTC CTCACACCAG CCAAGGTCAC AGGCAAGAGC 780  
AAGAAGAGAA ACTGACCTG AATGTTCAAT AAAGTTGATT CTTTGTAAAA AAAAAAAAAA 840  
50 AAAAAAAAAA AAAAAAAAAA AAAAA 865

55

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

5 TCATCATATA CAAAGTTTTT CGTCACACTG CAGGGTTGAA ACCAGAAGTT AGTTGCTTTG 60  
 AGAACATAAG GTCTTGTGCA AGAGGAGCCC TCGCTCTTCT GTTCCTTCTC GGCACCACCT 120  
 GGATCTTTGG GGTTCCTCCAT GTTGTGCACG CATCAGTGGT TACAGCTTAC CTCTTCACAG 180  
 10 TCAGCAATGC TTTCCAGGGG ATGTTCAATT TTTTATTCCT GTGTGTTTTA TCTAGAAAGA 240  
 TTCAAGAAGA ATATTACAGA TTGTTCAAAA ATGTCCCCTG TTGTTTGGGA TGTPTAAGGT 300  
 15 AAACATAGAG AATGGTGGAT AATTACAACG GCACAAAAAT AAAAATTCCA AGCTGTGGAT 360  
 GACCAATGTA TAAAAATGAC TCATCAAAAT ATCCAATTAT TAACTACTAG AAAAAAGTA 420  
 TTTTAAATCA GTTTTTCTGT TTATGCTATA GGAAGTGTAG ATAATAAGGT AAAATTATGT 480  
 20 ATCATATAGA TATACTATGT TTTTCTATGT GAAATAGTTC TGTCAAAAAT AGTATTGCAG 540  
 ATATTTGGAA AGTAATTGGT TTCTCAGGAG TGATATCACT GCACCCAAGG AAAGATTTTC 600  
 25 TTTCTAACAC GAGAAGTATA TGAATGTCCT GAAGGAAACC ACTGGCTTGA TATTTCTGTG 660  
 ACTCGTGTG CTTTGAAAC TAGTCCCCTA CCACCTCGGT AATGAGCTCC ATTACAGAAA 720  
 GTGGAACATA AGAGAATGAA GGGGCAGAAT ATCAAACAGT GAAAAGGGAA TGATAAGATG 780  
 30 TATTTTGAAT GAACTGTTTT TTCTGTAGAC TAGCTGAGAA ATTGTTGACA TAAATAAAG 840  
 AATTGAAGAA ACACATTTTA CCATTTAAAA AAAAAAAAAA ACTNGAGGGG GGGCCGTAC 900  
 35 CCAAATCGCC GCATAGTGAT CGTAAACAAT CT 932

## (2) INFORMATION FOR SEQ ID NO: 72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

50 CGCCTGGCAC CATGAGGACG CCTGGGCCTC TGCCTGTGCT GCTGCTGCTC CTGGCGGGAG 60  
 CCCCCGCCG GCGGCCCACT CCCCCGACCT GCTACTCCCG CATGCGGGCC CTGAGCCAGG 120  
 AGATCACCCG CGACTTCAAC CTCCTGCAGG TCTCGGAGCC CTCGGAGCCA TGTGTGAGAT 180  
 55 ACCTGCCCAG GCTGTACCTG GACATACACA ATTACTGTGT GCTGGACAAG CTGCGGGACT 240  
 TTGTGGCCTC GCCCCCGTGT TGGAAAGTGG CCCAGGTAGA TTCCTTGAAG GACAAAGCAC 300  
 60 GGAAGCTGTA CACCATCATG AACTCGTTCT GCAGGAGAGA TTTGTTATTC CTGTTGGATG 360

ACTGCAATGC CTTGGAATAC CCAATCCCAG TGACTACGGT CCTGCCAGAT CGTCAGCGCT 420  
 AAGGGAAC TG AGACCAGAGA AAGAACCCAA GAGAACTAAA GTTATGTCAG CTACCCAGAC 480  
 5 TTAATGGGCC AGAGCCATGA CCCTCACAGG TCTTGTGTTA GTTGTATCTG AAACTGTTAT 540  
 GTATCTCTCT ACCTTCTGGA AAACAGGGCT GGTATTCCTA CCCNGGAACC TCCTTTGAGC 600  
 ATAGAGTTAG CAACCATGCT TCTCATTCCC TTGACTCATG TCTTGCCAGG ATGGTTAGAT 660  
 10 ACACAGCATG TTGATTTGGT CACCTAAAAA GAAGAAAAGG ACTAACAAGC TTCACTTTTA 720  
 TGAACAAC TA TTTGAGAAC ATGCACAATA GTATGTTTTT ATTACTGGTT TAATGGAGTA 780  
 15 ATGGTACTTT TATCTTTTCT TGATAGAAAC CTGCTTACAT TTAACCAAGC TTCTATTATG 840  
 CCTTTTCTA ACACAGACTT TCTTCACTGT CTTTCATTTA AAAAGAAATT AATGCTCTTA 900  
 AGATATATAT TTTAYGTAGT GCTGACAGGA CCCACTCTTT CATTGAAAGG TGATGAAAAT 960  
 20 CAAATAAAGA ATCTCTTCAC ATGARAAAAA AAAAAA 996

25

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 785 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

35 GGCACGAGGG GCTTTGCGTA CACAATAGCT GCTAGGAGTA CCCAAGCCT GARTACARCC 60  
 TGCTGGTGTC ATGGCCACGT GTGAGCAGGC CAGCGTCAMA CGGCTCGCTG TGACCCGTCC 120  
 40 CGRAGACTGA AATGGGCCCTG GGTCTTCTCC TKGTCTCTGT ATWAAAGTCC TCTCTTGAAA 180  
 GTGGAGAGCA AAGGCACACA GAGGTGCGCG CTCACAAGAA TTCCTCCCGG TGACTGGGTA 240  
 ATCAATGTTA CTGCTGTTTC CTTTGCAGGA AAGACCACAG CAAGATTCTT TCATTCTCTT 300  
 45 CCTCCTAGCC TGGGGGACCA GGCTCGAACT GACCCTGGAC ATCAAAGGAG GGATTATGTG 360  
 GCTGCTAAAG CCATCGGCCC ACAGCCCTGT TCACRTCTTG GTGCTTCTCT TTCCAGAGG 420  
 50 CTGGTCCCAG CCAGGCACAC ACAAAGGCA GATTCTCGTA AACSCAGCCT CCCTCCCTGG 480  
 AGGCTGCCTC CTGCCCTGGA TCTGGAGTGG AGCTGCTCTG AGATTTTGAG TTCTTCTGCA 540  
 GAGATGATTA AATATATCCA AGAGACATTG GAAACCTGC TGAACATTTT ACATTGGTCT 600  
 55 GCTCAGCACA TGGCTGGATG CGGATATTTT TATAATTCCA GAAAGTCACA CAGCTCCTCT 660  
 GTATGAGACC AGTGGGCGCC ATTTAAAAGA ACAGGATGAG AATCTAAGAT ATATTATTAA 720  
 60 TAAATGTAAT GGATTTTTTT TTTGTAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 780

AAAAA

785

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(2) INFORMATION FOR SEQ ID NO: 74:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1069 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

20

TCCTCACCAT TCCCTAGGN CAGGTCCCTG CAGGTCCAC ACTTCTCCCA GGTCCTAAA	60
CTTGGGTCGG TCCTTCCCT GGAGTAGCTG GNTCTCCAG TCGAGGTCCC TGTTCAGTCG	120
GTCTTAGGC TCCTGCACAT GAAGGTGTGT GCCTGTGGTG TGTGGCTGC TCTAGGAGCA	180
GATACAGGCT GGTATAGAGG ATGCAGAAAG GTAGGGCAGT ATGTTAAGT CCAGACTTGG	240
CACATGGCTA GGGATACTGC TCACTAGCTG TGGAGGTCCT CAGGAGTGA GAGAATGAGT	300
AGGAGGGCAG AAGCTTCCAT TTTGTCTCTT CCTAAGACCC TGTTATTTGT GTTATTTCTT	360
GCCTTTCCGA GTCCTGCAGT GGGCTGCCCT GTACCCTGAA CCTCATGAGC CTCTAAGGGA	420
AAGGAGGAAC AATTAGGACG TGGCAATGAG ACCTGGCAGG GCAGARTACA AGCCCAGCAC	480
CAGTGTCCCA GCCTTACTGG GTCCTTACCC TGGGCCAAAC AGGGAGGGCT GATACCTCCT	540
TGCTCTTCCT AGATGCCCAC CTCCTACAAT CTCAGCCCAC AAGTCCTCTC CACCCTAGGG	600
GGCTTGCTGC ATGGCAATAA CTCATAATCT GATTGTGAGG TTGCCCCTT ACAGGGGCAG	660
ATTTTCTGCT CAGTTCAACA ATGAAATGAA GAGGAATCC CTCTTTCTAC AGCTCACTTC	720
TATCAGAGGC CCAGGTGCCT CAGAGCCACA TTGAGTTGCT TTTTCTGGGA TGAGGAAGTA	780
GGGTAAACT CCCAGTTTC CTGAGGGAGG CTCCTGACAG GTGCCCTTTG TCAGACCCTA	840
CCACAGCCTG GATAGGCAGC CACATGGTC CTCGCCCTTG CTCGGNACTC CGTGGTGGTC	900
CTGCCCTTCT CCCTGCATGC CTGTGGGTCT GCTCTGGTGT GTGAAGGTCG GTGGGTTAAC	960
TGTGTGCCTA CTGAACCTGG CAAATAAACA TCACCCTGCA AAGCCAAAAA AAAAAAAAAA	1020
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1069

55

(2) INFORMATION FOR SEQ ID NO: 75:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 base pairs

(B) TYPE: nucleic acid



(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

5 GGACATTAGA TCACTGTGGA CCTAAAACAA ACAAACAACT ATAAGGAAAA TGGCATTAGA 60  
 AATGGTCTGG GGATCAGTTT ATCACTGCAG TTGTTACATC ACCCCATGGT CTAAAATACA 120  
 10 GAGCTTTAGT CTGTCTCTGT TTCAGTTCAT TTTACAGGAG GTGAACATCA CACTTCCAGA 180  
 AAACTCTGTC TGGTATGAAA GGTATAAATT TGATATTCCT GTCTTTCCT TGAATGGCCA 240  
 GTTTCTGATG ATGCATCGAG TAAACACCTC AAAACTTGAA AAACAGCTCC TGAAACTGA 300  
 15 GCAGCAAAGT ACTGGARGCT GACTGATGCC CTCATGATTT TCCACCCTCT CTTCCCATAA 360  
 AGCATCTTCC TAAGGAAATG AMCATGGCCT GATACTCATT TTGTCACTTG TACAGAGCCC 420  
 20 TAAGGATGTT CTGAATTCAG TGGTGCCAAA TAAATGTTGA CATTCCCTTT TTGGTTGATG 480  
 GAAGTATCAG TGTGGGAACT GTTTGCTTAA TGGCATTTTA TAAAATAAKA AKAKCATATT 540  
 AGCAGGGAGG GAGATGATGG AGGAGGGGAG AAGTCCATTT GTCTTATTTA TCCTTTTTGT 600  
 25 ATTAATAGAG AAGCACTTCA CAGTCACTGG CAATGCCATT TATAGGAAGA AGGTTCTGCA 660  
 TTCTGTCTGC TCCCGGAGGG CTTAACTTTT TAATGAAAGA ATAAATGCTC TTCCACTCAG 720  
 30 TAGATAAAGT GAAATGTGAA TTGTTAATAA CTGTGCACGG TCAATAAAGC GATGTTTTAA 780  
 GGAATACAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAACTCG A 831

35

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 590 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TATATATAGA CNGTTAATAG TCGTGANTGN TGTGNACGAA CATTAAACGGA AGTAGCATGT 60  
 AGCCAGTCGA ATAACNTATA AGGACAAAGT GGAGTCCACG CGTGCGGCCG TCTAGACTAG 120  
 50 TGGATCCCCC GGCTGCAGGA TTCGGCACGA GCTGCCAGGT GAGGAGCAGA GAGACTGTTC 180  
 CCTTGGGTGG AGAGGTGTGG GCATGAGAGC CACCCATTGC CAAGCAGCAA GAATGTTCTG 240  
 55 GCTTTTTTCC CTTCACAAAT ATGCAGGGCT CAGGCTCCCA ATTCCGGGCC TGTCTGCTTT 300  
 GCTGTGTGTT CTCCTGTCCC TGTTCCTCCG GAGGGCCCAG GTGGAAGTCA CGACAGGGAG 360  
 GGAGACGCTT CCCAAAACCC TGCAGGGCTA TTTCCAGAA TTTGGTTTTT AAGTACAAAA 420  
 60

	CTTTTTGTCC TGTAAGATAT ATGCAGCCTC ACAGAAGCAG CCTCTGCCTC CACTTTACCA	480
	GCTACGTTTT TATCTTAAGC ACATGGGGCT CCCTTAGAAC TTA CTCCACT GATTTAAAAA	540
5	AAAAAAAAA AACTCGAGG GGGGGCCCG TACCCATTCG CCCTAAAAGT	590
10	(2) INFORMATION FOR SEQ ID NO: 77:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1274 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:	
20	GAGCCACCAC ACCTGGCCTG GAAGGAACCT CTAAAAATCA GTTACGTCT TGTATTTTGT	60
	TCTGTGATGG AGGACACTGG AGAGAGTTGC TATTCAGTC AATCATGTCG AGTCACTGGA	120
	CTCTGAAAAT CCTATTGGTT CCTTTATTTT ATTGAGTTT AGAGTTCCT TCTGGGTTTG	180
25	TATTATGTCT GGCAAATGAC CTGGGTTATC ACTTTTCCTC CAGGGTTAGA TCATAGATCT	240
	TGGAAACTCC TTAGAGAGCA TTTTGCTCCT ACCAAGGATC AGATACTGGA GCCCCACATA	300
30	ATAGATTTCA TTTCACTCTA GCCTACATAG AGCTTTCTGT TGCTGTCTCT TGCCATGCAC	360
	TTGTGCGGTG ATTACACACT TGACAGTACC AGGAGACAAA TGACTTACAG ATCCCCCGAC	420
	ATGCCTCTTC CCCTTGCAA GCTCAGTTGC CCTGATAGTA GCATGTTTCT GTTTCTGATG	480
35	TACCTTTTTT CTCTTCTTCT TTGCATCAGC CAATTCCTCAG AATTTCCCCA GGCAATTGT	540
	AGAGGACCTT TTTGGGGTCC TATATGAGCC ATGTCTCAA AGCTTTTAAA CCTCCTTGCT	600
40	CTCCTACAAT ATTCACTACA TGACCACTGT CATCTAGAA GGCTTCTGAA AAGAGGGGCA	660
	AGAGCCACTC TGCGCCACAA AGGTTGGGGT CCATCTTCTC TCCGAGGTG TGAAAGTTTT	720
	CAAATTGTAC TAATAGGSTG GGGCCCTGAC TTGGCTGTGG GCTTTGGGAG GGGTAAGCTG	780
45	CTTTCTAGAT CTCTCCAGT GAGGCATGGA GGTGTTTCTG AATTTTGTCT ACCTCACAGG	840
	GATGTTGTGA GGCTTGAAAA GGTCAAAAAA TGATGGCCCC TTGAGCTCTT TGTAAGAAAG	900
50	GTAGATGAAA TATCGGATGT AATCTGAAAA AAAGATAAAA TGTGACTTCC CTGCTCTGT	960
	GCAGCAGTCG GGCTGGATGC TCTGTGCCT TTCTGGGTC CTCATGCCAC CCCACAGCTC	1020
	CCAGGAACCT TGAAGCCAAT CTGGGGGACT TTCAGATGTT TGACAAAGAG GTACCAGGCA	1080
55	AACTTCCTGC TACACATGCC CTGAATGAAT TGCTAAATTT CAAAGGAAAT GGACCCTGCT	1140
	TTTAAGGATG TACAAAAGTA TGTCTGCATC GATGCTGTA CTGTAAATTT CTAATTTATC	1200
60	ACTGTACAAA GAAAACCCCT TGCTATTITAA TTTTGTATTA AAGGAAAATA AAGTTTTGTT	1260

TGT TAAAAAA AAAA

1274

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(2) INFORMATION FOR SEQ ID NO: 78:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

AGGATTTTTC	CTTGTTCAAC	CAAAATCTGA	GCATTCTTTC	TATGTTGAAA	ACACTGAAAA	60
ACTAATTTWA	GTTAATGAAC	TAGAAAGAAT	ATTGATTTTW	AAGAAACAGA	AAAATACTAC	120
TTATTTTCCT	TCTCAAATAA	CGTTTCTTTC	AAAAACTTCT	GGCTGAAGTA	TAACATGCTG	180
GTAGTTAACA	TAAATCTTGT	CTTCTCTTGT	TTCTTTATCT	TTCTTTGTTA	TTTAGATGCT	240
TGTATAAATG	TCTTTTGTTT	TTATTAAGTG	CCTAATTGAC	AGAGCTTAAT	TTGAAGAAGT	300
GCCCTAATTT	ATTGACCACT	TAAGAATTGC	CTTTATTGGG	GTATTTTATT	TGTTCTGCG	360
TCTTTTGTAT	GTGTTTCAGT	CTACTCATCC	CTGTGAGTAT	GTGTGGGGGA	CAGCTGATAG	420
AAGGGAGGAG	AGTGTGTCTA	TGCTCAGGAT	TGCCCTTTAG	CCACTCAGCC	AGAGATCCAC	480
AGGGAGCAAC	AAGGACAGTT	TCACATGCTT	AGACTTTCTT	GGAAGAAACA	GTGAGGAGGA	540
GTAAGTCGTG	AGTAGTGTCA	AGCTGGAGT	AGAATGTGTC	TAAGGCAGTT	GACCCACCT	600
TCCAACATGT	TTTCACTTTA	TTTGCCCTC	CCTACATTG	GGTTAGGTT	CATTTGGATT	660
TGCAGCAATA	ATGACTTTAT	TTCTCTCTG	GTCAGGATT	GGCACATAAA	ATCCTTTTAT	720
TATAGAATA	GCTATTTTAG	TTACATAGTA	ATGTAATAA	TGGAGAGATT	TATAGAGAAT	780
TTTGKTTTTG	CTGTCATATA	TGTCCATTTT	GGAGACAGAT	ATGATAGAAC	TAGAAATTAA	840
GTTGCATTTT	TGCAAGTGCC	ATTTGAATGA	ACTTCAAGTA	TCTTCTTAAT	TATTAAATTT	900
TCTGATGAAG	GCATTGTAAC	AAATATATAG	TATTATTAAA	TCTAATTAAT	ATTTGGAAAT	960
ATTAATAAAT	AGGTATTTTA	TTTACTGTAA	AAAGTCAAAC	TTCATTATGT	AGATAAATCT	1020
TATTCCTTTT	ATTCTTTCCC	CTGTTTACAT	CCTTTTACAA	AAGCTTAGTC	ACCAATTAAA	1080
GCTTTCCTAT	CAAAAAAAA	AAAAAAA	ACTCGAGACT	AGTTCTCTCT	CCT	1133

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(2) INFORMATION FOR SEQ ID NO: 79:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

GAATTCGGCA CGAGGGGAAA AGGATGCTGA ACGAGAGCAG AAAGCCTCTT TCCTTTGCTT 60  
10 CACGCCTTTC CAGTCTTTAT TTAAACTCG GGTCCCTTT CTGTGGTCGC AGCAACCTTT 120  
ACTCCACCTG CACTGCTGCT CCTGGGGGCT CCCAGGCCT CCCTCTGCCT TTCTACCCAG 180  
TGGCTGACGG GATGCCCTGTC TTGCCTGGAC GCACCACTGC TCTCCTGTCC CTCACCTTGG 240  
15 CTTTGTCTGT GCCCTGCTCT GGGGTGAAG CTGGCCCATG TGTCCCCCGG AGTCATGGCT 300  
GCTCCTCCTG GGAGGCCTCT GTGTGCGTCA CGTCTTCCAC ACCTGGGGGC AGCTGGCGAG 360  
20 CCCGTGCTCT GTTCCCTCG GCTGCTTGGC ACAGAGYTGC AGCCTGGGAY TCTCCGTGGA 420  
CCCAGACTGG GGATTTTGCC AGGGGGGCGA TGGGAGGAGC AGGTGCTTTG CCTGGCGGCT 480  
GTGTCTGCAT TTCTGGACGC CCCAGAGCAC AGAAGTTGCC GGCACCTTGA GGTCTTCCTC 540  
25 GGCATGTGCC AGATTACATG AGTGACGGCT GGAATATGT TTTCTTTTTT GTAATGGAGG 600  
CGTGTTCAC ATATAGTAAA GCTCACCAA AAGTAAAAA AAAAAAAAAA AAAAACTCG 660  
30 A 661

35 (2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1378 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

45 ATTGGGTACC GGGCCCCCCC TCGAAGTTTT TTTTTTTTTT TTTAATGAA AGCTCTCAAA 60  
TAAGCGATTT TATTCCTATC CATGATTGCA GACATTTACA AAACCATAAC ATCTGAGTTC 120  
ACCTTAAAAA ATAACCTATA TAAAGCAGTG ATATACACAG CACAAAATAG TTCAGGGAGG 180  
50 GGGCAGGAGC AACTTGTAAT AATTAAAATG TAAACGTGAA AAAAAGGATG GAATAAAAGT 240  
CCCTACTTAT TTCTACTTAA GATGTCATGT GATAATATTT TACAATGTCC TGTGGGTCAA 300  
55 TGTATGTATG TGTATATGTC TGTATAACAT ACACATATAC AGTACATTCT CTTTCCCACA 360  
CATATACATA CACACATAAT TATTTGCAGT TCAGTTTAGG GCAATTCTAA TATGCCACTC 420  
CGTACAGTTG TTTGAATCAC ATTTGGACCC GCTTTCTTCA CAAAAGAGGG GAGAGAGCAG 480  
60

	GAAATAAAAA GGTGTTTGTG GTGTGACTGA GATTCCTTTG TTAACTGTA CACTGTGATG	540
	AATAATTTTC TTCCGTAGTA GTTCTGTGAA GGGCTGACTC ACTGTGGTTT TCATGAGGAG	600
5	ACTTGGTAAT GGATCACACG CTCATTGTCA TGCTAGGGGA GTAACCTCA CTCTGAAAAG	660
	GATTTAAGAA ATTTCCCCC ATTTGCCCAT CATCCCTTGG AGTGCCCGGT TGATTACTCA	720
	GGCTCATATT ATTGGGAGAA TTCTTGAAA TACTGTCCAT ATCTCCTGAG CCTAAAGAGC	780
10	CATTCAATGTG ATGTGACTCC ATTCCTCCTA ATCCACCCAT GGGACCATCT GACCCAGGRC	840
	CCATTGGAAA ATTAGGTCTG TTAGGTCCAG GAGGTACTGC ATTCATTAAA GTATACATGT	900
15	TATCACCAGA GTTGGTTGAA TCTGCTGGAC TAGGCATGAT GGGTGTTCCT GGTGGCCCTC	960
	CACCTCCTGG AGGACCTACA TAATCCCAG GAGATGCTGA GGAGTATGGT ATTGAATTGG	1020
	CATTGTGTGG GTTTGGCCAA GGTCTACCAC CACCTGGACC CATGTTCAAT CCAGGCATTC	1080
20	CAGGGCCACC TAAAGCATTC AGTGGGGTC TCATTGCACC TCCATAGTTC TGTGGTCCTA	1140
	AGGGCACCAT TCCTCTTGA GGAGTCATTC TCTGCATTGG CCCACCCATA TTTGATGTC	1200
25	CTTGTGTGCG AGTTGGATCC ATTCCACTGG GGAGTAATGG CTGACTTCCT GGGACACCTC	1260
	CAAGTGCCTG ATTAGGTATC CTCAATGGG GCCTTGGACC TCCAGGTAC CGAGGTGACA	1320
30	TAAAAGGGTA ATCATGGAAG GCTTTTGCTT CACTTGAGTG TTCACATGTT TCACGTCT	1378

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

	ACTTTGTCCA AATGTGTCTG TCACATGTAG TCAGCTGNAG NAATTTAAAA TGAATTGCCA	60
45	AGTGAAGAGT CTGTGGATTA ATTGGCCGTT AATTACAGG CTTTATCAAT GTGTCCTCAA	120
	GGGAGAGGCC CAACCCTAAT TAAGGAGCTA AACTTCCTGA GTGAGGGGCT GTGAGGATGG	180
50	AGGTGGAGGA GGCATCTGGG GCGGGTGGTG GCCGGGCCAG CAGATGGCGC CTCCTGGCT	240
	GAGCTGCCCC CACCGCCAGT TCCCTCATTT CCACTCAGGA AGGCAGAGAA GGCAGAGTGA	300
	TCTCTCAAG GAAGAGCTTC CCCAGCCTTC GGGAGCAGCT GGCAGGGCGT CCGGAATAA	360
55	GCCCTACACG CCGCCGCTG CCTCCAATC ACTAACCTG CGCCTCTTGT CTTTCAGATT	420
	CAACGCGTTC AACAGAAGCC ATCCCCAGCC CAGCTTAAAT TATAAAGATA GACAATAACT	480
60	CTGTTCCAAT CTGCGTGGTG CTTCTTTAGT AAATACTGTA CAGATTTTAC CATGGAGAAC	540

	TTTTTTTTTA GTTTTTACCT TTTCTTAAT ACCCTTATTC CGAATGGACG AACACTTTCT	600
	ACCACTGCTG ACCATTGTAA AATACCGTGT ATATAAATCC CATTGAAATA ATGCCCTGGA	660
5	ATAGAACATC TCAAATGCTG CTTAATTACA GACTCAGGTC GATTACTTGT ATTTTCATGA	720
	ATGTTCTCTC AAGTTAGACA TCTGGTGCAA GACCAACCGG GAGACCATGG AATTGTCAAA	780
10	AGTACAACT GACAGTGTGT ATATTTAATT TAAAGACTTA TTTAAAACT CACAAGCTCT	840
	CACCTAGACT TTGGAGAGCA GTCTGTTTTT TGTAATGTCT GATACTAGAA ACTAATTTGC	900
	TTATTTTAGT TGTATTCAAG ATTTGAAGAT GTATTTTATA GACAAGTTCT GTTTTGAAC	960
15	TTTGTGGAAC TGTCCAATC AATCAATTC CCAGTTATGA TGAGTATTTA CATTATGAAT	1020
	GTATAACCCA GACATGATTT GTAAAGCCGA CAGTATGTTT CTATTACACA ACACTTTTTG	1080
20	ATACAGCGTC TCTGTCTTC ACTGATACTG GAGTCTCCGT TGTCTGCNNG GTCCCTTCGA	1140
	GTTTCTAGTT ACAGACACAA TCATACTGTG ATTTTATTTT TAATATGGAT ATGCTATCAA	1200
	ACTGTGATAC ACTTATAATT CACTGTCCT GCATCAGGAG ATGGAGTGGG GAAAACGTGA	1260
25	TTTAATACAG TTTGTATCTG AATAATCTGT ATGGTTTATA CAGTTTGTGT TGTTCAGAGA	1320
	TGTTTAAAGT TTGATCTTTG TTTTCTAAA GATTAAAAA GCACTTGCCC CACTGTAAAT	1380
30	ATACAGCATG TAAAATTTCT RTAGTATATA AATGCGAGCA AATCACAAAA AAAAAAAN	1440

35 (2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

45	CCCGGGCTGC AGGAATTCGK YACGAGGCCA GCAGTTGCTC CCAGTTCAGG AGGTGCTCCT	60
	GTACCCTGGC CACAGCCCAA TCCTGCCACT GCTGACATCT GGGGAGACTT TACCAAATCT	120
	ACAGGATCAA CTTCCAGCCA GACCCAGCCA GGCACAGGCT GGGTCCAGTT CTGACCTGAG	180
50	CACGGTTTTT CCTCATGTGA CTCTGGGAA GCGCTCCCT CATCTGGGCC AAAGGAAGGA	240
	GGACGAAGCC CTCCTCAGCT GGCCTGTGTT TGGGGCATGA ATCTCTCCTC TCCTCCTTGT	300
55	CTGGCTCTGT TGACAAACCG GGCATGTTG GCAGTAAATT GGCACCGTGT CACTGTGTTT	360
	CCTGGGATTC AAGTATGCAA CCAGAACACA GGAGAAGAAA AGCTCCAGGA TCCCTGTCCC	420
60	CATCTGTCCT CTTGATGTGA GAGAGACTCT GAGACTTCTT CCATCGCAAT GACCTGTATT	480

	AAACACAAGC CCCCCAAGCA AAAGAAGAGG TTGAGTTTGC TGCCAGGATT CAGATCAGCC	540
	CTTCCCAGGG TCTGCAGGTG TCACATGATC ACAGTTCAGC GGGAGGCTTT CCGTACCCAC	600
5	ACTGGCTGTA GCACTTCAGT CCATCTGCCC TCCAGAGGAG GGTTCCTTCC TGATTTTATG	660
	CAGGTTTAGA GGCTGCAGCT TGAGCTACAA TCAGGAGGGA AATTGGAAGG ATTAGCAGCT	720
10	TTTAAAAATG TTTAAATATT TTGCTTTGCT AATGTGCTGA TCCGCACTAA CTCATCTTTG	780
	CAAAAGGAAC TGCTCCCTCG GCGTGCCCCA GCTGGGGCCT CTGAAGGGAT TCCTCACTGT	840
	GGGCAGCTGC CCTGAGCTTC AGGCAGCAGT GTTCATCTCT GGCCAGTTGT CTGGTTTCCA	900
15	TGTATTCTAG GCCAGGTAGG CAACACAGAG CCAAGGCGGG TGCTGGAAGC CAGACGGAAC	960
	AGTGTGTTGGG CAGGAAGGTG GATGCTGTGTG TCATGGAGCT GTGGGAGTTG GCACTCTGTC	1020
20	TGCTGGTGGC CCTCTCGGCT CACATGTTCA CAGTGCAGCT CCTGGCAGAC TTGGGTTTTC	1080
	TCTTTGGTGG TTTCTAAAGT GCCTTATCTG CAAACAACTT CTTTCTCCT TCAGGAAGT	1140
	TGAATGGCTA GAAGAAGGAG CTCAGTAAAC TAGAAGTCCA GGGTTGCTTG GTTACTGGT	1200
25	TTATAAGAAA TCTGAAAGCA CCTCTGACAT TCCTTTTATT AACTCACCTC TCAGTTGAAA	1260
	GATTTCTTCT TTGAAAGGTC AAGACCGTGA ACTGAAAAA GTGTTGCCT TTTTGCGGGA	1320
30	CCAGATTTTT AAGATAAAAT AAATATTTTT ACTTCTGTCA AAAAAAAAAA AAAAAAATNT	1380
	C	1381

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(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1706 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

45	ACTGCACCAC TGCCAGGTC TCCCGGCTGG ATGAAGACGT GGTCCATGAG GAAGCTGGCT	60
	AGCTCAGACT GGAGAGTAGC TTCAGGAAAA AAGACAAGTG GCCTAAGGAA ATCACGGCCC	120
50	CCAACATCA TCTGAGGGCT AAAGATGAGA AGTAGTCAC TTAATAAGAC AAAAGCCTGT	180
	AGGGGGAAAA GAAAGGATGT TAAAAGGAC AGAATGTTTC CCAAGGTAGA AATGACACTG	240
55	TCAATTCTC CTGGAATGG GGCAGGGAT ACTCGCCTTG TTGCTCCAC TTGAGTCAGT	300
	ACTCACCTGC TCCTGGATCT CAGTATCCAC ATCTGAGAGG CAACTCTGGC AGAGTTCACA	360
	GAAGGCCACC ATTCTGTCCC TCAAACTCGA CAGCTGCTTC TGTGGGCACA GTGGCTTGAA	420
60	GGGAAGAAT GAAGACACAG ACTCCTCTGT TCCATTATC CCATCTAAGA CCCACACTCA	480

5 CCTGGGGAAG CATCTGATTT AGAAATGTGG GTTAGTGTCC AGAGAATGGA AAAATAGACA 540  
 AGACTCAAGG CTGGCAGGAT AACCTGTAAC AACAAAGGGT TTGAAAAATG AGGTTTGGGT 600  
 TAGGAGAGGG AGAGACAGAT AGCCAGAAAC ACACCACTGA AGAGGAGAGA AAATGAGTAA 660  
 AGGGAGAGCT AATTCCTTTT CCAGTGGAAA ATGAGTGATA TTCTGGACAT TCTTCAGAGG 720  
 10 CATCTACACG AAGTAGAAAT GTCACCGCTC CCTAATTTAC TCTACGTCTT CTAGAATCCC 780  
 TCAATATTAT CCTTGGCTTC CAGGAAATCC AAGAAGACCC TGGAAAGTAGA GTCCACCTTC 840  
 TAAGAGAGGA ATGTAAGAGG TGACCCCCAC CCACCTGATC TTCCTCGCTT TGTCCTCTCC 900  
 15 ACGCACTGAG ACTTGACACA CCTAGTGGCC ACCTAGAACG TAGGTCCTTA AAATYTAGCC 960  
 CCCAGCCCC CAACCCATCT CTAGCCTGTC CACTCACCTG GTGAGGAACY TYTCCTGTGT 1020  
 20 CCACAGCYTT CTGCAGGAGT TGGCAACATG GCTCATAGAG CTCCCAGCGA GTCAGGTCAT 1080  
 GAGTGCTTTG GGGGAGAAAG GGAATGTTA TACTGGAAAA GAACAGAGGG AACCAACTCC 1140  
 ACAGACACCA GTAAAAACGG GATGGGGAAG AGGAGGAAAG CCACTCACTT GTAGAAGGCA 1200  
 25 GAGAGGCGTT TCAGAGTGGC TGCCAGATTA TATACCTCAT CCTCATCTAG GAAGGACGAC 1260  
 TGAGAAGGAA AGAAGATCCA CAATAGCATT TCCCCAGAA CTCATCAGTC CACATCCCCC 1320  
 30 GTCTTGCAGC CCCTCCCACC CTGTGTTGGG GTGTCCCATT GTCCAGCCCC AGCTCCTACC 1380  
 TGTAACAGCT CTTCAAGCTC CTGCTGGAAR CGGTCACTCA GCAAACTTAC TAGCTGGCTG 1440  
 CGGGCAAAGT CCGCCCGGCT GAAGAAAGTG AATTCGGGAT TACAGAGCAG GTAAGAGCAT 1500  
 35 GCGCCCCAGC CTCAAGCACC GCTGGCTCTG CATGCTTCAC CACCACCTCC TGGAGTTGCT 1560  
 GCAGGAACAG CTCCAGGTGC TGAGAAGAAA AGGCAGAAGA TGGTGTGCTG TGGGGATGGG 1620  
 40 AGGAGGACAC TCTTCTGGCG GGAAGTGGA CGGGGTTAAA AGCATTAAC TTCAAGGATA 1680  
 AGATGCCTAA RAAAAAAAAA AAAAAA 1706

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(2) INFORMATION FOR SEQ ID NO: 84:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

60 GAATTCGGCA CGAGCTTGGT AGCCTTAGAA CTGCATGAGC TGCTTTACCA CTGGGAAACA 60  
 60 CGAGCACAGC CTAGCTTGAT TTTGTATGTG GTATCAGATC TAAGGTGGAT GGAATTCAGG 120



ACTTCCTGTC TACTCTTTGA TTTTGTTTTA TTTTGTAGAA TGTTTTATTT TGTTTTATTC 180  
ATTTATTTCAT CTTTCAGAGAC ATGGTCTGGC TCTGTGTGCC AGGATGGAGT GCATGGTGTG 240  
5 ATCATAGGCC ACTGCAGTGT TGAGCTCCCG GGCTCAGGCG ATCCTCCTGC CTCAGCTYCC 300  
TTAGTAGCTG GGACTATAGG CACATGCCCT ACCATGCCCTG GCTTTGTCTA CTTTTTGAAT 360  
GATGTCYCAA ACTAGAAGGT CTATTAATTT AAAAAATTAA GGATAGCATG CCATAATTAA 420  
10 AAATAATAAC AGTGGGAAAA GGCACCTTCC AATGATTCAG ACATCAACTT GTGATTTAAA 480  
AAAACGAAAA ATAAATAATA GGAAAAAAG GGGAAAAAGT TAAATAAAAA TAAAATTAAA 540  
15 AAAAAAAAAA AAAAACTCGA GGGGGGCCCG GTA 573

20 (2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

30 CTCTTTGGCT GTGTCTACCT CCTTCATCTG CTGCGCGAC ATAAGCACCG CCCTGCCCCT 60  
AGGCTCCAGC CGTCCCGCAC CAGCCCCCAG GCACCGAGAG CACGAGCATG GGCACCAAGC 120  
CAGGCCTCCC AGGCTGCTCT YCAGTCCCT TATGCCACTA TCAACACCAG CTGCGCCCCA 180  
35 GCTACTTTGG ACACAGCTCA CCCCCATGGG GGGCCGTCTT GGTGGGCGTC ACTCCCCACC 240  
CACGCTGCAC ACCGGCCCCA GGGCCCTGCC GCCTGGGCCT CCACACCCAT CCCTGCACGT 300  
40 GGCAGCTTTG TCTCTGTTGA GAATGGACTC TACGCTCAGG CAGGGGAGAR GCCTCCTCAC 360  
ACTGGTCCCG GCCTCACTCT TTTCCCTGAC CCTCGGGGGC CCAGGGCCAT GGAAGGACCC 420  
TTAGGAGTTC GATGAGAGAG ACCATGAGGC CACTGGGCTT TCCCCCTCCC AGGCCTCCTG 480  
45 GGTGTCATCC CTTACTTTA ATTCTTGGGC CTCCAATAAG TGTCCCATAG GTGTCTGGCC 540  
AGGCCACCT GCTGCGGATG TGGTCTGTGT GCGTGTGTGG GCACAGGTGT GAGTGTGTGA 600  
50 GTGACAGTTA CCCCATTTCA GTCATTTCTT GCTGCAACTA AGTCAGCAAC ACAGTTTCTC 660  
TGAAAAAAAA AAAAAAAAAA AAAC 684

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(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1036 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

TGGAGGCAGA TGCACAGGAG AAAGGTTCCC GTCCGCACCC TCTCAGACCT GAGGCTGAGC 60  
TTGCAGTGAG GGCTTCTCCT CGGCCCTCG CCCGCCCCA GAGCTGCCAT CCTGCTGTT 120  
10 ACAAGCCAGA GGAGCCCGGA TGTGAGGCC CAGATCACCT CCAGGGACTT GGGGTTCCTA 180  
TCTGAAATCC TTTATTTTGT TACCATGGGG TGGGCCCCGG GCTGAGAAGG AAGAAGCACC 240  
15 CTCTCCCCGG CCTCCTCTGT CTGCACCGT GGGGCTGTGA CTTACTCCTG CCTCCAGGG 300  
CGGGCGGGG CCCCTGGGA CCTCTTAAGG CCCAAGGTGG GCCCCAGGAC CTYTGGGCAG 360  
AGTGGAYTGC TCATGGCAGA TGTGTGGCAA TGTCTGGCTG WGTCTTTCCG GCAMCTGCGT 420  
20 YCCCTYTCCC GGGYTCCCT GCTGCATGGT GGATGTGCTC CTTCTGGCC CGGTCACATT 480  
GCCTCCTTGA GCCTTAGTCC AGGGGGTCAC TYCTCCCACC CCACCTACCT CACAGGGTTG 540  
25 TTGTGAGGGT GCACAGAGGA GCAAAGTCCC TGAAGGCCCT CAGGCAGTAT ATAGGGGCCG 600  
CCCACCTTCA GCTGCCCTGG GATGGGAAGG ACCCAGCCCG ACCCTGGGC ATAACACTGT 660  
GTTTGCAAAT GGAGATTGAG GTATTGGGGA TGCAGTTGT GGGGAGCTGG CCTGGCAGAG 720  
30 TAGGGGTAGT TGGCTTGGCC TTCTCTTGG TGATCCCACC CCCAGCCATT TGCATTGCTG 780  
GCCCAGCGCC TGGCCTGGGG GCGGGGAGA GGCAGCAGAA GGGGCTGGC AGGGGCGGTG 840  
35 GAGGACTCAG GAACTGCCCC GGGAGAGTGG GTATGGCGGC TGAGCCAGGG GCCCTCCTGT 900  
GTTTGACTTC CCGGATGGG TCCTTGCTTC TCAGCTGTGT CCGACCCAC CATGTAATAA 960  
AACCCAAAGG AACAGCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1020  
40 CCCNGGGGGG GNCCCG 1036

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## (2) INFORMATION FOR SEQ ID NO: 87:

## (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 908 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TTAAACAAAT GGAATCATGC AATATGTGAC CTTTTCGTC TGGCTTATTT TATTTAGCAT 60  
AATGTTTTTG AGGTTTCATC AAGCTGTAGC ATGTATCAGC ACCTCATTTT TTTTCTGGC 120  
60 TGAATATTAT TCCATTATAT GGATTTACCA CAATTCATTT ACCTATTCAT CTTTGTTC 180

341

5 TGCTGTCTGG CTATTGTGAA TAATGCTTCG ATAAACATTC ATATACAAGT TTCTATGTGG 240  
CTTTATGTTT TCATTTCCTCT TGGCTATCTA CATGGGAGTA GAATTCTAGG TCATAATATA 300  
ATTTTATGTT TAACTTCTCA AAGAATTGCC AAAAGGTTTT TCATAGTGGC TGCATCATTT 360  
ACATTCCCAC CGGCAATGTA CAAGGATTTC TATTTTTCCTA TATCCTTGCA CTTACCAACA 420  
10 CTTCTMTTTC GTWATWATTT TGTMTTTCCTA TTATTGCCAC CCTAGTGGAT GTGAAATGGC 480  
ATCTTATGTT TTTGATTGTC ATTTCTCTAA TGACAAATGA TATCATACTT TTTTATGTG 540  
CTTACGGATC AAAGGTATTT CCTTGGAGAA ATGTCCCTTC AAGTCCTTTG CCATTTCAAA 600  
15 ATTTGGTTAT TTGTCCTTTA TTATTCAGTT TTAAGAAATT CTGGCCAGGC GCAGTGGCTC 660  
ACCTGTAATC MTAGCACTTT GGGAGGCCAA GGCGGGCAGA TCACTTGAGK TCAGGACTTC 720  
20 GAGACCAGCC TGGCCAACAT GGTGAAACCC CATCTTACTA AAAATACAAA AATTAGCTGG 780  
GCGTGGTGGC AGGTGCATGT AATCNTATCT ACTCAGGAGG CTGAGGCAGG AGAATCGCTT 840  
GAACCCAGGA GGCGGAGGCT GCAGTGAGCC AAGATCACGC CATTGCACTC TAGCCTGGGT 900  
25 GACACAGA 908

30

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 655 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

TGCACTGGTT CCTTCTCCCC AGCAAATACT GCCTTCTTGT TTTTCTCTGA TGTGGCAGGT 60  
GACTACAAAA TCCGCCTTGG TATTCTTCAA ATGCATATAT ATTCCCTTCT TGTCAGCTCC 120  
45 CTCTCTTCTT AGATTAGAAA ACTGCCTCAT TTTCTGCTCA CTGGATGTGC AGTCCCAGCT 180  
TGCTCTTCTC TCCTCCCCC CTGTTGCAGG TGTCTTTTTT TTTTCTCTC TCTCCCCACT 240  
GGGCAGCAAA AGTTGTTCCT CAGTGGAAAW TTAGGCATCC TCAAGTTTCY TCCCAGCTTC 300  
50 TGCTGTGTTT TCTTAGAGTA AATTGCCAAT TTCTGTTTTT ACAGGAAATC CTTTTTTAAA 360  
AATGGAATCA GTGTGGTCCC CATCTACTCT GCAAAAATG CATTTTTCTC TATTTTCAAA 420  
55 TGAGATTTGT TCAAGTTTCA AAACCACGTG AAATAATAAA TGTATAGTAG TTTTCTTTTC 480  
CTTGGGCATT GCTWGATATG TGAAATGGGT TTATGAAAAA TAATAAAATC ATAACGCTAT 540  
TTGTTTGACT TTCAATTTC TGGGAATTTT TCTCAGCTAA ACTCTAAATG GTGATTARGC 600  
60

AAAAAAAAA AAAAAAAACY GRAGGGGGC CCGGTACCAA TTCGCCCTAT AATGA

655

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(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TTTTTTTTTTT ACCATTTTAAA ATAAATGAA AGTGACCTTC TGTTTATAAA AATCTTTGTC 60  
TGCATCTCTG CTTATTTCCT TAGAAGAGAT TCCAAGAAGC GGTGAGTGAT TTCACGGCAG 120  
20 CAGAGGGTTG GGACATATTA CGGGCGCGGA TCCCTCTTGG AGTGAGATGA CTCTCCGGAG 180  
AGATTITAGTC GTCACCCCTCG CGTGTGAGGC TCGTTCACAC CCCAGGGATG TGTCTATCAA 240  
GATGGAAGAT CTTTTACACG CTCTTGATTT TGTGTGSCY TTTTCTATT ACTAGTGAGA 300  
25 AKGAAACTTT TTATATGATT ATTATCCATC ATAATCCAAC ACAAATTACT GCTTCATGTT 360  
CTTTTACTTT CCTGTGAAGG TTTTAGTGCC TTTTAAAAAT TGCTATATAT TAAGCTTGTT 420  
30 AATACTTCCA TGCTGTATTT GTGGSCATCA RTTCCCCCG GNACAGGCNT GCACATTTTG 480  
CCTTCACACG CTGGGTGGTT TTTCATTTTC AMTCTATTT CTCGTTCTTC TATCGTTTTA 540  
TGTTTCAGACG GGTTCCTCCG TGTAGAAAGC AGTTTATGAA GATTTACTTT CGACAGTCTT 600  
35 CTCTCTACTT TCTACAGTGA ATTCTCTGAT GTGTCTGGA GTTTGGGGGT CTGGGTAAGA 660  
RTCCCTCTCT CACCTATTC TCTATTACGA TCCACAGCCT CATGCTTTAT GARATTGGTG 720  
40 GCCGGGARGC GGGGAGATTT GCGGATCCCC CAAGCCAGAC TTTATCCCCC TATCCCTGCC 780  
TCTGGATCCC ACGTACAGGC CTGGGAAGTC CCTGTGGGTA GGGGCAATG GTCTCGCACT 840  
CTCACCTGTA CCCCAGGGCT GGCACAGGAT GGTCAAGGAG AGAGGCTGCC CAAGCGCATC 900  
45 CYTCTGGTGT CCCCTGACA CGCCTCCAAA GTGAGCAGGT AGGTTTCAAC AGCCCCACGT 960  
TGCAGGTGGG AGATGAAGCT CAGGGTGGAG ACCAGTATCT CACAGTTCTC TTTGCATGGC 1020  
50 CGGGTACTTG TTAGTCAACT GATCAAGTGA AAATTCTAGC CCCAGAGGCA GGAGAATCCG 1080  
GAACAAAATT AAACCAGCCA GG 1102

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(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1533 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

	GGCACGAGCC GNCACGGGCA GCGCCCCATA GCGCCAGGGA CCCCTGGCA GCGGGAGCCG	60
	CGGGTCGAGG TTATGGATCC AGCGGGCGGC CCCCGGGCG TGCTCCCGCG GCCCTGCCGG	120
10	TGNCCTGGTGC TGCTGAACCC GCGCGGCGGC AAGGGCAAGG CCTTGCAGCT CTTCCGGAGT	180
	CACGTGCAGC CCCTTTTGGC TGAGGCTGAA ATCTCCTTCA CGCTGATGCT CACTGAGCGG	240
15	CGGAACCACG CGCGGGARCT GGTGCGGTGC GAGGAGCTGG GCCGCTGGRA CGCTCTGGTG	300
	GTCATGTYTG GAGACGGGCT GATGCACGAG GTGGTGAACG GGCTTCATGG AGCGGCCTGA	360
	CTGGGAGACC GCCATCCAGA AGCCCCGTG TAGCCTCCCA GCAGGCTCTG GCAACGCSCT	420
20	GGCAGCTTCC TTRAACCATT ATGCTGGCTA TRAGCAGGTC ACCAATGAAG ACCTCCTGAC	480
	CAACTGCACG CTATTGCTGT GCCGCCGGCT GCTGTCACCC ATGAACCTGC TGTCTCTGCA	540
25	CACGGCTTCG GGGCTGCGCC TCTTCTCTGT GCTCAGCCTG GCCTGGGGCT TCATTGCTGA	600
	TGTGGACCTA GAGAGTGAGA AGTATCGGCG TCTGGGGGAG ATGCGCTTCA CTCTGGGCAC	660
	CTTCTGCGT CTGGCAGCCC TGCGCACCTA CCGCGGCCGA CTGGCCTACC TCCCTGTAGG	720
30	AAGAGTGGGT TCCAAGACAC CTGCCTCCCC CGTTGTGGTC CAGCAGGGCC CGGTAGATGC	780
	ACACCTTGTG CCACTGGAGG AGCCAGTGCC CTCTCACTGG ACAGTGGTGC CCGACGAGGA	840
35	CTTTGTGCTA GTCCTGGCAC TGCTGCACTC GCACCTGGGC AGTGAGATGT TTGCTGCACC	900
	CATGGGCCCG TGTGCAGCTG GCGTCATGCA TCTGTTCTAC GTGCGGGCGG GAGTGTCTCG	960
	TGCCATGCTG CTGCGCCTCT TCCTGGCCAT GGAGAAGGGC AGGCATATGG AGTATGAATG	1020
40	CCCCTACTTG GTATATGTGC CCGTGGTCGC CTTCCGCTTG GAGCCCAAGG ATGGGAAAGG	1080
	TGTGTTTGCA GTGGATGGGG AATTGATGGT TAGCGAGGCC GTGCAGGGCC AGGTGCACCC	1140
45	AAACTACTTC TGGATGGTCA GCGGTTGCGT GGAGCCCCCG CCCAGCTGGA AGCCCCAGCA	1200
	GATGCCACCG CCAGAAGAGC CTTATGACC CCTGGGCCGC GCTGTGCCTT AGTGTCTACT	1260
	TGCAGGACCC TTCTCCTTC CCTAGGGCTG CAGGGCCTGT CCACAGCTCC TGTGGGGGTG	1320
50	GAGGAGACTC CTCTGGAGAA GGGTGAGAAG GTGGAGGCTA TGCTTTGGGG GGACAGGCCA	1380
	GAATGAAGTC CTGGGTCAGG AGCCCAGCTG GCTGGGCCCA GCTGCCTATG TAAGGCCTTC	1440
55	TAGTTTGTTC TGAGACCCCC ACCCCACGAA CCAATCCAA ATAAAGTGAC ATTCCCAAAA	1500
	AAAAAAAAAA AAAAAAAAAA ANCCCGNGGG GGG	1533

## (2) INFORMATION FOR SEQ ID NO: 91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

ATCCTCTGGA ATCTAGGTGG AAGCCACCAA GCCTTCTTCA CACTTGCGTT CTGAGCATCT 60  
GCAGACTTAA CCCCATGTGG CAATCACCAA GGCTTATGGC TTGTGTCTC CAGAACTGTG 120  
GCCAGAGCTG TACCTGGGCC CCTTTGAGCT GAGGCTGAAG CCAGAGTCTG AAGCTCAGCA 180  
GGGCAGTARG GCCCTGGGCC TGGCCCTGA AACCATTCTT TTCTCCTAAG CCTCTGGGCC 240  
TTTGATGGGA RGGGCTGTCC TCAAGATTTT TGAAATGCCT TTGGAGGGTT TTTGCCTTGT 300  
CTTGATATT GGCTTCCTTT TAGTTATGCT CATCTCTCTA GCAAGTGAAT GTTTCACAAC 360  
CTGCTTGGAT TCTTTCTCTA CCACAGARCC AGGCTGCAAA TTTTACAAAC TTTTCACTC 420  
TGTTCCTCTT TTAAATATAA ATTTCAATGT TAAGTCACTT CTTTGCTCCC ATATCTGATT 480  
TAGGTTGCTG GAAGTAGCCA AGTCACCTCT TGAATGCTTT GCTGCTTAGA AATTTCTCT 540  
ACTAGGTAGC CTGGGTCATC AACTTAAGT TCAAA 575

## (2) INFORMATION FOR SEQ ID NO: 92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

TCCTTTTCATC TTAAGCACCA CCCGACAGGG CAGGTACTAT TACCATCTCC GTTTGACAGA 60  
TNAGGAACCT GGCACAGGAA GCATTTAAGT GGATTCCCCA GGATCGCCCC ACTGTCAGGA 120  
GCAGANTCAG AATGGGCCTC AGCATCAGGC TCCCAATCCT GGCTTCTAAC TGCTGCGCTC 180  
TGCCCTTCYC TCWCCCCACC TCCCCACTCC AGTGCCTTTG GTCATGCCAC TGCAGCTTTC 240  
AGGCCAATAC TGGATTAGCC TCTTAGTGTT CTTGTCCCTG CAGCCATTTC CCCAGGCAGC 300  
AATTCCATGT GCCCTCACTG ATGTAGGTGG CTCTGTGTGTC ATTGTGACA TCCTATGAA 360  
TTGTTTATGC ATCTTGTTCA CACTCACAGC ACCCTCCCTC TCACACGTCC TCCTTATAAA 420  
AATGTCCCTC AGTGTCTGCT ATGAGCCAGG TGCAGACTTA AGTGACAGGG CTGCTACGGG 480

345

AAATAAAAAA TTAACAAGGA GCACCTGCCT CTTAATGCAC AGTAACAAAC TATGTTAAGT 540  
GTCAGGAAGG AAAGGTTAAG GATGCCAGGA AGGCTTTTAA TAAATAACCT GACTTAGATG 600  
5 GGCAGGTGGT GCTGARGATT AAGAACGTGT TCTTCTCGA 639

10 (2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 744 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

20 GAATTCGGCA CGAGAGTGGC TGGAGTCTGG CTGCAGAGGG AAGACATCAG CAGGGAGGGA 60  
GCCAGGGCCT GTACATCTTT TCCTCTGGCC ATTGTCCTGG TCTTTGTAAG CCCAGAATCT 120  
CCCCCTCCCT GAAGGGAGGC CAGCACCCCA GGAGGGCAGC AGGTGTGCTG TGAGGGTTGG 180  
25 AGTAGTGTGA GAGGTCAGGG TACACTAGAA TGGCCATGGA CACCATGTGG GGGTGCTCTG 240  
GGCTGGGCCA CAGAACAGTG TCCTTCCTGC TGCTCCTCCC CTGCAGCTTC CCCCACCTT 300  
30 GTNGTTTATT TGGTTTGATA CCAATCAGCA GACCCTGCAA GGTGGAAGCT CCCAGGCTCT 360  
CAGTCCCACS ACTCTCATGT GCCAGTCACC CNTACTGTAA CTGCCCAATG AGTACTTCTT 420  
GCCCCTGCC AAGATAGAGC CAGTTTACCA AGACAGGGGA ATTGCAGTAG AGAAAGAGTT 480  
35 GAATATACAT AGAGCCAGCT AAATGGGAGA GTGGAGTTTT CTTATTACTT AAATCAGCCT 540  
CCCYTAAAT TCAGAGGTGA GAATTTTCA AGGACAGTTT GGTGGSCAGG CCTAGGGAAT 600  
40 GGATGCTGCT GATGGCTAG GGATGCAATC ATAGGGGTGT AGAAAAGTWC CTTGTGCACT 660  
GAGTCCACTT TTGGTGAGAG CTACCAAGGA GCTGCTGGTC TGCTGGTCCC GGTAGAGCCA 720  
TCTGGTGTCA GGAATGCAAA AGTG 744  
45

50 (2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 526 base pairs  
(B) TYPE: nucleic acid  
55 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

60 GCAGGGGAAT TCGGCCACGG AGGGGTTTCA ACAGGGCCCG TGGGGTGAGG TGCARACACA 60

AAGCCCATAA GTGCTGGCCT GTTGGGACAA ATGAGAGAAA TCCCATAGGG TGGTGATGAC 120  
AGCGCAYTCA GCCATCYTAY TCCTGGGGAA AATGAAACTT GTGCTCCTAT CAAATGCTCA 180  
5 GTTGTAAGAAC TGGAAAAAAA TTTTAGAAGA CATCTGTCC AGCATCTGTG TTTATGTCTA 240  
TAAAATGTAG AAAACTAAAG CACAGAGATG TTAAATGTTT TGTCCAAGGT CCAACAGCTG 300  
GTTAGCARGC TTGGTCTGGT GACCTTTCTA CTGAACCACA GTGCCGCTGG GGGAAGTCCT 360  
10 CAGCACAGAT GGCTGCTGCT ATAGCTGGGG TATGGGCAGT ATTAGTAGTT AACCAGTCAA 420  
CCCAAGTTCC CATAGTCTAG GTTCTGCTTC AGCTGGAGGT TAGGGAAAAA CACAAGAAAA 480  
15 TCCCTTACCA CTCTACCACT GCTGGGGGAT GTACTAAGAG ATCCCC 526

20 (2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 426 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

30 GGCACAGGC AGGAGAGACT TGGTCCATGG GGAGAAGCCT GCAGTATAGA TGGGACCTCC 60  
AGGAGCCCAA GTAGCATAGA CCCTGCTGAT CCGGGGCCAT TGAGCCAGAG GATTTGGGCT 120  
GAATGTCCCC AGAGACAAAA GGGAAAGGTA GATCCTTTCC CTAAAGATG AAAGCCATCG 180  
35 CCCGGGCTTG CTTATGCTC TCTCTCCTGG TCCTTCACA TGTGTCTTCT GAACATTTGT 240  
TCTGGCATCA CAATCCCGT CATCTGTCA TCTGGCCCTT CCCACCTTTC CACCTTATCT 300  
40 CTTGCACTGT CTCCGCTCG ACCTGGCACC TGGGTGAARG CTGCTCTTG CTGGTGCCCA 360  
TAGCCCCCAG TGTATGTCT TGAMCTCCCC AGCCATATGG ARACCCACCT CAGGAGGGCC 420  
CCTCGA 426  
45

50 (2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 844 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

60 GGCACAGCG CACGAGATAG GAAGCTTGGC AGGGGCAGCT CCCCCAGTGC GCATTGCCCT 60



	GTAACCTCGAG CGCCTGGGAG TGGGGAGAGG CTGGAATG GAGCAGGGTG GTGGACCTCG	120
	TCTTCTCCTG CTCATCCAG GCCTCCTCCA TAACACCTAC CTAGCACGGC CTGGGGACTT	180
5	CCCAGCCCAA GGAACAACCTG AGAATACTGA GTGCCAGGGT AGCCCTAGCC CCATTTTACA	240
	CCTGGGCAAA GTGAGGTCAC TGGATTCAAA CACTCAGATT TAAACCTCCT CTGTGTCTGC	300
	AGCACCTGTA TATAACTGCC AGCCTCTGCT GCCCTCTCC AAAAAGTCTC TGCCCTTGTC	360
10	TTTGGCACCT GTCTCTGTCC TCCCATTTCT CTGCTCCTCC TTTCTCCAAC TCAGANTCAC	420
	CCTGTTAGTT CAGCAAATGT TCATCGAGCT CCATAATGTA GCAGGACAGG NCTGTCTAAC	480
15	AGATTCTGGN CTTGCAAGGG TGAGACAAGT ACTCTCCATC TTTCTCTCAT CTTACAGAT	540
	GGTCTGCTCA ACAACTTTGC ACTGAATTGT AAATAATTGA TACTGCATAA AACATTGATG	600
	TTCTTTAAGG GTAGTCCAGC AAGGTGGCAA GTCTTATAAT GATAACTGCT CAAGGATCTC	660
20	TCAGTGAAGC ATTTGGGGST GCTAGCTCTG CCTATGGGTG AGGTCAGCTA TCTCACGCCA	720
	TCTACTTCCA CNTGCCCCC CATGCCAGGC TCACCCTGAG CTGAGATGCC TGAGCAGGTG	780
25	GCAGAAAGGA GCCACCTGGT TTATGCTTCG GGACCACAAA CTCCTCTATC CAGANGACAG	840
	TTTT	844

30

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

	AGCCCTGCTG AAGTACAGGT TCTTCTATCA GTTCTGTTG GGCAATGAAC GAGCAACAGC	60
	AAAGGAGATC AGGGATGAAT ATGTGGAGAC GCTGAGCAAG ATTTACCTGT CTTACTACCG	120
45	CTCTTACCTG GGGCGGCTCA TGAAGGTGCA GTATGAGGAA GTCGCTGAGA AAGATGATCT	180
	AATGGGTGTG GAAGATACAG CAAAGAAAGG ATTCTYCTCA AAGCCATCGC TCCGCAGCAG	240
50	GAACACCATT TTCACCCTAG GAACCCGCGG CTCTGTCATC TCCCCACTG AACTTGAGGC	300
	CCCCATCCTG GTGCCTCACA CAGCGCAGCG GNAGAGCAGA GGTATCCATT TGAGGCCCTC	360
	TTCCGCAGCC AGCACTACGS CTCCTAGAC AATTCTGCC GCGAATACCT TTTCATCTGT	420
55	GAATTTTTTG TTGTGTCTGG CCCAGYTGCA CACGACCTGT TCCATGCTGT CATGGGCCGT	480
	AACTCAGCA TGACCCTGAA ACACCTGGAT TCTTATCTAG CTGACTGCTA CGATGCCATT	540
60	GCTGTTTTTC TCTGTATCCA CATTGTTCTC CGGTTCGTA ACATTGCAGC AAAGAGGGAT	600

	GTTCTGCCCC TGGACAGGTA CTGGGGAACA GGTGCTTGCC TTGCTATGGC CACGGTTTGA	660
5	ACTGATCCTG GAGATGAATG TTCAGAGCGT CCGAAGCACT GACCCCCAGC GCCTAGGGGG	720
	GTGGAATACT CGGCCCCACT ATATCACACG CCGCTATGCA GAGTTCTCCT CCGCTCTTGT	780
	CAGTATCAAC CAGACAATTC CTAATGAACG GACCATGCAA TTGCTGGGAC AGCTGCAGGT	840
10	GGAGGTGGAG AATTTTGTCC TCCGAGTGGC AGCTGAGTTC TCCTCAAGGA AGGAGCAGCT	900
	TGTGTTTCTG ATCAACAACAT ATGACATGAT GCTGGGTGTG CTGATGGAGC GGGCTGCAGA	960
15	TGACAGCAAA GAGGTGAGA GCTTCCAGCA GCTGCTCAAT GCTCGGACAC AGGAATTTCAT	1020
	TGAAGAGTTG CTGTCTCCCC CTTTGGGGG TTTAGTGGCA TTTGTGAAGG AGGCTGAGGC	1080
	TTTGATTGAG CGTGGACAGG CTGAGCGACT TCGAGGGGAA GAAGCCCGGG TAACTCAGCT	1140
20	GATCCGTGGC TTTGGTAGTT CCTGGAAATC ATCAGTGGAA TCTCTGAGTC AGGATGTAAT	1200
	GCGGAGTTTC ACCAACTTCA GAAATGGCAC CAGTATCATT CAGGGAGCGC TGACCCAGCT	1260
25	GATCCAGCTC TATCATCGCT TCCACCGGGT GCTGTCCCAG CCGCAGCTCC GAGCCCTCCC	1320
	TGCCCCGGGCT GAGCTCATCA ACATTACCA CTTTATGGTG GAGCTCAAGA AGCATAAGCC	1380
	CAACTTCTGA TGTGCCAGAA ACCGCCCTGA GATCTGCCGG TCATCTCCAT GGACTTCTGC	1440
30	ACCCCATTC ATACCTTCTT TCACCTGGGG TACCCCTTCC AGTTTTCCTC TTGCTTCCCA	1500
	GGCCCTTGAC ATGGCTTACC TGCCTTCACT CCCAGCACCT TGCCCAACAG GATAAGCTGG	1560
35	ATCCCTTGG CCTTCTGAAT ATCCAGTGT CTTAGGTTT CCCAAGACCA CTTCCCTGTG	1620
	GGCTTCCAAA ATGGCCTTTA TCATTTCTCC AGTCTGTAC CCTCCTTTCC TGCTCCATA	1680
	CACCCAAGGC TTGTTTCTTC CCTGTAAAA ACCACTGCCT CAATCTCTGG TTCACTCAAC	1740
40	TAGTCACCAT GTCCTGAGGC ATGAAGCCTC CTCAGCTCTT GGAATTGCTG GCAAGGGGTG	1800
	ACTGCCTCTG AGTCATTGTG TTTTCAAAG TGATTTCTTT TCTGTAGCTT TTTGACCTAA	1860
45	GATCTCAGCA ATTTGAACAC TAACCTCTCC CCTCCTGGCT CAAGAATTAC TCCGAAGTCA	1920
	GTCTGCAGAA AATAAATATT TAGTATGACA TGAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1980
	AAAAA	1985

50

(2) INFORMATION FOR SEQ ID NO: 98:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1416 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

	ATATGAAGGG AAAGAATTGG ATTATGTTTT CTCAATTGAT GTCAATGAAG GTGGACCATC	60
5	ATATAAATTG CCATATAATA CCAGTGATGA CCCTTGGTTA ACTGCATACA ACTTCTTACA	120
	GAAGAATGAT TTGAATCCTA TGTTCCTGGA TCAAGTAGCT AAATTTATTA TTGATAACAC	180
10	AAAAGGTCAA ATGTTGGGAC TTGGGAATCC CAGCTTTTCA GATCCATTTA CAGGTGGTGG	240
	TCGGTATGTT CCGGGCTCTT CGGGATCTTC TAACACACTA CCCACAGCAG ATCCTTTTAC	300
	AGGTGCTGGT CGTTATGTAC CAGGTTCTGC AAGTATGGGA ACTACCATGG CCGGAGTTGA	360
15	TCCATTTACA GGAATAGTG CCTACCGATC AGCTGCATCT AAAACAATGA ATATTTATTT	420
	CCCTAAAAAA GAGGCTGTCA CATTTGACCA AGCAAACCCT ACACAAATAT TAGGTAAACT	480
20	GAAGGAAC TT AATGGAAC TG CACCTGAAGA GAAGAAGTTA ACTGAGGATG ACTTGATACT	540
	TCTTGAGAAG A TACTGTCTC TAATATGTAA TAGTTCTTCA GAAAAACCCA CAGTCCAGCA	600
	ACTTCAGATT TTGTGGAAG CTATTAAC TG TCCTGAAGAT ATTGTCTTTC CTGCACTTGA	660
25	CATTCTTCGG TTGTCAATTA AACACCCCAG TGTGAATGAG AACTTCTGCA ATGAAAAGGA	720
	AGGGGCTCAG TTCAGCAGTC ATCTTATCAA TCTTCTGAAC CCTAAAGGAA AGCCAGCAAA	780
30	CCAGCTGCTT GCTCTCAGGA CTTTTTGCAA TTGTTTTGTT GGGCAGGCAG GACAAAAACT	840
	CATGATGTCC CAGAGGGAAT CACTGATGTC CCATGCAATA GAACTGAAAT CAGGGAGCAA	900
	TAAGAACATT CACATTGCTC TGGCTACATT GGCCCTGAAC TATTCTGTTT GTTTTCATAA	960
35	AGACCATAAC ATTGAAGGGA AAGCCCAATG TTGTCACTA ATTAGCACAA TCTTGGAAAT	1020
	AGTACAAGAC CTAGAAGCCA CTTTETAGACT TCTTGTGGCT CTTGGAACAC TTATCAGTGA	1080
40	TGATTCAAAT GCTGTACAAT TAGCCAAGTC TTTAGGTGTT GATTCTCAA TAAAAAGTA	1140
	TTCTCAGTA TCAGAACCAG CTAAAGTAAG TGAATGCTGT AGATTTATCC TAAATTTGCT	1200
	GTAGCAGTGG GGAAGAGGGA CGGATATTTT TAATTGATTA GTGTTTTTTT CCTCACATTT	1260
45	GACATGACTG ATAACAGATA ATTAAAAAAA GAGAATACGG TGGATTAAGT AAAATTTTAC	1320
	ATCTTGTAAG GTGGTGGGGA GGGGAAACAG AAATAAAATT TTTGCACTGC TGAAAAAAA	1380
50	AAAAAAAAAA AAAAGGAAAC TCGAGGGGGG GCCCGG	1416

## (2) INFORMATION FOR SEQ ID NO: 99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1935 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

5	NICTACCCCTA ATCAAGATGG GGACATACTT CGCGACCAGG TTCTTCATGA ACATATCCAG	60
	AGATTGTCTA AAGTAGTGAC TGCAAATCAC AGAGCTCTTC AGATACCAGA GGTTTATCTT	120
	CGAGAAGCAC CATGGCCATC TGCACAATCA GAAATCAGGA CAATAAGTGC TTATAAAACC	180
10	CCCCGGGACA AAGTGCAGTG CATCCTGAGA ATGTGCTCTA CGATTATGAA CCTCCTGAGC	240
	CTGGCCAATG AGGACTCTGT CCCTGGAGCG GATGACTTTG TTCCTGTGTT GGTGTTGTG	300
	TTGATAAAGG CAAATCCACC CTGTTTGCTG TCTACTGTGC AGTATATCAG TAGCTTTTAT	360
15	GCTAGCTGTC TGCTGGAGA GGAGTCCTAT TGGTGGATGC AGTTCACAGC AGCAGTAGAA	420
	TTCAATTAATA CCATCGATGA CCGAAAGTGA CCAAGACCAA GGCCACCAA GGCAGCAGAC	480
20	TGTTAATCAG ACAACAGAT CTCTGAGAAG GTGCATCAGC TGCTTTGAAG GCTGAAGATT	540
	GTTTGTATG ATACTGCACA GCATCAGGCA TTTTAAAGCA GATCTTTACT AAACAGGTTA	600
	ATGAGCTAAC AAGCAGGTTT TCTCGTCTTT GGGCTCTTTC CTTTCTGAGT TGCATATTCT	660
25	ATTTTCTTGT CCCCAAGTAG AGACTAGTAC TACAAAAGG GACCACATTT TTCAAGTATT	720
	TCTAAGTATA AAAAACAAAA CAAAAATCTC TTAGGAAATG TCTAGACCTC CATTCCTGGA	780
30	TTCCCTTTCT TTCTTTTAT TTTAAAAAAG AACAGTACCC CTCTTTAAAG ATGCTGTCTT	840
	ACATTAATGA GCATCTAATG GAAAGAAGGT ATGAGTTGCA CTGAGGATTA GAATAGTGGT	900
	GCGTTAGTGG CATTATCTAT AAATACACTC ACCTAAATG AAAGCTAAGA AGGAAATGTA	960
35	AATATAATAT ATATTTATAT TTGATGTAAT ATGGACATCT GCAGATTCTA ATAAACAAGG	1020
	ACTATGCTG ATAGTAGGCT GTGACATACT GTCTGTGAA ATGGTTTCCT TGACAAAATT	1080
40	TAAGCTGAGC TTAAAAGCAA AAAAACAAAA AGTACACAGA AATATTTATT AAAATGTAAT	1140
	ACAGTTTAT GAACCTTCTA GGTATGGAGT TTGATGGACA GGGCTGCCTY TAATGAGTGT	1200
	GAAGGTCAT AAGTCACTTA GACATCTCAC CGTGAAGTT TGTGAGCCTG CATTAGGAGA	1260
45	TAGACTGATT ACCATACATG ACATAAAAAG GAACAGTGA TAGCTCATAC TTTATGGTGG	1320
	TTCTTCTCCT CCGAAATAAT ATACTGCAGA AATCCAGAC AGAGCTCCTT ACAAACCTTT	1380
50	AATTGTAATA TATTTTGTAT GATTATTCAC ATTGAATGCA CAGACCAAGA ATTCAGTGAA	1440
	TGTCATTTTT TAAAAACTA ATTTGTATTG TCTGCTCTAG TGATACAAGT TTTACTAGTG	1500
	ATAAACTATT TTAATCAACC ATACTATTCT TATGAAAAA AATATCTATT TTGGCAGGTT	1560
55	TCTGTGCCTT TATTTCCCTC TTCTGAAAAA AAGTCTGTGT TTTCATAGTT TGGTTTGCAT	1620
	TGTATATCAA TAATTAATCA GGAATGGGTT TTGGTGCCTG AAAAATTGGC CATGGAGGCA	1680
60	CACCAAAGCT TCAAGCACA GTCTGTGACA TGGGCCATCA CTGTCTGGTT TCACTTCGTG	1740

TGTTTCCTAA ACACATTTAG CTGCTTTTTT AACAACTCA GCCCCATACT TGAGTCCCTT 1800  
GTTGTTGGGA GCATTTCCAG GCATCTTTTA AGGGAACTGT GACAAACAGC CTCGGGCAGA 1860  
TGAACACGGA GGCTCTCTGT TGTCTGTCTC TGAGATCTTT GTGTCTGGGA ATGCCTAAAG 1920  
NTTTTGNTTT TTTT 1935

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

GAATTCGGCA CGAGCGTCCA CGCAGCCGCC GGCCGGCCAG CACCCAGGGC CCTGCATGCC 60  
AGGTCGTTGG AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCCTCA GCCTCCTCTT 120  
CCTCATCCTG ATGGGCACTG AACTCACTCA AGACTCCGCT GCCCCCGACT CCCTGCTGAG 180  
AAGTTCAAAG GGCAGCACGA GGGGTCTTT GGCTGCTATT GTCATCTGGA GGGGAAGAG 240  
TGAGAGCCGG ATAGCCAAGA CCCCAGGCAT TTTCAGAGGT GGCGGGACCT TAGTCCTACC 300  
CCCAACACAC ACCCCTGAGT GGCTCATCCT CCCTTTGGGC ATAACGCTGC CCTTGGGGGC 360  
TCCAGAAACA GCGGTGGGG ATTGTGCCGC TGAGACCTGG AAGGGCAGCC AGCGTGCCGG 420  
CCAGCTGTGT GCATTGCTGG CTTAATATGC AGGGCTTGGG GGGCTGTGGC CACATGCCCC 480  
GCAGGAGGTG AGTGAGGAGC CCTGTGGCGT GCTGGTGTGG GGATCGTGGG CATTTCAAAC 540  
GGGCTTGTCTG TACCCTGAAC AATGTATCAA TAGAGAAAAA AAAAAAAAAA AAAACTCGA 599

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

GAATTCGGCA CAGAAAAAAA AGAGAGACTG GGTCTTACTG TGTGCCCCAG ACTTGTCTTG 60  
AACTCCTGCC TCAGCCTCTC AAGTACTTGG GATTATAGGC CAAGAAGCCA CCATGCCTAG 120  
CTTCTTCCTG TCATTGATCC AGACTAATAC TCTGGGGTCA GCCTCATTTT TTCTCTTTCT 180

	CACATTGCAC ATCCACTTGT CACCAAATCK RGTTCATTCT GCATCCTAAG TAAGTCCTTT	240
5	GATTCCTCCA GTTGTTCATT AGTAATGTCT CAARTGTAAT TTTTCTAGT AGTTTTCAGC	300
	CTGTCTTTCC KGCCTTCAGT CTAACTTCT CCAGTACATA KGCCACATTG TTGTCAGCAK	360
	GATCAWATTT TATTTAAAAA TACTTTACAW AKGTTTATKG CCAAATATTA GRAAATACAG	420
10	ATTCATGGAA AGAAAAATCA CTGTCCCAAG GAGGTCACCTG GCATGGTGAG GTTAAGGGGT	480
	GATTTTAATT TTTAAAAATG TATATTTTTT CCTGTGTAGA GTAGTAACAC CCTTGAAAAC	540
15	ACAWTCCCTT GTAAAGTCTC TAATTCTGTA CTCCGCATCT AGSTGRTCTC TTCTTTCTCA	600
	GATATTTTAC AATTTCAATT ATCACCACCT TTCTCTAGCC TTTACCCGTC TCTTCAATAT	660
	TWACATATGC AGAAGTTTCT CCTAACAAAC ACCTGCCTCT GCCTCAGTTC TGCTACCACC	720
20	CTGTTGCTTT CTTTCCCTTC ACAATCAAAT TTAAGAGTGT CAAAAAAAAA AAAAAAAAAA	780
	TCGA	784

25

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1035 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

	AGAGGCCTGG CTGCGTTGCC CTATCTCCGT CTCGCCACC CACTTAGCGT TTAGGCATC	60
40	AATTACCAGC AGTTTCTCCG CCACTATCTG GAAATTACC CGATTGCTCC CGGCAGAATA	120
	CAAGAGCTTG AAGAACGCCG CAGTTGCGTG GAAGCCTGCA GAGCAAGGGA AGCAGCGTTT	180
	GATGCCGAAT ATCAGCGAAA TCCTCACAGG GTGGACCTCG ATATTTTAAC CTTTACGATA	240
45	GCTCTGACTG CCTCTGAAGT TATCAACCCT CTGATAGAAG AACTTGGTTG CGATAAGTTT	300
	ATCAATAGAG AATAGTTAGG TGGTGACACT ACTTCAAGAG AACCTCTGCA TTCCAGTCAT	360
50	ACCAATCCTG CAACTTGATT TTCAGAAGTC AAGAGTATAT CGCGATAAGA CAGTGACACG	420
	GTGGAGGGGA AAAAAAGGGG GAGGGGAAG CTTATCTTGA AAAAGCATCA CAGAAGTAGA	480
	AAAAAATGTC GAAAGCATTA TAACTGTAAC GTTCTTTGAG TTTGTGATTG ATCCACATTT	540
55	TTCCCCCTGC ATTATGAAA ATGTCTCTCA GCATTGCTTT ATTACAAAGT AAAGGATGGT	600
	TTTATAAAT TGAGACTGAT GAAACATCAA TACTAGAGCC CATGAGGATG AAAGAAATTA	660
60	TCAAATAGTG CTGAACAGAA TAAGATGTTA ACGCTGAGTT ATTAGGACTG GAAGGCTATG	720

AAAAGAACTT GAAATTGTCG GAATATGTGC TCTCTTCATG TCATATTCAA TAGAAGTTTC 780  
 TAGTTTAAGA TTGATTTTGT GTTTTCTTAG GCATTTCAAG TGACAAGCAA AGTAAATGTA 840  
 5 TATATTATGT GATAAATCAT GTTTTCAAGA ACGTCAAATT TCTGGACTTT TTTCTTTCAA 900  
 TTTTAAATTT TTAAAGTTTT TTTGGTATTA AAAAATCYAT TCACAAGCCA AAAAATWIWT 960  
 WAAATWIWCM GCGAAAAGCC AAAAAAAAAA AAAAMMAGGG GGGGCCGGGC CCCATCCCCC 1020  
 10 CAAGGGGGTC CNGNT 1035

15

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

25

AGGTATTAGG CCCTTTTGTG GGAGCCCCAT GTTTTGTGTTT TCTGAGTTGG TGGGGAGGGA 60  
 SGGAGGGGGA GGGCTGAATT GTTTTGCAGA GGAAGATGGC ATCTGTGCTT TAAATTTCTC 120  
 30 ATTACTGGGT TAGAAAACAA AGAGGGAKTG CCCTGCACAT TTTCTTTTGT GCTTTTAAAT 180  
 GTTCTTAAAG TTGGAACAGG TTTCCTCGGG CCTGTTTGA CTGATTGCTG GAGTGCAITTT 240  
 GATAGTTAAA AATTACTAAT TGGTTTTATT TCCCTTCACA CTCTGCCTCC CCACTTCCTC 300  
 35 CCCCCTTACT GAAAAATAAC CATTTTAGTG TCAGGCTAGA AATTGAATTG CTGAGTTTGT 360  
 TGTATCCTTT AAATTAATAA CCACAAGTGT TTATTGTAGT GGTAAACTG TAGCATCTCA 420  
 40 GCATCTGGGT GGAAGCTGCC TATATTTCTT CCCAGTTTAA CTGGGGACCA TCTGTGAAAT 480  
 TAATTTTCCA TCCAGACAGC TGCTGTGAGC AAATGAACAT AAATGCTCCG TGGAAATTTA 540  
 CTAACCAAGT TTTATATTGA CCTGCAGTGT AAAAAGCACA TTTAATTATA AACAATATAT 600  
 45 TCAAAATGGG CAAATTTTAT TTTCAAATGC AGTGTAGAGC TAGATTAAAA GCAACTCTTT 660  
 GCCACCTACT CTGCCCTTTT GGCAAAGTTA CCTTGAACAA AGAATCTTAA GGGTTTATTA 720  
 50 AGAACTCTTT ATTTTCTTCA TACCCTGTTT TCTGCAGTGC TTTCTAACAG CTTCTGGGTG 780  
 CAGATTTTCT TCGGCATCCT TTGCACTCA GCTTATTACA GGTAGGTAGT GCTTAAGAAA 840  
 AGTCATGGAG GACTAAAGCC TAAGTCCTTT TCACTTTTCC TCCATCTGAA GGTAGGTGAG 900  
 55 TTCATCCTCT TCATAGTAAT GCTGTTTAC CAAGACTTTA TAGCAGATGG ACCCAGAAAG 960  
 AATTTTCTGC TATTGTGTTT ACTACAACAG GATAGGGACA TCAGACAGCC CCAGAAACCC 1020  
 60 CTTCCAGATC TGATATGGGA CTATTAATTT TTATGCTGTT AATTGGTATT CATTACAAT 1080

	GCAGTTGAAG GGGGAAGGCT CCACTGCATT CTTGGCTAA GGCCTGAATG CTTGCTCATC	1140
5	TGTAAGATCT ATACTCGAGG TTTTGTTTC CTTTAAAT TCTTAGGGA GAGAGGGATG	1200
	GTTTCTGAGG GGTCTGAAA GTATGATTCA ATGTGCAACA TACAGGTAGG TCTTCAGCAT	1260
	AAGCTGAAAT ATATGCATGT AAAAATTG ACATCTTTT TTTAATTTT CCACTTCTT	1320
10	CTTAACCTTA CTCTCTTTT TGTCCCCC CCATCTTACA GAAGTTGAGG CCAAGGGAGA	1380
	ATGGTAGGCA CAGAAGAAAC ATGGCAAAC GCTCTGTGCT TTCAAACCA AGTGTCCCC	1440
15	CCAACCCCA ATTTGTCTAA GCACTGGCCA GTCTGTTGTG GGCATTGTTT TCTACAACCA	1500
	AATTCTGGGT TTTTCTTC TTTCTTAA CATAGAGGTA CCACCACAAG GGATGCCCTA	1560
	CTCTCTCGCA GCTCTGAAA GCATCTGTTT GAGGAAAGG TCTCTGGCA AGCAAGTGGT	1620
20	TATTTGGATT GCTTGCTTC CTTTTCAC CTGGGACATT GYAATCATAA AATAACAGTA	1680
	AATTCCAAAC CTCAAAACT ATTATGGCCT GAGCACAGCT GAAATCTAGC AGAGTTAAC	1740
25	TCTTCTGCCT CCATGCTGT CACTATAAT TCAGGTTCTG CTGTTGGCTT CAGAACATGA	1800
	GCAGAAGAAT CGTTTATGC TAGTTATGC ATTCATGGTT GAAACTCAAC TTAGGGAAAG	1860
	GGTTCCAATG TATTAAGCAA TGGGCTGCTT CTCCCAATC CTCCCTAACA ATTGTTGTG	1920
30	TGGACTTCTC ATCTAAAAGG TTAGTGGCTT TTGCTGGGA TCAGTGCTCT CTATGATGT	1980
	TCTTGCTGGT CTCCAGACAC ATTCCTGTG CATTAAGACT TGAAAGACTT GTAGATGTGT	2040
35	GATGTTTCAGG CACAGGATGC TGAAAGCTAT GTTACTATTC TTAGTTGTA AATTGTCCTT	2100
	TGATACCAT CATCTGTTT TCTTTTGTA GGTATAATA AAAACTGT TGACAATAAA	2160
40	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA	2218

## (2) INFORMATION FOR SEQ ID NO: 104:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

	CTTCACAGAC TGACAGAATG GTTTGTTTT GTTTGTTTT GTTTGTTTT GTTTTGAGA	60
55	TGGACTCTAG CTCTGTCACC CAGGCTGGAG TGCAGTGGT CGATCTCGGC TCACTGCAAG	120
	CTCCGCCTCC CGGGTTCTCA CCATTCTCCT GCCTCAGCCT CCCGAGTAGC TGGGACTACA	180
60	GGCGCCACC ACCACGCCG GCTAATTTT TGTATTTTT AGTAGAGACG GGGTTTACC	240



	ATGTTAGCCA GGATGGTCTC GATCTCCTGA CCTCGTGATC CGCCCGCYTC GGCTCCCAA	300
	AGTGCTGGGA TTACAGGCGT GAGCCACCGT GCCTGCCCCA GAATGGTTT TAAAGCCACA	360
5	GTTGAGARGC CACCCATTGC CCGGCGCCTG GACAGTGATC ATCTTGTTCA TCTTGTTTCA	420
	TCCTTTCTTG TGTGATTGGA ATTATTCATC CCCTTTGAAA GATGAGAAGG TTGAGATGCA	480
10	AAGAGTCTAC CTTTCCAAGT TCTCACTGCT GGAAAGARCT AGAAGCACAG TTCAAAGTTC	540
	TGGNTTCTGG ACTCTGCAGT CCAGGTYTCC CTTYTCCCAC TTGCCTACCC TCAATGCCAC	600
	ACTGTTTTTG AAGTGGCCCA TAACTTGAAG GRAAAGTTTA AAGACAGTTC AATTTAATCA	660
15	TCAGRATGCA TTCTTTTTTT TTTGCGARAC GGAKTTTCAC TCTTGCTGCC CASGCTGGAG	720
	TGCAATGGTG CAATGATCTC GGCTCACTGC AACCTATGCC TCCTGGGTTC AAGNGATTAT	780
20	CCAGCCTCAG CCTCCCGAGT AGCTGGGATT ATGGGCGCCC ACCACCATGC CCAGCTAATT	840
	TTTGATTTTT TTTTTTAGT AGAGATGGGG TTTCGCCAGG TTGGCCAGGC TGKTCTTGTC	900
	AAYTCCTGGC YTCAGGTGAT YTGCCACYT CATCYTCAA AAGTGCTGGG ATTACAGGCA	960
25	TGAGCCACTG CGCCTGGCYT CAGAATGCAT TCTTACACAT CTATCCTAGA CATTTATAAG	1020
	CACTCTAATG GATAACAATC CAAGAATAAA TGATTGTAAA AGATGATGCC GAAGAGTTGA	1080
30	TGTCAATCTT TTTTTCCTAA GAAAAAAGT CCGCGAGTAT TAAATATTTA GATCAATGTT	1140
	TATAAAATGA TTACTTTGTA TATCTCATTA TTCCTATTTT GGAATAAAAA CTGACCTTCT	1200
	TTAATCATAT ACTTGTCTTT TGTAATAGC AGCTTTTGTG TCATTCTCCC CACTTTATTA	1260
35	GTTAATTTAA ATTGGAAAAA ACCCTCAAAC TAATATTCTT GTCTGTTCCA GTCTTATAAA	1320
	TAAAACTTAT AATGCATGTA AAAAATAAAA A	1351

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(2) INFORMATION FOR SEQ ID NO: 105:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2066 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

	GGCACGAGGC GCGGAGGGC CACAATCACA GCTCCGGGCA TTGGGGGAAC CCGAGCCGGC	60
55	TGCGCCGGGG GAATCCGTGC GGGCGCCTTC CGTCCCGGTC CCATCCTCGC CGCGCTCCAG	120
	CACCTCTGAA GTTTTGACAGC GCCCAGAAAG GAGGCGAGGA AGGAGGGAGT GTGTCAGAGG	180
	AGGGAGCAAA AAGCTCACCC TAAACATTT ATTTCAAGGA GAAAAGAAAA AGGGGGGGCG	240
60	CAAAAATGGC TGGGGCAATT ATAGAAAACA TGAGCACCAA GAAGCTGTGC ATTGTTGGTG	300

	GGATTCTGCT CGTGTTCCTAA ATCATCGCCT TTCTGGTGGG AGGCTTGATT GCTCCAGGGC	360
5	CCACAACGGC AGTGTCTCTAC ATGTCTGGTGA AATGTGTGGA TGCCCGTAAG AACCATCACA	420
	AGACAAAATG GTTCGTGCCT TGGGGACCCA ATCATTGTGA CAAGATCCGA GACATTGAAG	480
	AGGCAATTCC AAGGGAAATT GAAGCCAATG ACATCGTGTT TTCTGTTCAC ATTCCCCTCC	540
10	CCCACATGGA GATGAGTCTT TGGTTCCTAAT TCATGCTGTT TATCCTGCAG CTGGACATTG	600
	CCTTCAAGCT AAACAACCAA ATCAGAGAAA ATGCAGAAGT CTCCATGGAC GTTTCCTGG	660
15	CTTACCGTGA TGACGCATTT GCTGAGTGA CTGAAATGGC CCATGAAAGA GTACCACGGA	720
	AACTCAAATG CACCTTCACA TCTCCCAAGA CTCCAGAGCA TGAGGGCCGT TACTATGAAT	780
	GTGATGTCTT TCCTTTCATG GAAATTGGGT CTGTGGCCCA TAAGTTTAC CTTTAAACA	840
20	TCCGGCTGCC TGTGAATGAG AAGAAGAAAA TCAATGTGGG AATTGGGGAG ATAAAGGATA	900
	TCCGGTGGT GGGGATCCAC CAAAATGGAG GCTTCACCA GGTGTGGTTT GCCATGAAGA	960
25	CCTTCTTAC GCCCAGCATC TTCATCATT TGGTGTGGTA TTGGAGGAGG ATCACCATGA	1020
	TGTCCCGACC CCCAGTGCTT CTGGAAAAAG TCATCTTGC CCTTGGGATT TCCATGACCT	1080
	TTATCAATAT CCCAGTGGAA TGGTTTCCA TCGGGTTGA CTGGACCTGG ATGCTGCTGT	1140
30	TTGGTGACAT CCGACAGGGC ATCTTCTATG CGATGCTTCT GTCCTTCTGG ATCATCTTCT	1200
	GTGGCGAGCA CATGATGGAT CAGCACGAGC GGAACCACAT TGCAGGGTAT TGGAAGCAAG	1260
35	TGGGACCCAT TGCCGTGGC TCCTTCTGCC TCTTCATATT TGACATGTGT GAGAGAGGGG	1320
	TACAACCTAC GAATCCCTTC TACAGTATCT GGACTACAGA CATTGGAACA GAGCTGGCCA	1380
	TGGCCTTCAT CATCGTGGCT GGAATCTGCC TCTGCCTCTA CTTCCTGTTT CTATGCTTCA	1440
40	TGGTATTICA GGTGTTTCGG AACATCAGTG GGAAGCAGTC CAGCCTGCCA GCTATGAGCA	1500
	AAGTCCGGCG GCTACACTAT GAGGGGCTAA TTTTATAGTT CAAGTCTCTC ATGCTTATCA	1560
45	CCTTGGCCTG CGCTGCCATG ACTGTCATCT TCTTCATCGT TAGTCAGGTA ACGGAAGGCC	1620
	ATTGGAATG GGGCGGCGTC ACAGTCCAAG TGAACAGTGC CTTTTCACA GGCATCTATG	1680
	GGATGTGGAA TCTGTATGTC TTTGCTCTGA TGTCTTGTA TGCACCATCC CATAAAACT	1740
50	ATGGAGAAGA CCAGTCCAAT GGAATGCAAC TCCCATGTAA ATCGAGGGAA GATTGTGCTT	1800
	TGTTTGTTC GGAACCTTAT CAAGAATTGT TCAGCGCTTC GAAATATTCC TTCATCAATG	1860
55	ACAACGCAGC TTCTGGTATT TGAGTCAACA AGGCAACACA TGTTTATCAG CTTTGCAATT	1920
	GCAGTTGTCA CAGTCACATT GATTGTACTT GTATACGCAC ACAAATACAC TCATTAGCC	1980
	TTTATCTCAA AATGTTAAAT ATAAGGAAAA AAGCGTCAAC AATAAATATT CTTGAGTATA	2040
60	AAAAAAAAA AAAAAAAAAA AAAAAA	2066

5 (2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1705 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

15 AATTCGGCAK AGGGCAGCTG TCGGCTGGAA GGAAGTGGTC TGCTCACACT TGCTGGCTTG 60  
CGCATCAGGA CTGGCTTTAT CTCCTGACTC ACGGTGCAAA GGTGCACTCT GCGAACGTTA 120  
AGTCCGTCCC CAGCGCTTGG AATCCTACGG CCCCCACAGC CGGATCCCCT CAGCCTTCCA 180  
20 GGTCTCAAC TCCCGYGGAC GCTGAACAAT GGCCTCCATG GGGCTACAGG TAATGGGCAT 240  
CGCGCTGGCC GTCTGGGCT GGCTGGCCGT CATGCTGTGC TCGCGCTGC CCATGTGGCG 300  
25 CGTGACGGCC TTCATCGGCA GCAACATTGT CACCTCGCAG ACCATCTGGG AGGGCCTATG 360  
GATGAAGTGC GTGGTGAGA GCACCGGCCA GATGCAGTGC AAGGTGTACG ACTCGCTGCT 420  
GGCACTGCCG CAGGACCTGC AGGCGGCCCG CGCCTCGTC ATCATCAGCA TCATCGTGGC 480  
30 TGCTCTGGGC GTCTGTCTGT CCGTGGTGGG GGGCAAGTGT ACCAACTGCC TGGAGGATGA 540  
AAGCGCCAAG GCCAAGACCA TGATCGTGGC GGGCGTGGTG TTCCTGTGGG CCGGCCTTAT 600  
35 GGTGATAGTG CCGGTGTCTT GGACGGCCCA CAACATCATC CAAGACTTCT ACAATCGCT 660  
GGTGGCCTCC GGGCAGAAGC GGGAGATGGG TGCCTCGCTC TACGTGGCT GGGCCGCTC 720  
CGGNTGCTG CTCCTTGGCG GGGGGTGTCT TTGCTGCAAC TGTCCACCCC GCACAGACAA 780  
40 GCCTTACTCC GCCAAGTATT CTGCTGCCCC CTCTGCTGCT GCCAGCAACT ACGTGTAAAG 840  
TGCCACGGCT CCACTCTGTT CCTCTCTGCT TTGTTCTTCC CTGGACTGAG CTCAGCGCAG 900  
45 GCTGTGACCC CAGGAGGGCC CTGCCACGGG CCACTGGCTG CTGGGGACTG GGGACTGGGC 960  
AGAGACTGAG CCAGGCAGGA AGGCAGCAGC CTTAGCCCTC TCTGGCCCAC TCGGACAACT 1020  
TCCCAAGGCC GCCTCCTGCT AGCAAGAACA GAGTCCACCC TCCTCTGGAT ATTGGGGAGG 1080  
50 GACGGAAGTG ACAGGGTGTG GTGGTGGAGT GGGGAGCTGG CTTCTGCTGG CCAGGATGGC 1140  
TTAACCTGA CTTTGGGATC TGCTGCATC GGTGTGGCC ACTGTCCCA TTACATTTT 1200  
55 CCCCCTCTG TCTGCCTGCA TCTCCTCTGT TGCGGGTAGG CCTTGATATC ACCTCTGGGA 1260  
CTGTGCCTTG CTCACCGAAA CCGCGCCCA GGAGTATGGC TGAGGCCTTG CCCACCCACC 1320  
TGCCTGGGAA GTGCAGAGTG GATGGACGGG TTTAGAGGGG AGGGGCGAAG GTGCTGTAAA 1380  
60

5 CAGGTTTGGG CAGTGGTGGG GGAGGGGGCC AGAGAGGCGG CTCAGGTTGC CCAGCTCTGT 1440  
GGCCTCAGGA CTCTCTGCCT CACCCGCTTC AGCCAGGGC CCCTGGAGAC TGATCCCCTC 1500  
10 TGAGTCCTCT GCCCCTTCCA AGGACACTAA TGAGCCTGGG AGGGTGGCAG GGAGGAGGGG 1560  
ACAGCTTCAC CCTTGAAGT CCTGGGGTTT TTCCTCTTCC TTCTTTGTGG TTTCTGTTTT 1620  
GTAATTAAAG AAGAGCTATT CATCACTGTA ATTATTATTA TTTTCTACAA TAAATGGGAC 1680  
15 CTGTGCACAG GRAAAAAAAA AAAAG 1705

15 (2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

25 TGCAGGAATT CGGCAGAGGT TTTCCGCTAG ACTCTGGCAG TTGGTGAGCA TCATGGCAAC 60  
CGTTACAGCC ACAACCAAAG TCCCGGAGAT CCGTGATGTA ACAAGGATTG AGCGAATCGG 120  
30 TGCCCACTCC CACATCCGGG GACTGGGGCT GGACGATGCC TTGGAGCCTC GGCAGGCTTC 180  
GCAAGGCATG GTGGGTCAGC TGGCGGCACG GCGGGCGGCT GCGGTGGTGC TGGAGATGAT 240  
CCGGGAAGGG AAGATGCGG GTCCGGCAGT CCTTATTGCT GGCCAGCCGG GCACGGGGAA 300  
35 GACGGCCATC GCCATGGGCA TGGCGCAGGC CCTGGGCCCT GACACGCCAT TCACAGCCAT 360  
CGCCGGCAGT GAAATCTTCT CCCTGGAGAT GAGCAAGACC GAGGCGCTGA CGCAGGCCTT 420  
40 CCGGGCGTCC ATCGGCGTTC GCATCAAGGA GGAGACGGAG ATCATCGAAG GGGAGGTGGT 480  
GGAGATCCAG ATTGATCGAC CAGCAACAGG GACGGGCTCC AAGGTGGGCA AACTGACCCT 540  
45 CAAGACCACA GAGATGGAGA CCATCTACGA CCTGGGCACC AAGATGATTG AKTCCCTGAC 600  
CAAGGACAAG GTCCAGGCCG GGGACGTGAT CACCATCGAC AAGGCGACGG GCAAGATCTC 660  
CAAGCTGGGC CGCTCCTTCA CACGCGCCCG CGAACTACGA CGCTATGGGC TCCAGACCA 720  
50 AGTTCTGTGA GTGCCAGAT GGGGAGCTCC AGAAACGCAA GGAGGTGGTG CACACCGTGT 780  
CCCTGCACGA GATCGACGTC ATCAACTCTC GCACCCAGGG CTTCCTGGCG CTCTTCTCAG 840  
GTGACACAGG GGAGATCAAG TCAGAAGTCC GTGAGCAGAT CAATGCCAAG GTGGCTGAGT 900  
55 GGC GCGAGGA GGGCAAGGCG GAGATCATCC CTGGAGTGCT GTTCATCGAC GAGGTCCACA 960  
TGCTGGACAT CGAGAGCTTC TCCTTCCTCA ACCGGGCCCT GGAGAGTGAC ATGGCGCCTG 1020  
60 TCCAGCAGGT CTATGGGGAT GCCGTGAGGG CTCTGGTAGC TGGTGCCCG GATTCCCGTG 1080

ATGCCACGGT TGGTGGCCTC GTGCCGAATT CCTGCAGCCC GGGGGATCCA CTAGTTCTAG 1140  
AGCGGCCGCC ACCGCGGTGG ANCTCCN 1167

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(2) INFORMATION FOR SEQ ID NO: 108:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1907 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCACAGGGG AATCATCGTG TGATGTGTGT GCTGCCTTTG TGAGTGTGTG GAGTCCTGCT 60  
20 CAGGTGTTAG GTACAGTGTG TTTGATCGTG GTGGCTTGAG GGGAAACCTT GTTCAGAGCT 120  
GTGACTGCGG CTGCACTCAG AGAAGCTGCC CTTGGCTGCT CGTAGCGCGG GGCCTTCTCT 180  
25 CCTCGTCATC ATCCAGAGCA GCCAGTGTCC GGGAGGCAGA AGGTACCGGG GCAGCTACTG 240  
GAGGACTGTG CGGGCCTGCC TGGGCTGCCC CCTCCGCCGT GGGGCCCTGT TGCTGCTGTC 300  
CATCTATTTT TACTACTCCC TCCCAAATGC GGTCCGCCCG CCCTTCACTT GGATGCTTGC 360  
30 CCTCCTGGGC CTCTCGCAGG CACTGAACAT CCTCCTGGGC CTCAAGGGCC TGGCCCCAGC 420  
TGAGATCTCT GCAGTGTGTG AAAAAGGGAA TTTCAACGTG GCCCATGGGC TGGCATGGTC 480  
35 ATATTACATC GGATATCTGC GGCTGATCCT GCCAGAGCTC CAGGCCCGGA TTCGAACTTA 540  
CAATCAGCAT TACAACAACC TGCTACGGGG TGCAGTGAGC CAGCGGCTGT ATATTCTCCT 600  
CCCATTGGAC TGTGGGGTGC CTGATAACCT GAGTATGGCT GACCCCAACA TTCGCTTCCT 660  
40 GGATAAACTG CCCAGCAGA CCGGTGACCG TGCTGGCATC AAGGATCGGG TTTACAGCAA 720  
CAGCATCTAT GAGCTTCTGG AGAACGGGCA GCGGGCGGGC ACCTGTGTCC TGGAGTACGC 780  
45 CACCCCTTG CAGACTTTGT TTGCCATGTC ACAATACAGT CAAGCTGGCT TTAGCGGGGA 840  
GGATAGGCTT GAGCAGGCCA AACTCTTCTG CCGGACACTT GAGGACATCC TGGCAGATGC 900  
CCCTGAGTCT CAGAACAAC TCCGCCTCAT TGCCTACCAG GAACCTGCAG ATGACAGCAG 960  
50 CTTCTCGCTG TCCCAGGAGG TTCTCCGGCA CCTGCGGCAG GAGGAAAAGG AAGAGGTTAC 1020  
TGTGGGCAGC TTGAAGACCT CAGCGGTGCC CAGTACCTCC ACGATGTCCC AAGAGCCTGA 1080  
55 GCTCCTCATC AGTGAATGG AAAAGCCCTT CCCTCTCCGC ACGGATTTCT CTTGAGACCC 1140  
AGGGTCACCA GGCCAGAGCC TCCAGTGGTC TCCAAGCCTC TGGACTGGGG GCTCTCTTCA 1200  
GTGGCTGAAT GTCCAGCAGA GCTATTTCTT TCCACAGGGG GCCTTGCAGG GAAGGGTCCA 1260  
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GGACTTGACA TCTTAAGATG CGTCTTGTC CCTTGGGCCA GTCATTTCCTC CTCTCTGAGC 1320  
CTCGGTGTCT TCAACCTGTG AAATGGGATC ATAATCACTG CCTTACCTCC CTCACGGTTG 1380  
5 TGTGAGGAC TGAGTGTGTG GAAGTTTTTC ATAAACTTTG GATGCTAGTG TACTTAGGGG 1440  
GTGTGCCAGG TGTCTTTCAT GGGGCCTTCC AGACCCACTC CCCACCCTTC TCCCCTTCCT 1500  
10 TGCCCGGGG ACGCCGAAC CTCTCAATGG TATCAACAGG CTCCTTCGCC CTCTGGCTCC 1560  
TGGTCATGTT CCATTATTGG GGAGCCCCAG CAGAAGAATG GAGAGGAGGA GGAGGCTGAG 1620  
TTTGGGTAT TGAATCCCCC GGCTCCACC CTGCAGCATC AAGGTGCTA TGGACTCTCC 1680  
15 TGCCGGCAA CTCTTGCCTA ATCATGACTA TCTCTAGGAT TCTGGCACCA CTCCTTCCC 1740  
TGGCCCTTA AGCCTAGCTG TGTATCGGCA CCCCCACCC ACTAGAGTAC TCCCTCTCAC 1800  
TTGCGGTTTC CTTATACTCC ACCCCTTTCT CAACGGTCCT TTTTAAAGC ACATCTCAGA 1860  
20 TTAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGGG CGGCCGC 1907

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(2) INFORMATION FOR SEQ ID NO: 109:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 611 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

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ATGAATTAA GCCAAGCTNT NAATAGGGAC TCACTATGGG GGAAAGNTGG GTAACGCCTG 60  
CAGGTACCGT TCCGGAATTC CCGGTCGAC CCACGCGTCC GATGGGGCTT TAGTAAATCA 120  
GGCTTGCAGG CTCAAAGCTG CAATCTGCCC ACTCTCAGGT ACTGAGACTT TGTGGGCCTC 180  
AGACACCAGG AAGAAAGTTG GGATACAGTC ATTGAGTTA AAAAGGGAAT GACCCCTCAG 240  
AAACCCGCAT TAGCAGTGTT ACTCTTGAA GTGCCTTTAC TTTAAGCCT CTCTGTTCTG 300  
AAAAAGAGGT GTTTGGTTAC GTGTGAGCCA ACATCACGTT TTGTTAGCTG TGATTACCT 360  
TTGTCCGTTT AAAAGACTTC ACGGAGCCAT TCTGTATACA AGGTGTGCTC TTTCCAATGT 420  
AGAAGGGGTT ATGGAAGAG GTGCGATCCT TTGCTGTAAA CTGGAGAGAC CAGTCCCAA 480  
CAGAGGGGAA TTTAAGCCC TTCTCATCAC CCAATTGGAT GTTTTGTCTT ATAGCAAAT 540  
CCTGCAAAAT AAATAAATA ATATTGCAA AACTAAAAA AAAAAAAAAA AAAAAAAAAA 600  
55 GGGGGNCCN C 611

## (2) INFORMATION FOR SEQ ID NO: 110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2632 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

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TCCCAGCTCT CAGGACAAGG GCCCTGGGCG ATCTTTTAAA AAAGCCGATT GGGTGTCTTT 60  
CTAAAANTAC AACCACTACT TCATCGTCAA GTTCTGGA AGGGAGTCCC CTCCAGATTC 120  
TCATGGAGTG ACAAATCTTG ACTCTGCTC CTGGAATTTT TCAGGCCCAA ACTAGCGTTT 180  
CTACAATGAT TTTTGGCA AATTTGTCTT GATTATGGGT GGCTGATGAG GAACGTGCTT 240  
TTGTTAGGAA CCGAACTGG GCGGCGTGA GGGCGTGAC GCAATGAGTC CGGAAGAGGG 300  
TGAAATGCTT TCGGTAGGCA CTCCACGGCT GTGAAGATGG CGGCGGCTGC GTGGCTTCAG 360  
GTGTGCTG TCATTCTCT GCTTCTGGA GCTCACCGT CACCACTGTC GTTTTTCAGT 420  
GCGGACCGG CAACCGTAGC TGCTGCCGAC CGGTCCAAAT GGCACATTCC GATACCGTCG 480  
GGGAAAAATT ATTTAGTTT TGGAAAGATC CTCTCAGAA ATACCACTAT CTTCTGAAG 540  
TTTGATGGAG AACCTTGTA CCTGTCTTTG AATATAACCT GGTATCTGAA AAGCGCTGAT 600  
TGTTACAATG AAATCTATAA CTTCAAGGCA GAAGAAGTAG AGTTGTATTT GGAAAACTT 660  
AAGGAAAAA GAGGCTTGTG TGGGAAATAT CAAACATCAT CAAATGTGTT CCAGAACTGC 720  
AGTGAAGTCT TTAAACACA GACCTTTCT GGAGATTTTA TGCATCGACT GCCTCTTTTA 780  
GGAGAAAAAC AGGAGCTAA GGAGATGGA ACAAACCTTA CTTTATTTG AGACAAAACC 840  
GCAATGCATG AACCATGCA AACTTGGCA ATGCACCAT ACATTTTAT TGTACATATT 900  
GGCATTTTCT CCTCAAAGGA ATCATCAAAA GAAATTCAC TGAGTAATCT TTTTACCATG 960  
ACTGTTGAAG TGAAGGTCC CTATGAATAC CTCACACTG AAGACTATCC CTTGATGATT 1020  
TTTTTCATGG TGATGTGTAT TGTATATGTC CTGTTGGTG TTCTGTGGCT GGCATGGTCT 1080  
GCCTGCTACT GGAGAGATCT CCTGAGAATT CAGTTTGGG TTGGTGCTGT CATCTTCTG 1140  
GGAATGCTTG AGAAAGCTGT CTTCTATGCG GAATTTTCTG ATATCCGATA CAAAGGAAAA 1200  
TCTGTCCAGG GTGCTTTGAT CCTTGCAGAR CTGCTTTCAG CAGTGAAACG CTCCTGGCT 1260  
CGAACCTGG TCATCATAGT CAGTCTGGGA TATGGCATCG TCAAGCCAG CCTGGAGTCA 1320  
CTCTTCATAA GGTGTAGTA GCAGRAGCCC TCTATCTTTT GTTCTCTGGC ATGGAAGGGG 1380  
TCCTCAGAGT TACTGGGGCC CAGACTGATC TTGCTTCTT GGCCTTTATC CCCTTGGCTT 1440  
TCCTAGACAC TGCCTTGTGC TGGTGGATAT TTATTAGCCT GACTCAAACA ATGAAGCTAT 1500

TAAAACTTCG GAGGAACATT GTAAACTCT CTTGTATCG GCATTTCACC AACACGCTTA 1560  
 TTTTGGCAGT GGCAGCATCC ATTGTGTTTA TCATCTGGAC AACCATGAAG TTCAGAATAG 1620  
 5 TGACATGTCA GTCGGACTGG CGGGAGCTGT GGGTAGACGA TGCCATCTGG CGCTTGCTGT 1680  
 TCTCCATGAT CCTCTTTGTC ATCATGGTTC TCTGGCGACC ATCTGCAAAC AACCAGAGGT 1740  
 10 TTGCCTTTTC ACCATTGTCT GAGGAAGAGG AGGAGGATGA ACAAAGGAG CCTATGCTGA 1800  
 AAGAAAGCTT TGAAGGAATG AAAATGAGAA GTACCAAACA AGAACCCAAT GGAAATAGTA 1860  
 AAGTTAACAA AGCACAGGAA GATGATTTGA AGTGGGTAGA AGAGAATGTT CCTTCTTCTG 1920  
 15 TGACAGATGT AGCACTTCCA GCCCTTCTGG ATTCAGATGA GGAACGAATG ATCACACACT 1980  
 TTGAAAGGTC CAAATGGAG TAAGGAATGG GAAGATTGC AGTTAAAGAT GGCTACCATC 2040  
 AGGGAAGAGA TCAGCATCTG TGTCACTCTT CTGTACGGCT CCATGGGATT AAAGGAAGCA 2100  
 20 ATGACATCCT GATCTGTTCC TTGATCTTTG GGCATTGGAG TTGGCGAGAG GTGTCAGAAC 2160  
 AAAGAGAACA TCTTACTGAA AACAAGTTCA TAAGATGAGA AAAATCTACG AGCTTCTTAT 2220  
 25 TTACAACACT GCTGCCCCCT TTCCTCCCAG ACTCTGACAT GGATGTTTAT GCAACTTAAG 2280  
 TGTGTTGTTT CTGAACTTTC TGTAATGTTT CATTTTTTAA ATCTGACAAA CTAAAAAGTT 2340  
 TAACGTCTTC TAAAGATTG TCATCAACAC CATAATATGT AATCTCCAGG AGCAACTGCC 2400  
 30 TGTAATTTT ATTTATTTAG GGAGTTACAT AGGTGATGGG GGAAATGTT AACTACCTTT 2460  
 CATTTTCTCG GGAAGTCAAG GTTACATCTT GCAGAGGTTG TTTTGAGAAA AAAGGGCCCT 2520  
 35 TCTGAGTTAA GGAGCCATAG TTCTATCAAT GATCAAAAGA AAAAAAAAAA AACTCGATCG 2580  
 GCACGAGGGG GGGCCCGGTA CCCAATTCGC CCTATGGGAN TCGAATGAGA CC 2632

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(2) INFORMATION FOR SEQ ID NO: 111:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GAATTCGGCA CGAGCTCACC GTGCTGCGTG ACACAAGGCC AGCCTGCGCC TACGAGCCCA 60  
 TGGACTTTKT RATGGCCCTC ATCTACGACA TGGTACTGSW TGTGGTCACC CTGGGGCTGG 120  
 55 CCCTCTTCAC TCTGTGCGGC AAGTTCAAGA GGTGAAGCT GAACGGGGCC TTCCTCCTCA 180  
 TCACAGCCTT CCTCTCTGTG CTCATCTGGG TGGCCTGGAT GACCATGTAC CTCTTCGGCA 240  
 60 ATGTCAAGCT GCAGCAGGGG GATGCCTGGA ACGACCCAC CTTGGCCATC ACGCTGGCGG 300



	CCAGCGCTGG	GTCTTCGTCA	TCTTCCACGC	CATCCCTGAG	ATCCACTGCA	CCCTTCTGCC	360
5	AGCCCTGCAG	GAGAACACGC	CCAACTACTT	CGACACGTCG	CAGCCCAGGA	TGCGGGAGAC	420
	GGCCTTCGAG	GAGGACGTGC	AGCTGCCGCG	GGCCTATATG	GAGAACAAGG	CCTTCTCCAT	480
	GGATGAACAC	AATGCAGCTC	TCCGAACAGC	AGGATTTCCC	AACGGCAGCT	TGGGAAAAAG	540
10	ACCCAGTGGC	AGCTTGGGGA	AAAGACCCAG	CGCTCCGTTT	AGAAGCAACG	TGTATCAGCC	600
	AACTGAGATG	GCCGTCGTGC	TCAACGGTGG	GACCATCCCA	ACTGCTCCGC	CAAGTCACAC	660
15	AGGAAGAMAC	CTTTGGTGAA	AGACTTTAAG	TTCCAGAGAA	TCAGAATTTC	TCTTACCGAT	720
	TTGCCTCCCT	GGCTGTGTCT	TTCTTGAGGG	AGAAATCGGT	AACAGTTGCC	GAACCAGGCC	780
	GCCTCACAGC	CAGGAAATTT	GGAAATCCTA	GCCAAGGGGA	TTTCGTGTAA	ATGTGAACAC	840
20	TGACGAAC TG	AAAAGCTAAC	ACCGACTGCC	CGCCCCCTCC	CTGCCACACA	CACAGACACG	900
	TAATACCAGA	CCAACCTCAA	TCCCCGCAAA	CTAAAGCAAA	GCTAATTGCA	AATAGTATTA	960
25	GGCTCACTGG	AAAATGTGGC	TGGGAAGACT	GTTTCATCCT	CTGGGGGTAG	AACAGAACCA	1020
	AATTCACAGC	TGGTGGGCCA	GACTGGTGTT	GGTGGAGGT	GGGGGGCTCC	CACTCTTATC	1080
	ACCTCTCCCC	AGCAAGTGCT	GGACCCAGG	TAGCCTCTTG	GAGATGACCG	TTGCGTTGAG	1140
30	GACAAATGGG	GACTTTGCCA	CCGGCTTTGC	CTGGTGTTT	GCACATTTC	GGGGGGTCAG	1200
	GAGAGTTAAG	GAGGTTGTGG	GTGGGATTCC	AAGGTGAGGC	CCAACTGAAT	CGTGGGGTGA	1260
35	GCTTTATAGC	CAGTAGAGGT	GGAGGGACCC	TGGCATGTGC	CAAAGAAGAG	GCCCTCTGGG	1320
	TGATGAAGTG	ACCATCACAT	TTGGAAAGTG	ATCAACCACT	GTTCCCTCTA	TGGGGCTCTT	1380
	GCTCTAGTGT	CTATGGTGAG	AACACAGGCC	CCGCCCCCTC	CCTTG TAGAG	CCATAGAAAT	1440
40	ATTCTGGCTT	GGGGCAGCAG	TCCCTTCTTC	CCTTGATCAT	CTCGCCCTGT	TCCTACACTT	1500
	ACGGGTGTAT	CTCCAAATCC	TCTCCCAATT	TTATTCCCTT	ATTCATTTC	AGAGCTCCAA	1560
45	TGGGGTCTCC	AGCTGAAANS	CCCTCCGGGA	GGCAGGTTGG	AAGGCAGGCA	CCACGGCAGG	1620
	TTTCCGCGA	TGATGTCACC	TAGCAGGGCT	TCAGGGGTTT	CCACTAGGAT	GCAGAGATGA	1680
	CCTCTCGCTG	CCTCACAAGC	AGTGACACCT	CGGGTCCTTT	CCGTTGCTAT	GGTGAAAATT	1740
50	CCTGGATGGA	ATGGATCACA	TGAGGGTTTC	TTGTTGCTTT	TGGAGGGTGT	GGGGGATATT	1800
	TTGTTTGGT	TTTCTGCAG	GTTCCATGAA	AACAGCCCTT	TTCCAAGCCC	ATTGTTTCTG	1860
55	TCATGGTTTC	CATCTGTCTT	GAGCAAGTCA	TTCTTTTGTT	ATTTAGCATT	TGGAACATCT	1920
	CGGCCATTCA	AAGCCCCCAT	GTTCTCTGCA	CTGTTTGGCC	AGCATAACCT	CTAGCATCGA	1980
	TTCAAAGCAG	AGTTTTAACC	TGACGGCATG	GAATGTATAA	ATGAGGGTGG	GTCCTTCTGC	2040
60	AGATACTCTA	ATCACTACAT	TGCTTTTCTT	ATAAACTAC	CCATAAGCCT	TTAACCTTTA	2100

AAGAAAAATG AAAAAGGTTA GTGTTTGGGG GCGGGGGGAG GACTGACCGC TTCATAAGCC 2160  
 AGTACGTCGT AGCTGAGTAT GTTCAATTA ACCTTTGTGAT ATTTCTCAAA AAAAAAAAAA 2220  
 AAAAAANCCCG GGGGGGGGGC CGGACTGG 2249

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(2) INFORMATION FOR SEQ ID NO: 112:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

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GATACTATAA GGCAAGTCAC TCACGGGTGC GCCGTTAGAC TAGTGGATCC CGGGTGCAGG 60  
 AATTCGGCAG AGCGCCGCCG GAGCGGAGT GCTGGCGCCC CCGCGGCCGC TGCCTCCGCG 120  
 GANCCCCAAA TCATGAAGT CACCGTGAAG ACCCCGAAGA AAAGGAGGAA TTCGCCGTGC 180  
 CCGAGAATAG CTCCGTCCAG CAGTTTAAGG AAGAAATCTC TAAACGTTTT AAATCACATA 240  
 CTGACCAACT TGTGTGATA TTTGCTGGAA AAATTTTGAA AGATCAAGAT ACCTTGAGTC 300  
 AGCATGGAAT TCATGATGTA CTTACTGTTT ACCTTGTCAT TAAACACAA AACAGGCCTC 360  
 AGGATCATTC AGCTCAGCA ACAATACAG CTGGAAGCAA TGTTACTACA TCATCAACTC 420  
 CTAATAGTAA CTCTACATCT GGTCTGCTA CTAGCAACCC TTTTGGTTTA GGTGGCCTTG 480  
 GGGGACTTGC AGGTCTGAT AGCTTGGGT TGAATACTAC CAACTTCTCT GAACTACAGA 540  
 GTCAGATGCA GCGACAACCT TTGTCTAACC CTGAAATGAT GGTCCAGATC ATGGAAAAC 600  
 CCYTTGTTC GAGCATGCTC CTCGAATCCT GACCTGATGN AGACAGTTAA TTATGGCCAA 660  
 TCCACAAATG CAGCAGTTGA TACAGAGAA TCCCAGAAAT TAGTCATATG TTGAATAATC 720  
 CAGATATAAT GAGACAAAG TTGGAACCTG CCCAGGAATC CAGCAATGAT GCAGGAGATG 780  
 ATGAGGAACC AGGACCGAC TTTGAGCAAC CTAGAAAGCA TCCCAGGGGG ATATAATGCT 840  
 TTAAGGCGCA TGTACACGA TATTCAGGAA CCAATGCTGA GTGCTGCACA AGAGCAGTTT 900  
 GGTGGTAATC CATTTGCTTC CTTGTTGAGC AATACATCCT CTGGTGAAGG TAGTCAACCT 960  
 TCCCGTACAG AAAATAGGA TCCACTACCC AATCCATGGG CTCCACAGAC TTCCAGAGT 1020  
 TCATCAGCTT CCAGCGGCAC TGCCAGCACT GTGGGTGGCA CTA CTGGTAG TACTGCCAGT 1080  
 GGCACCTCTG GGCAGAGTAC TACTGCGCCA AATTGGTGC CTGGAGTAGG AGCTAGTATG 1140  
 TTCAACACAC CAGGAATGCA GAGCTGTGTG CAACAAATAA CTGAAAACCC ACAACTTATG 1200

CAAAACATGT TGTCTGCCCC CTACATGAGA AGCATGATGC AGTCACTAAG CCAGAATCCT 1260  
 GACCTTGCTG CACAGATGAT GCTGAATAAT CCCCTATTTC CTGGAAATCC TCAGCTTCAA 1320  
 5 GAACAAATGA GACAACAGCT CCCAACTTTC CTCCAACAAA TGCAGAATCC TGATACACTA 1380  
 TCAGCAATGT CAAACCCTAG AGCAATGCAG GCCTTGTTAC AGATTCAGCA GGGTTTACAG 1440  
 ACATTAGCAA CGGAAGCCCC GGGCCTCATC CCAGGGTTTA CTCCTGGCTT GGGGGCATTA 1500  
 10 GGAAGCACTG GAGGCTCTTC GGAACATAAT GGATCTAACG CCACACCTAG TGAAAACACA 1560  
 AGTCCCACAG CAGGAACCAC TGAACCTGGA CATCAGCAGT TTATTCAGCA GATGCTGCAG 1620  
 15 GCTCTTGCTG GAGTAAATCC TCAGCTACAG AATCCAGAAG TCAGATTTCA GCAACAACCTG 1680  
 GAACAACCTCA GTGCAATGGG ATTTTGAAC CGTGAAGCAA ACTTGCAAGC TCTAATAGCA 1740  
 ACAGGAGGTG ATATCAATGC AGCTATTGAA AGGTTACTGG GCTCCCAGCC ATCATAGCAG 1800  
 20 CATTTCTGTA TCTKGAAAAA ATGTAATTTA TTTTGTATAA CGGCTCTTAA ACTTTAAAAT 1860  
 ACCTGCTTTA TTTCAATTTG ACTCTTGGA TTCTGTGCTG TTATAAACAA ACCCAATATG 1920  
 25 ATGCATTTTA AGGTGGAGTA CAGTAAGATG TGTGGGTTTT TCTGTATTTT TCTTTTCTGG 1980  
 AACAGTGGGA ATTAAGGCTA CTGCATGCAT CACTTCTGCA TTTATTGTAA TTTTTTAAAA 2040  
 ACATCACCTT TTATAGTTGG GTGACCAGAT TTTGTCTGC ATCTGTCCAG TTTATTGCT 2100  
 30 TTTTAAACAT TAGCCTATGG TAGTAATTTA TGTAGAATAA AAGCATTAAA AAGAAGCAAA 2160  
 AAAAAAAAAA AAAAATTCCT GCGCCCGCA ATTCTTCT 2198

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(2) INFORMATION FOR SEQ ID NO: 113:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1043 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

CTGAAGTGTA TGTGGTGAGG AAGAAGAGGC TCCTACTGTA GACAGCCTTG TTCTACAGAT 60  
 50 CCTCCCAGAA ATCTCTGGGC CAGGTGGAAC CCAGGGTCAG AGAGGGATGG GAGAGAGGTT 120  
 TAATTTTCCA TGATAAATAA AAATCTATAA AATAATAAAC AAGAGAAAAG AGATTGGAAA 180  
 CAGCCAGGTT GGAGCAGTGA GTGAGTAAGG AAACCTGGCT GCCCTCTCCA GATTCCCCAG 240  
 55 GCTCTCAGAG AAGATCAGCA GAAAGTCTGC AAGACCCTAA GAACCATCAG CCCTCAGCTG 300  
 CACCTCCTCC CCTCCAAGGA TGACAAAGGC GCTACTCATC TATTTGGTCA GCAGCTTTCT 360  
 60 TGCCCTAAAT CAGGCCAGCC TCATCAGTCG CTGTGACTTG GCCCAGGTGC TGCAGCTGGA 420

5 R G A C T T G G A T G G G T T T G A G G G T T A C T C C C T G A G T G A C T G G C T G T G C C T G G C T T T T G T G G A 480  
 A A G C A A G T T C A A C A T A T C A A A G A T W A A T G A A A T G C A G A T G G A A G C T T T G A C T A T G G S C T 540  
 C T T C C A G A T C A A C A G C C A C T A C T G G T G C A A C R A T T A T A A G A G T T A C T C G G A A A C C T T T G 600  
 C C A C G T A G A C T G T C A A G A T C T G C T G A A T C C A A C C T T C T T G C A G G C A T C C A C T G C G C A A A 660  
 10 A A G G A T T G T G T C C G G A G C A C G G G G A T G A A C A A C T G G G T T A G A A T G G A A G K T T G C A C T G T 720  
 T C A G G C C G G C C A C T C T T C T A C T G G C T G A C A G G A T G C C G C C T G A G A T K A A A C A R G G T G C G G 780  
 G T G C A C C G T G G A R T C A T T C C A A G A C T C C T G T C C T C A C T C A R G G A T T C T T C A T T C T T C T T 840  
 15 C C T A C T G C C T C C A C T T C A T G T T A T T T T C T T C C C T T C C C A T T T A C A A C T A A A A C T G A C C A G 900  
 A G C C C C A G G A A T A A A T G G T T T T C T T G G C T T C T C C T T A C T C C C A T C T G G A C C C A G T C C C C 960  
 20 T G G T T C C T G T C T G T T A T T T G T A A A C T G A G G A C C A C A A T A A A G A A A T C T T T A T A T T T A T C G 1020  
 A A A A A A A A A A A A A A A A A A C T C G A 1043

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(2) INFORMATION FOR SEQ ID NO: 114:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 703 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

G A A T T C G G C A C G A G T G C G C G G C A C C A C G G C G G T T T T T C G A C G C T G G C G G T G G A C G C A G G 60  
 C A G C A T G G A C C A C G G T T G C T G G C G G A T G G G A G C G T C T A T G G T C A G T T G C C T T A G A A G T 120  
 40 G G T G A G A T G G A A G C T G C A G T T G G A A G A C C C T G G A G G A T G C C T G A C A A G G G G A T G T C T G A 180  
 C A C A T G A T T G G A G C T C T T T T T G A A A T G T T T C T T G C C C T T C C T G G A G C A G A G G A G C C A T T A 240  
 45 T T T A T G C A G G T A C A T C G A A G T C T T T T G A C C T C C A T A C A G T G A T T A T G C T T G T C A T C G C T G 300  
 G T G G T A T C C T G G C G G C C T T G C T C T G C T G A T A G T T G T C G T G C T C T G T C T T T A C T T C A A A A 360  
 T A C A C A A C G C G C T A A A G C T G C A A A G G A A C C T G A A G C T G T G G C T G T A A A A A A T C A C A A C C 420  
 50 C A G A C A A G G T G T G G T G G G C C A A G A A C A G C C A G G C C A A A A C C A T T G C C A C G G A G T C T T G T C 480  
 C T G C C C T G C A G T G C T G T G A A G G A T A T A G A A T G T G T G C C A G T T T T G A T T C C C T G C C A C C T T 540  
 55 G C T G T T G C G A C A T A A A T G A G G C C T C T G A G T T A G G A A A G G T G G G C A C A A A A A T C T T C A T G 600  
 A G C A A T A C T T C T T A G T A G A T T G T T T T G T T A T T C A A A T C A A G T T C T A G T G T T T T A T G T G A 660  
 G A T T A T A T A A T T T A C A G T G T T G T T T A T A T A C T T T T G A A T A A A 703  
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## (2) INFORMATION FOR SEQ ID NO: 115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3684 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GGCAGAGGGG GCATGAGCAG GAGGAGGATT ACCGCTACGA GGTGCTCAGC GCCGAGCAGA 60  
TTCTACAACA CATGGTGGNA ATGTATCCGG GAGGTCAACG AGGTCATCCA GAATCCAGCA 120  
ACTATCACAA GAATACTCCT TAGCCACTTC AATTGGGATA AAGAGAAGCT AATGGAAAGG 180  
TACTTTGATG GAAACCTGGA GAAGCTCTTT GCTGAGTGTC ATGTAATTAA TCCAAGTAAA 240  
AAGTCTCGAA CACGCCAGAT GAATACAAGG TCATCAGCAC AGGATATGCC TTGTCAGATC 300  
TGCTACTTGA ACTACCCTAA CTCGTATTTT ACTGGCCTTG AATGTGGACA TAAGTTTGTG 360  
ATGCAGTGCT GGAGTGAATA TTAACTACC AAAATAATGG AAGAAGGCAT GGGTCAGACT 420  
ATTTCTGTGC CTGCTCATGG TTGTGATATC TTAGTGGATG ACAACACAGT TATGCGCCTG 480  
ATCACAGATT CAAAAGTTAA ATTAAAGTAT CAGCATTTAA TAACAAATAG CTTTGTAGAG 540  
TGCAATCGAC TGTAAAGTG GTGTCCTGCC CCAGATTGCC ACCATGTTGT TAAAGTCCAA 600  
TATCCTGATG CTAAACCTGT TCGCTGCAA TGTGGGCGCC AATTTTGCTT TAACTGTGGA 660  
GAAAATTGGC ATGATCCTGT TAAATGTAAG TGGTTAAAGA AATGGATTAA AAAGTGTGAT 720  
GATGACAGTG AAACCTCCAA TTGGATTGCA GCCAACACAA AGGAATGTCC CAAATGCCAT 780  
GTCACAATTG AGAAGGATGG TGGTTGTAAT CACATGGTCT GTCGTAACCA GAATTGTAAA 840  
GCAGAGTTTT GCTGGGTGTG TCTTGGCCCA TGGGAACCAC ATGGATCTGC CTGGTACAAC 900  
TGTAACCGCT ATAATGAGGA TGATGCAAAG GCAGCAAGAG ATGCACAGGA GCGATCTAGG 960  
GCAGCCCTGC AGAGGTACCT GTTCTACTGT AATCGCTATA TGAACCACAT GCAGAGCCTG 1020  
CGCTTTGAGC ACAAACCTATA TGCTCAGGTG AAACAGAAAA TGGAGGAGAT GCAGCAGCAC 1080  
AACATGTCCT GGATTGAGGT GCAGTCCTG AAGAAGGCAG TTGATGTCCT CTGCCAGTGT 1140  
CGTGCCACAC TCATGTACAC TTATGTCTTC GCTTCTACC TCAAAAAGAA TAACCAGTCC 1200  
ATTATCTTTG AGAATAACCA AGCAGATCTA GAGAATGCCA CAGAGGTGCT CTCGGGCTAC 1260  
CTTGAACGAG ATATTTCCCA AGATTCTCTG CAGGATATAA AGCAGAAAGT ACAAGACAAG 1320  
TACAGATACT GTGAGAGTCG ACGAAGGGTT TTGTTACAGC ATGTGCATGA AGGCTATGAA 1380  
AAAGATCTGT GGGAGTACAT TGAGGACTGA GAATGGCCCT GCATAAAATG AACTCTGAAA 1440

	ACTTTACCAT CTAGAGTGCT CATGCAATTA AAACAAAACA AACACAAACA AGGAGGCACT	1500
5	AAGCCTATTC TGACACCACT GGTCTGTAGT ACCAGAATTG TTTTGTAAAT GGAAAGTTTA	1560
	AGTAAATTAT ATTGTAATAA AAAGGTAGAT AAACCATGT ACAACAGTAT TCTAGGCCGC	1620
	CAACAAAAGT GTGACAGACA CACTAAAAGC CCTCCAACTT TAACTTGTA CGTAGCTTCA	1680
10	TTCTCAAAGC TGA CTCTCTTT TTTTCTTTT TCCTTTTCCT GAGTGTAGTA CAGTTAAAAT	1740
	TTCAACAGC TCCTTGACAC TGCTTTTCAT GTTCAAACCA GCCATTTTGT TGTACTTTGG	1800
15	TAAAGGACCT CTTCCCTTC CTCCCTACA CATAAGATA CACCCACACA CAGACTGACT	1860
	CTCTTTCTCT CATAACCCAA GGTGATGAGT GAATGATGCT TAGTTCCTTG TAAAGAAAAT	1920
	CTTGGGATGG GGAAAGGGT AGGCAGCAAG AGGATTCAAC AAACGAAAAA CATAAAAACT	1980
20	TTGTATATGA CTTTAAAC AAGAGGACAA CACAGTATTT TTCAAAATTG TATATAGCGC	2040
	ATATGCATGG ACAAGCAAG CGTGGCACGT GTTGCATAA TGTTTAATTA CAAAAAATA	2100
25	TTTATCTTTT AAAATCTTC AAGATTATGT CTATTGCTG TGCAATTTCT TTCAGTTTGC	2160
	TTATCTTTCC CGGGTTGGGG TTGGGATAAA GGTGTGTCGG TTTAGCACCT CTGGAAGACC	2220
	TATCTAGAGC TCTTTCACIT TCCTGAGGTT ATTTTGCCCY TTCTGGTGT TGTATGTCTG	2280
30	TTGCCGGCCA TGGGCTNCAY GCCTGAATT CCTGCTCTTG ATCAGGGACA AGGGAGGTCA	2340
	AGCTCTGACT AATGCCATGA CTTGATTAAG GGTACAGCA GGGAGTTTGT TTGCTACAGC	2400
35	TCATGAATTA ACCTGTCCA ACCTAATCCC CCTCCATGGC ATCATGCCTC TACCCAAGCC	2460
	TTTGTGTGCC CATGTTATGC ACACAGCTGT AGGCATTCTT AAGTCCCCTG TCGCATCCAG	2520
	TGGAAGCATT TTAATAATTC TTTTACTTTT TGGTTTCCC TTAATGCTG CTTTTCAGAT	2580
40	TTTAGTTATG GCTCGTCTGC TCACCCCTTC TCTACATTAG GGTGTCAAAG AGAATGTTTT	2640
	GCTTTAAATA TAAATAGCCA TTCATTTAGT CTCAGATTGT GAATTTAAAA TGGTGGATAC	2700
45	CGAAATTGCT TGTGTGTGTT GCTGTGGGTT TGGTTGAAG GCAAACACCC CTAGAACATG	2760
	ATATTCCCAT CTAGTGCAAT TAAATAGAAA TCACTGAGTT TGCTGCTTTT TTATTGTCAG	2820
	CAGATAGGAG AATTAATAAT GCATTTIAGC TGTGATGTCC ATTTTATGA AATTCCTACT	2880
50	AAGAGCTATG TTAAGTAAGT AGGATGGTGG TGGTTGTATT AACTATATAC CTGTTTAGGC	2940
	CATTCTGGCT GTGGTATTTT TCAATAGGTC AGCATCTGTA AATCTGTCAG TTTTATACAG	3000
55	GAGTGCAGAG TGAAGTAGGC AACTAGATTA AGAGGTCTAA ATATGAAATA CCAGTTGAGG	3060
	CTGAGGACCT CTTCGTCTTC CTTTAAATGT CTTTGCCTA GGGAGTGTIT ACCATTGTG	3120
	AGGCAGCTTT GTCTGCTCTT AACTGTACA TCCTATTACT CCATTGGGAA GTAGGTTTAC	3180
60	TTTCTCTGG CTTTGTGCTT AAGTTAGGCT TTGCTGAATC AACCTACTT TTCCTTTAG	3240

AAAAGGTTGT TACAGGAGAT TTACTGGCAA CTGTTCTTTT CCCATCAAAA ATCAGTGAAT 3300  
 GTTGTCTGAG TATAAATGCT GCTTCCTTAA ACCACTTGTC GCTTTAGGAT CAACTTTACC 3360  
 5 TGTACCTTTT CTCCTTTCCT CCCTTGCCAC CTCAGGTGCA AATCTGAACT CAGTGTCTGC 3420  
 TTCTTCCATT TTCTCGTCTC TCTCCCTCTT TCCCCATTA TCCATATGAC ATTATTTTAC 3480  
 10 TTCAAATGAC AGCATCAATC TTAAAAAGAT ATACATTAAA ACTAAGGAGT TTTTMTAAAG 3540  
 AAAGCCTGAA TAAGTTCCTT TCCCTGGTAA CTTTGAAAAG CAGTCAGAGT TGCTATATAG 3600  
 ATATATGTGG CTCCTTTAAA ATGCTTTGTG TATGTGTGGT GTTTAAAAAA AAAAAAAAAA 3660  
 15 TTCGGGGGGG GGCCCGGTNC CCAT 3684

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(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1965 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

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AAGAAAGGTT ATTTAAATTC TAGATCACAT ATGGACCCGG GAAGGTTTTT NACCCTCTGT 60  
 TAGTGACATC GAGTCTCCCA CTAGACAAAA TAGGTGGAAA AATCTCTCGA GGGCTCACAT 120  
 35 TGTTTTGTC TCTTCAGGAA AAACACCACC AGGCCATACC ACAGCCTGCC CAGTGAGGCG 180  
 GTCTTTGCCA ACAGCACCGG GATGCTGGTG GTGCCCTTTG GGCTGCTGGT GCTCTACATC 240  
 CTCTGGCTT CATCTTGGA GCGCCAGAG CCGGGGATCC TGACCGACAG ACAGCCCCTG 300  
 40 CTGCATGATG GGGAGTGAAG CAGCAGGAAG GGGCTCCCAA GAGCTCCTGG TGGTGCAGCC 360  
 TGTGCTCCCC TCAGAAAGTC TGCTCTTCCC AGGGCTCCCG GCTGGTTTCA GCAGGCGACT 420  
 45 TTCTTCCAAT GCTGGGCCCA GACTTCTTGC CTGGGTGCTG GCCTGCCCTC TCCGNCCTG 480  
 TTGCTGCCTG TCTGCTTCC TTGGTGGYTT TGCTGGGTGC TGGGCTGCC CTCTCCGGCC 540  
 GCTTGCTGCC TGTCTGCTT CCTTGGTGGC TTTGCTGGGT GCTGGGCTG CCTTCTCTGG 600  
 50 CTGCTTGCTG CCTGTCTGCT TTCCTTGGTG GCTTGGCTT CTGCACTCCT TGGCGTCASC 660  
 TCTCAGGTCC TCCATTACA CGAGGTCCTC CTCGCTCTGG CCGCTCTTGC TGCTCCTGTC 720  
 55 TGAAGAWATC AGACTGATTT CCTCTAAGA CTCCTAGGGA TGTGGTGAAG AGCTGGGACT 780  
 CAAGTGCACT CCACGGTGTG AAACATGAGG GARGTGAGGT GTCCGTCCAC TTCCCCCATA 840  
 AAGGTGTGCA TTTCAGTTAG GCTGCCCCGC CACAGAGCAG GCTTCATCTG CTCTGCCATC 900

60

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CAGCCCCATC TGGATGTGAG GTGGGGTGA GACATCATGG GGTGATTGCA GAAAGGGGA 960  
 GTGGCGGCCC ACGCAGCTTC TGCTGAGGAG CTGACCGCTC TGAGCTGTTT TGTTCGTAT 1020  
 5 TGCTGCTCTG TGTCTGCATG TATTGTGACC GTGCGGCTCC ACCTCTTCCA GCTGCTGCTA 1080  
 CAGCTGAGGC CTGGATCCCG GCCTTTCCCT GTGACTTACG TGTCTGTCAC CGGCANGCAG 1140  
 10 CCCTACAAAT CCTGGTGACC TGCTCTCCCA AGAACAGAGC CTGTCCCCAG ATGTCCCACT 1200  
 AGCGATGAGT AACAGAGGTG GCTGTGGACT TCCTCTACTT CTCCTTGCTG GATCAGGGCC 1260  
 TTCCTGCCTC CCGCTGGGCA GGTCTGGCCT TGCTCTCTTG GCAGGGCCCC AGCCCCCTG 1320  
 15 ACCACTCTGC AGCTACCAT GCAGCTGATG CCAAAGTTGT GGTGTCCAGT GTGCAGCAGC 1380  
 CCTGGGAGCC ACTGCCACCT TCAGAGGGGT TCCTTGCTGA GACCCACATT GCTTCACCTG 1440  
 GCCCCACCAT GGCTGCTTGC CTGGCCCAAC CTAGCGTTCT GTGCCATGCT AGAGCTTGAG 1500  
 20 CTGTTGCTCT TCTTCAGGG AGGAAATAGG GTGGAGAGCG GGAAGGTCT TGCTCCTAAG 1560  
 TGTGTGCTGT GTGGCTTTT TGCTTCTCC AAAGACGCAC TGCCAGGTCC CAAGCTTCAG 1620  
 25 ACTGCTGTGC TTAGTAAGCA AGTGAGAAGC CTGGGGTTTG GAGCCACCT ACTCTCTGGC 1680  
 AGCATCAGCA TCCTACTCCT GGCAACATCA GGCCAACGTC CACCCAGCC TCACATTGCC 1740  
 AGATGTTGGC AGAAGGGCTA ATATTGACCG TCTTGACTGG CTGGAGCCTT CAAAGCCACT 1800  
 30 GGGATGTCCT CCAGGCACCT GGTCCCATG ACCAGCTCCC CGTCTCCATA GGGGTAGGCA 1860  
 TTTCCTGGT TTATGAAGCT CGAGTTTCAT TAAATATGTT AAGAATCAA GCTGTCTTTG 1920  
 35 TTCAGGCTGC TATAACAAAA ATATAATAGC CTGGGTGGCT TAAAC 1965

40 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 base pairs

(B) TYPE: nucleic acid

45 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

50 AGTGATCCCC TTGCCTCGGC CTCCCAAAT GCTGGAATTG TAAGCGTGGG CCTCTGCACC 60  
 CGGCTTGGTC CGCAATTTAA AAACGCACAG CCACCATTC CTYTCCAGAA AGCACCCAGA 120  
 TGCCTTTGGG AGAACCAGCC TCCTCCATGG AGGAAAGCTT GGGATCTGCC TTCCACCTG 180  
 55 GGGAGGAGAG GGATCTGTGG AAAATCCTTC TGACGGACTT CCCCTCAGTG CCTGATCCAT 240  
 ACTCAATAGT AGAAAAAGTA AGAAATATAC AAAGATAGCA GATACACGGA GACAGTTCCC 300  
 60 CAAATAGCTG AGCGAWTAGC GCAGAAGCAA TATTGAAGAC CTAATAGCTG AGACATTTC 360



AGAACTGATA AAGTGCATCC AGCCACAGAT CAAGCAGCCC AGAAAATTCC AGGCAGCATC 420  
 AAAAAATAAA TAGCCCCACA TGCACCCGTG AAAATGCAGA AGACCAAACA AAAAAGTCCG 480  
 GTCAACAGCC AGAGTTAAAG AGG 503

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(2) INFORMATION FOR SEQ ID NO: 118:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

GGCACAGCTT GGAATGAACC CCTGTGGATA AGGGGGACTA TTAGATAGAA TAAACATCAA 60  
 TAAATGCTTG ATGAATAAAC GCTAATCCTA CCTTCCCAGC CTGACACCTC CCAGTGGACA 120  
 CCACACTTCA CTTGAAGCCT TAGAAACCTT TCCCACCCAT GCTTCCAGCC CTGGCTTCAT 180  
 GTTGCCATTT CTCACCCCA GAACAGGCCG CCCGCCTGAA GAACTACAA GAGCAAGAGA 240  
 AACACAGAA AGTGGAGTTT CGTAAAAGGA TGGAGAAGGA GGTGTCAGAT TTCATTCAAG 300  
 ACAGTGGGCA GATCAAGAAA AAGTTTCAGC CAATGAACAA GATCGAGAGG AGCATACTAC 360  
 ATGATGTGGT GGAAGTGGCT GGCCTGACAT CCTTCTCCTT TGGGAAGAT GATGACTGTC 420  
 GCTATGTCAT GATCTTCAAA AAGGAGTTTG CACCCTCAGA TGAAGAGCTA GACTCTTACC 480  
 GTCGTGGAGA GGAATGGGAC CCCAGAAGG CTGAGGAGAA GCGGAACNTG AAGGAGCTGG 540  
 CCCAGAGGCA ANGAGGAGGA GGCAGCCCAG CAGGGGCCCTG TGGTGGTGAG CCCTGCCAGC 600  
 GACTACAAGG ACAAGTACAG CCACCTCATC GGCAAGGGAG CAGCCAAAGA CGCAGCCCAC 660  
 ATGCTACAGG CCAATAAGAC CTACGGCTGT KTGCCCGTGG CCAATAAGAG GGACACACGC 720  
 TCCATTGAAG AGGCTATGAA TGAGATCAGA GCCAAGAAGC GTCTGCGGCA GAGTGGGGAA 780  
 GAGTTGCCGC CAACCTCCTA GCGCCCCGC CCAGCTCCCT TTGACCCCTG GGCAGGGCA 840  
 GGGGGCAGGG AGAGACAAGG CTGCTGCTAT TAGAGCCCAT CCTGGAGCCC CACCTCTGAA 900  
 CCACCTCCTA CCAGCTGTCC CTCAGGCTGG GGGAAAACAG GTGTTTGATT TGTACCGTT 960  
 GGAGCTTGA TATGTGCGTG GCATGTGTGT GTGTGTGTGA GAGTGTGAAT GCACAGGTGG 1020  
 GTATTTAATC TGTATTATTC CCCGTTCTTG GAATTTTCTT CCCATGGGGC TGGGGTACTT 1080  
 TACATTCAAT AAATACTGTT TAACCCAAAA AAAAAAAAAA AAAAGAAAGA AGN 1133

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## (2) INFORMATION FOR SEQ ID NO: 119:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

GGGCACAGCT GAAGCTGCAG ACCTCCCCAG GGGATGGCTC CTCTCCCCCA GGAGCCCCGA	60
GGCAGGGGAG GCAGAAAGCC TGGGCTCTGG GGGGTGGCCT GCGGACAGCT GTGCTGTGGG	120
15 CCGGGGGCTG GGCCTGTCCC ACAGGNCGT GGAGCTCGTG GTTCTGAGCA GCCAGCTGGG	180
TGGTGTCTGG GGATAGCTGG GAGGCACAGC GGCTGCCATG TGGGACTGGG ACTGGAGTGC	240
20 TCCCTGGTCT TGGCCTCTGT GGCTCAGCCT TGCTCTGGTC TGCTGAGTG CAGGGGCCAA	300
GGGGCACAGG GCCAGTGAGG CCGGCCACGC TCGGGCCCTC ACCTGTGAGA TGGGGTCGGA	360
ATTTKACACA GCCTANGGCT TGGTTCTTGG TKGTNGAMCG TGGACTYCTK AGAACGGGAG	420
25 TGCTGGTCCT .GAAAGGCGTG GTTGGAGACC AGCTGCTTTT CTCGCTGTTT TTCTCTTAGG	480
AGATTAAACA AAAACAGAAA GCACAAGACG AACTCAGTAG CAGACCCAG ACTCTCCCCT	540
30 TGCCAGACGT GGTTCAGAC GGGGAGACGC ACCTCGTCCA GAACGGGATT CAGCTGCTCA	600
ACGGGCATGC GCCGGGGGCC GTCCCAAACC TCGCAGGGCT CCAGCAGGCC AACCGGCACC	660
ACGGACTCCT GGGTGGCGCC CTGGCGAACT TGTMTGTGAT AGTTGGGTTT GCAGCCTTTG	720
35 CTTACACGGT CAAGTACGTG CTGAGGAGCA TCGGCAGGA GTGAGGCCCA GCGCCGAGA	780
CCCAAGGCGC CACTGAGGGC ACCGCGCACC AGAGCGTGAC CTCGGCAGGC TGGACACACT	840
40 GCCCAGCACA GGCAGACCCA CCAGGCTCCT AGGTTTAGCT TTTAAAAACC TGAAAGGGGA	900
AGCAAAAACC AAAATGTGTG ACTGGGCTTT GGAGGAGACT GGAGCCTCAG CCCTGTCTCTG	960
GCCACGGGCC GCTGGGGCTG GTGTGGGTGG GCCTTGTGTG CTGGATTGT AGCTTATCTT	1020
45 CCGTGTGTG TTTGGACCTG TTTTAGTAAA CCCGTTTTTC ATTTTAAAAA AAAAAAAAAA	1080
AAACTTTGGG GGGGGGCCCC N	1101

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## (2) INFORMATION FOR SEQ ID NO: 120:

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

AGCTTCTCTG TCCAGTCTTG AACTCTGGGS TCTCTTGGAA CTTTCCTCAC CCCTCTCAGC 60  
 5 CTGAATATTC CTTCCATGGA TTCCACTCAA CCAGACTTTG GATCTGTGCC TACTTAATCA 120  
 ACCTTATCTT TGCATATGT TCGGGCCAC CTTCCACTCC TTGGTTCTTG TTCTCCTTG 180  
 GCCTAACTTG TCCCTTCTCC ACTTCACATC CCGGTGGGA CAGCATTCCT CTTCTCTCCC 240  
 10 AACCTCCCTC CGTCTCARAA AAAAAAAAAA AAAAAAAAAA TT 282

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## (2) INFORMATION FOR SEQ ID NO: 121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2635 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

25 TAAGGGGGTG TGTGCTCACC TCCTCCTGAC CCTTAACACT CCTGTCCTGC CCAGACCAAC 60  
 AGAGAGAGCT GTCCTTGAGA CCCCGGAGAG AAGCAGCTGC CGAAAGCTGC AGCCTTTCCG 120  
 30 CACTCTGAGA CATGATCTT CCTCTGCCA GGGGAGAGCC ACCCACAGGC CATGTCCAGC 180  
 CCCACTTCCC TCAGCCCCCA GGGYTCCTT CTGGCCCCC TGAGGATTCC CTAGGGCTGC 240  
 CCCGCAGAGG GGYTTCCCCA AGCTCTGTTT TGAAGCCTGC AATGTGGAAA AGTGAGAAGT 300  
 35 CAGAGGGAAC AGGACAGTG CAGCCGGGCT CTGAGGCCAC ACCTCACACC TCGCTGTTC 360  
 CCAACATCCC CTGAGCAGTG TGAGCTCATC TCACCAGATG AGAAGAGGCC CTGTGCATTT 420  
 40 YTTTGTGTTG TTTGTTGCTG TTTTCCCCCA CCCATCCAGT TCTCCTCAGC AAAGCAAATT 480  
 CCTTAACACC TTTGGTGGAG AATTCTTAC CCAGACTTGG GGCTGTGATG CCCTTCAGTG 540  
 CGTGGTGACT GCAGCGTGTG TCGTGTGCC TGTGTGTGAA CCTGGGGGCC ATCCTGGTGG 600  
 45 CCTGGGAGCG TGAGGAGAGG CCCCCTGTGT GCTGGGTGAG TGGTGGGTGT GGGGTCAATG 660  
 CAGTGAGGCT CTCTGGGTGA GGCTCCCAAC CTGGCAGTCC CCAGCCTCCC AGCATCTGTG 720  
 50 AGCGTCTGTT GGACTTTACA GAAGAGCCTC ATCCYGTCTG CCCCTCACTC TGCCCTGGAA 780  
 TCAACATCTT CCGAGTCCTT CTGGGGGAA ATAGCAGAGC CCCACTTAAC TCCATAAACT 840  
 GCTTCCCATT CCGCAGCCCA GTTCTGATTG TTGAGGTGTC GCGTCGTTCC AGGTCCCCCA 900  
 55 GTCCCTCTT TCTCCTGTCC TCTCTGTGTC CTTACCTCC CCACTCCAGC CCCGGCTCAG 960  
 TTCAGGGAAA TGCTGTCCA YATCAGCCCT CTGCTCTCTG AGGCAGCCGC GCCTCTGACT 1020  
 60 CGGAGCTACT TGAAACTTCT GCTCTTGCTA GGATTGGAGT CTACCTATCT CTTCCATTG 1080

	TCCCAGCTGG AGTTCCTGGAA CTTTCCTCCT CGGGGTGGGG GTGGGGGTTG TTACGGATGC	1140
5	TGGGGGGCCT GGGGAAGGAA GGAGTTCAGA GGAGGGGTGT CCCCCTGTCT CTTGATGTCA	1200
	CCCTCCGCTC CTGGGACACG TGCTCTCTCT GTCTCTGGGT CTTCTGGGTTG TGCACGTTTG	1260
	TGTGTCTTTG TAAATATGTT TTAGGAAGAA AGCAAAAGGG ACTGAAGTAG CCTTTGGTAG	1320
10	GATTGCAGGG GTCCAGCCTT GCCTGTTTCC GAAGCCCCCA CACTGCTTTT CGCCCCACTG	1380
	AGACTGGTCC CCTCAAAGG TAGACAAAC AGCAGCTCCC TGTGGAGCTG AAGGGCGGCC	1440
15	TCAAAGTGGC TTTTGTAG ACAAGGTAA GGTTCCTCA TGAGCAAGT TGTAGATCGG	1500
	TCCTTCTCA GCTCCTTGAT TTGTGACCTT GACCAAGGGG CCTGCCATCC AGCCCTCCA	1560
	GTGCCCTCTC CTCGATGCTT CGCTCCTTCC TGCCCCCACT CCCCTGGGTT AGGAGGTAG	1620
20	GGGAATTAGG GCCATGCTGG AAGAAGCTTA ACCATGTGTT CAAAGAGCGG TTTCTTGCTT	1680
	GCTTGGTCCT GGAATCCCC TTGGCTGCCC CAGGCCTCCT TGGCCCATGG GTGCTGGGGG	1740
25	AGGTGGATGT CAGATCTGGT AGGTTGCAGC AGAGAAATA AATGTGCTTT GAGAGACCAC	1800
	TCAGAGAGGG TCCAAGGGTG ATGGAGAAGG AAGCATGGCC TGGGAGCTTG GAAAGGARGG	1860
	GTGGTGGGTG GCGGCATCTT GACTGCCCCC TGTGTGCCC CACGTGGGGG GTGCTCACCC	1920
30	CYCTTCACTC CAGCCCGCCT GCCTTCAGCC TTCCATGAGC TTCACCTGCT TCCACTTCA	1980
	CTTTGGAGGG GGTGGGGTCC GTTGGCATCA ACACGGGGAC CCTCTGCTTC ACTAAGCCC	2040
35	GAGCCCTCAG CCCCTGGGGA GAACAAATGG CTGAGCTTTG ATACCTGGGG TCTCGAGAG	2100
	GCTGCGGGCT GCGGGCAGTC CCAGGGGAGA GACGCCACAG AAGGAGATCC AGACATCCCG	2160
	AGGAAGTTCC CAGCAGAGCA AACTGCTTTC CAGCCTGAAG CCTGCTTAAA CTGTGTGATG	2220
40	TGCAATAACT GAGCTTAGAG TTAGGAATTG TGTTCAGTG CTTGGATTTC CGTCTGTAGA	2280
	TTTAACTGCT GAAATTGTAT CTCTCAGTAA TTTTAGAGT CTTTAAAAA ATTGAAAAC	2340
45	AAAGTGTTAG ACTGTGTGCG TGTGCGTTGA TGGGCACTCA AGAGTCCCTT GATCATCCA	2400
	GCCCTGCCTT TCCCCTGCGC CCCCATCCTC TCAGTCCCG CCC/GCCTCC ACTTGGGGAC	2460
	CCTGCCTCGT GTGCTCTTTA TCTGCCTATT ACTCAGCCTA AGGAAACAG TACACTCCAC	2520
50	ACATGCATAA AGGAAATCAA ATGTTATTTT TAAGAAAATG GAAAATAAA ACTTTATAAA	2580
	CACCAAAAAA AAAAAAAAAA ACCCNGGGGG GGGGCCGGTA ACCCATTTGG CCTAA	2635

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(2) INFORMATION FOR SEQ ID NO: 122:

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(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 994 base pairs

375

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GAATTCGGCA GAGGTTGGC GAAGATAGG AATAAGGAAG CACAGGAGTA GGGGAGAAGG 60  
AAGCACAGGA GTAGGGGAGA TATACAGCGG TCAGGATAAG GGGGAAAGGG CCGTGGTTGC 120  
SCAAGAGGTG AAACAAGATG TGAGAGACAA GGGGTAGGGA AGAAATGGGG CAGCGGTTAG 180  
GTTCAGAAGC GCATAGACCG TGGCGGACGG GCAATGCGAG GGGCACAGAA AGGAACTGAG 240  
GGGTGGGCTA TTTTAARGGA GATGGTCCTT CAGCCCTCTT YTTTCTGCG TAGTTCTCCT 300  
CCTCCAGGCC GCGCGGGAT ATGTCGTCCG GAAACCAGCC CAGTCTAGGC TGGATGATGA 360  
CCCACCTCCT TCTACGCTGC TCAAAGACTA CCAGAATGTC CCTGGAATTG AGAAGGTTGA 420  
TGATGTCGTG AAAAGACTCT TGTCTTTGGA AATGGCCAAC AAGAAGGAGA TGCTAAAAAT 480  
CAAGCAAGAA CAGTTTATGA AGAAGATTGT TGCAAACCCA GAGGACACCA GATCCCTGGA 540  
GGCTCGAATT ATTGCCTTGT CTGTCAAGAT CCGCAGTTAT GAAGAACACT TGGAGAAACA 600  
TCGAAAGGAC AAAGCCCACA AACGCTATCT GCTAATGAGC ATTGACCAGA GGAAAAAGAT 660  
GCTCAAAAAC CTCGTAACA CCAACTATGA TGTCTTTGAG AAGATATGCT GGGGGCTGGG 720  
AATTGAGTAC ACCTTCCCC CTCTGTATTA CCGAAGAGCC CACCGCCGAT TCGTGACCAA 780  
GAAGGCTCTG TGCATTGGG TTTCCAGGA GACTCAAAG CTGAAGAAGC GAAGAAGAGC 840  
CTTAAAGGCT GCAGCAGCAG CCCAAAACA AGCAAAGCGG AGGAACCCAG ACAGCCCTGC 900  
CAAAGCCATA CCAAAGACAC TCAAAGACAG CCAATAAATT CTGTTCAATC ATTTAAAAAA 960  
AAAAAAAAA AAAAAAAAAA AAAAAGGGGA GGGG 994

## 45 (2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1542 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

GGCASAGCCA CCTCGGCCCC GGGCTCGAA GCGGCTCGG GGGGCCCTTT CGGTCAACAT 60  
CGTAGTCCAC CCCCTCCCCA TCCCAGCCC CCGGGGATTC AGGCTCGCCA GCGCCCAGCC 120  
AGGGAGCCGG CCGGGAAGCG CGATGGGGC CCCAGCCGCC TCGCTCCTGC TCCTGCTCCT 180  
GCTGTTGCCC TGCTGCTGGG CGCCCGCGG GGCCAACCTC TCCCAGGACG ACAGCCAGCC 240

	CTGGACATCT GATGAAACAG TGGTGGCTGG TGGCACCGTG GTGCTCAAGT GCCAAGTGAA	300
5	AGATCACGAG GACTCATCCC TGCAATGGTC TTAACCCCTGC TCAGCAGACT CTCTACTTTG	360
	GGGAGAAGAG AGCCCTTCGA GATAATCGAA TTCAGCTGGT TAMCTCTACG CCCCACGAGC	420
	TCAGCATCAG CATCAGCAAT GTGGCCCTGG CAGACGAGGG CGAGTACACC TGCTCAATCT	480
10	TCACTATGCC TGTGCGAACT GCCAAGTCCC TCGTCACTGT GCTAGGAATT CCACAGAAGC	540
	CCATCATCAC TGGTTATAAA TCTTCATTAC GGGAAAAAGA CACAGCCACC CTAAACTGTC	600
15	AGTCTTCTGG GAGCAAGCCT GCAGCCCGGC TCACCTGGAG AAAGGGTGAC CAAGAACTCC	660
	ACGGAGAACC AACCCGCATA CAGGAAGATC CCAATGGTAA AACCTTCACT GTCAGCAGCT	720
	CGGTGACATT CCAGGTTACC CGGGAGGATG ATGGGGCGAG CATCGTGTGC TCTGTGAACC	780
20	ATGAATCTCT AAAGGGAGCT GACAGATCCA CCTCTCAACG CATTGAAGTT TTATACACAC	840
	CAACTGCGAT GATTAGGCCA GACCCTCCCC ATCCTCGTGA GGGCCAGAAG CTGTTGCTAC	900
25	ACTGTGAGGG TCGCGGCAAT CCAGTCCCCC AGCAGTACCT ATGGGAGAAG GAGGGCAGTG	960
	TGCCACCCCT GAAGATGACC CAGGAGAGTG CCCTGATCTT CCCTTTCCTC AACAAGAGTG	1020
	ACAGTGGCAC CTACGGCTGC ACAGCCACCA GCAACATGGG CAGCTACAAG GCCTACTACA	1080
30	CCCTCAATGT TAATGACCCC AGTCCGGTGC CCTCCTCCTC CAGCACCTAC CACGCCATCA	1140
	TCGGTGGGAT CGTGGCTTTC ATTGTCTTCC TGCTGCTCAT CATGCTCATC TTCCTTGGCC	1200
35	ACTACTTGAT CCGGCACAAA GGAACCTACC TGACACATGA GGCAAAAGGC TCCGACGATG	1260
	CTCCAGACGC GGACACGGCC ATCATCAATG CAGAAGGCGG GCAGTCAGGA GGGGACGACA	1320
	AGAAGGAATA TTTTCATCTAG AGGCGCCTGC CCACTTCCTG CGCCCCCAG GGCCCTGTGG	1380
40	GGACTTGCTG GGGCGTCAC CAACCCGGAC TTGTACAGAG CAACCGCAGG GGCGSCCCT	1440
	CCCGNTTGT CCCCAGCCCA CCCACCCCTT TGTTACAGAA TGTYTKGTTT GGGGTGCGGT	1500
45	TTTGTWATTG GTTTNGGATN GGGGAAGGA GGGANGCGG GG	1542

50 (2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

60 CAAGCTCTAA TACGACTCAC TATAGGGAAA GCTGGTACGC CTGCAGGTAC CGGTCCGGAA 60

377

	TTCCCGGGTC GACCCACGCG TCGGGGCTC AGGGTGGACG CATGGTTCTG CACTGAGGCC	120
	CTCGTCATGG TGGCGCCTGT GTGGTACTTG GTAGCGGCGG CTCTGCTAGT CGGCTTTATC	180
5	CTCTTCCTGA CTCGCAGCCG GGGCCGGGCG GCATCAGCCG GCCAAGAGCC ACTGCACAAT	240
	GAGGAGCTGG CAGGAGCAGG CCGGGTGGCC CAGCCTGGGC CCCTGGAGCC TGAGGAGCCG	300
10	AGAGCTGGAG GCAGGCCTCG GCGCCGGAGG GACCTGGGCA GCCGCCTACA GGCCCAGCGT	360
	CGAGCCCAGC GGGTGGCCTG GGCAGAAGCA GATGAGAAGC AGGAGGAAGC TGTCATCCTA	420
	GCCCAGGAGG AGGAAGGTGT CGAGAAGCCA GCGGAAAYTC ACCTGTCGGG GAAAATTGGA	480
15	GCTAAGAAAC TCGGAANNT GGAGGAGAAA CAAGCGCGAA AGGCCAGCK TGAGGCAGAG	540
	GAGGCTGAAC GTGARGWCG GAAACGACTC GAGTCCCAGC GCGAATGAGT GGAAGAAGGA	600
20	GGAGGAGCGG CTTGCGCTGG AGGAGGAGCA GAAGGAGGAG GAGGAGAGGA AGGCCCGCGA	660
	GGAGCAGGCC CAGCGGGAGC ATGAGGAGTA CCTGAAACTG AAGGAGGCCT TTGTGGTGA	720
	GGAGGAAGGC GTAGGAGAGA CCATGACTGA GGAACAGTCC CAGAGCTTCC TGACAGAGTT	780
25	CATCAACTAC ATCAAGCAGT CCAAGTTGT GCTCTTGAA GACCTGGCTT CCCAGGTGGG	840
	CCTACGCACT CAGGACACCA TAAATCGCAT CCAGGACCTG CTGGCTGAGG GGACTATAAC	900
30	AGGTGTGATT GACGACCGGG GCAAGTTCAT CTACATAACC CCAGAGGAAC TGGCCGCCGT	960
	GGCCAACTTC ATCCGACAGC GGGGCCGGGT GTCCATCGCC GAGCTTGCCC AAGCCAGCAA	1020
	CTCCCTCATC GCCTGGGGCC GGGAGTCCCC TGCCCAAGCC CCAGCCTGAC CCCAGTCCTT	1080
35	CCCTCTTGA CTCAGAGTTG GTGTGGCCTA CCTGGCTATA CATCTTCATC CCTCCCCACC	1140
	ATCCTGGGGA AGTGATGGTG TGGCAGGCA GTTATAGATT AAAGGCCTGT GAGTACTGCT	1200
40	GAGCTTGGTG TGGCTTGGTG TGGCAGAAGG CCTGGCCTAG GATCCTAGAT AAGCAGGTGA	1260
	AATTTAGGCT TCAGAATATA TCCGAGAGGT GGGGAGGGTC CCTTGAAGC TGGTGAAGTC	1320
	CTGTCTTAT TATGAATCCA TTCATTCAAG AAAATAGCCT GTTGCAAAAA AAAAAAAAAA	1380
45	AAAAACTCGA	1390

50 (2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1288 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

60 GGCGCGCGG TGAAAGGCGC ATTGATGCAG CCTGCGCGG CCTCGGAGCG CGCGGASCA 60

	GACGCTGACC ACGTTCCTCT CCTCGGTCTC CTCCGCCTCC AGCTCCGCGC TGCCCGGCAG	120
5	CCGGGAGCCA TCGACCCCA GGGCCCCGCC GCCTCCCCGC AGCGGCTCCG CGGCCTCCTG	180
	CTGCTCCTGC TGCTGCAGCT GCCCGCGCCG TCGAGCGCCT CTGAGATCCC CAAGGGGAAG	240
	CAAAAGGCGC ATCCGGCAGA GGGAGGTGGT GGACCTGTAT AATGGAATGT GCTTACAAGG	300
10	GCCAGCAGGA GTGCCGTGGT GAGACGGGAG CCCTGGGGCC AATGGCATTG CGGGTACACC	360
	TGGGATCCCA GGTCCGGATG GATTCAAAGG AGAAAAGGGG GAATGTCTGA GGGAAAGCTT	420
	TGAGGAGTCC TGGACACCCA ACTACAAGCA GTGTTTCATG AGTTCATTGA ATTATGGCAT	480
15	AGATCTTGGG AAAATTGCGG AGTGTACATT TACAAAGATG CGTTCAAATA GTGCTCTAAG	540
	AGTTTGTGTC AGTGGCTCAC TTCGGCTAAA ATGCAGAAAT GCATGCTGTC AGCGTTGGTA	600
20	TTTCACATTC AATGGAGCTG AATGTTTCAGG ACCTCTTCCC ATGAAGCTA TAATTTATTT	660
	GGACCAAGGA AGCCCTGAAA TGAATTCAAC AATTAATATT CATCGCACTT CTTCTGTGGA	720
	AGGACTTTGT GAAGGAATTG GTGCTGGATT AGTGGATGTT GCTATCTGGG TTGGCACTTG	780
25	TTCAGATTAC CCAAAAGGAG ATGCTTCTAC TGGATGGAAT TCAGTTTCTC GCATCATTAT	840
	TGAAGAATA CCAAATAAAA TGCTTTAATT TTCATTTGCT ACCTCTTTTT TTATTATGCC	900
30	TTGGAATGGT TCACTTAAAT GACATTTTAA ATAAGTTTAT GTATACATCT GAATGAAAAG	960
	CAAAGCTAAA TATGTTTACA GACCAAAGTG TGATTTTACA TGTMTTTTAA TCTAGCATT	1020
	TTCATTTTGC TTCAATCAAA AGTGGTTTCA ATATTTTTTT TAGTTGGTTA GAATACTTTC	1080
35	TTCATAGTCA CATCTCTCA ACCTATAATT TGGGAATATT GTGTGGTCT TTTGTTTTTT	1140
	CTCTTAGTAT AGCATTTTTA AAAAAATATA AAAGCTACCA ATCTTTGTAC AATTTGTAAA	1200
40	TGTTAAGAAT TTTTTTTATA TCTGTTAAAT AAAAAATTATT TCCMACAACC TTAAAAAAA	1260
	AAAAAAAAA AAAAAAAAAA AAAAAANAA	1288

45

(2) INFORMATION FOR SEQ ID NO: 126:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

	AGTGGCTTAA AGGCATCGTT TTAGGGATTA CTGGGAAGTA TCTTCAAAGT AATACATGAG	60
60	AAACATTCTT TCCTAAATCC TTTATTATAT TGAATATCGT ATTAATTGGT TTTCAGAGGT	120



TAAATTAACC ATGTATTCCT GCAATAAATG TCACTTGINT CTGTATATA ATCTTTTSTA 180  
 TATATTACCG GATTGATTCA TTAGTATTTT GTTGAGGATT TTTGTGTCTA TATTCATAAG 240  
 5 AGATGCTGGT CTGCAGTTTT CTTTTTTTGT GATAATCTGG TTTTGTATC AGTAATACAG 300  
 GCCCCATGAA ACGAGTTGGG AAGTGTTCAC CTCTCTTGTA TTTTTTCAAG AGTTTGTGAA 360  
 GAATGCTAT TAATCTTTTA AATGTTTGGT AGAATCTACC ATTGAAATCA TGTGCTCTGG 420  
 10 GCTTTTTTTT GAGGGAAGTG TTCTGATAAC TAATTCAGTA TCTACTTTTT ATAGCTCTGT 480  
 TCAGATTTTG CTCTTCCTG AGTTAGTTTT GGTAATTTGT GTATCTCTAG GATTTTGTCC 540  
 15 ATTTCAATTA TCTCATTTGT TGGCATAAAT TAAACTAAAT TTGGCCTGAG CCTACCTGTA 600  
 TATCTTGAGT CCCTCTGTAA GGAAGTGTAG CCTAAGTTGT ACATAAACAA ACTGAAATCC 660  
 TAAATTAGGA ATGTAGTTTT TGTAACAGCT CCTGAGTCTC AGGCAGTCAC AGCAGYCAAG 720  
 20 TCTGTCAATT GCAGGCTGCT AACTAAGCAG CCCATGSTCA AATGAGGCAA AAACCTTTGC 780  
 TTTTAACACA TAGTATAGCT TTGTAATCCT TTTCTTGCAC ACTCGGGTAA TTTCTTCCTT 840  
 25 TTTCAATCCC KGWATTTTCC AKGAATATGA RTCTYCCTTT TTTCCCTCC TGTCAGTCTA 900  
 GCTAATGGTT TGTCAATTTT GTTGATCTTT TGAARAACAA ACCTTTGGTT CCACTTTCTT 960  
 GTTGTCATATG CTGARTATTC TCATAATTGG AGTGGAAAGC TGATCTTTGA TTAATTATTT 1020  
 30 TACTTAGGGC TGAGGAGTTC ATGGACTTCG CAAAACCTCC TTGAATCTAA ATTGCATCTT 1080  
 CTTTCCTGGT TTCTGGGCTG AAACATGTTT TTTCCCATCT WANAWACCCT TGGTCTTTTC 1140  
 35 ATKGGCGATT AAGACTAGAG AAAGTTCTAG ATMCCCTGTC CTTTTATGCT GTCATTTTGT 1200  
 TTAAAGGCTT TCTATGTAGT AAACTATCT ATATAGACAA AATAGAGCCT TGAGTTGTGG 1260  
 TCTTGAATTT GATCAACATG ATTTACCACA TTCTGTACTG GATATTTCTT CACCTGCTGC 1320  
 40 TACTGTAAAC CATTTTATTC TTGGATCTTC TGTAGAGTAT ATTATCACAG GTACTTTTSTA 1380  
 CAGGGGTGTC TAATCTTTTG GCTTCCCTGG GCACATTGAA AGAAGAAGAA TTGTCTTGGG 1440  
 45 CCACACATCA AATACGCTAA CACTAATAAT AGTTGATGAG CTAAAAAAA AAAAAAAG 1500  
 GCAAAAAAGN CCAAAA 1517

50

(2) INFORMATION FOR SEQ ID NO: 127:

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1073 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

TGAATCTATT CTTTGAACAT TCTACAACAA GAATTACATT ATACTGTTAT ACCAGAGTAC 60  
 TTCTGCAGTG TGAAATAGAT TGGTTTGGAA AATGAACCTG GCTTTGCTAT AAATTACATT 120  
 5 CACAGGCCTT TTTGCAAATG TGTAACCTGC CTATCAAAGT AGTTTGTAGG GCAAATGCAG 180  
 AATATATGTC TCCATCTGGT AAAGTACCTT WTATCATGT GGGAAATCAA GTAGTATCAG 240  
 10 AACTTGGTCC AATAGTCCAA TTTGTTAAAG CCAAGGGCCA TTCTCTTAGT GATGGGCTGG 300  
 AGGAAGTCCA AAAAGCAGAA ATGAAAGCTT ACATGGAATT AGTCAACAAT ATGCTGTTGA 360  
 CTGCAGAGCT GTATCTTCAG TGGTGTGATG AAGCTACAGT AGGGRMGATC ACTCATGMTA 420  
 15 GGTATGGWTC TCCTTACCCT TGGCCTCTGW WTCATATTTT GGCCTATCAA AAACAGTGGG 480  
 AAGTCAAACG TAAGNTGAAA GCTATTGGAT GGGGAAAGAA GACTCTGGAC CAGGTCITAG 540  
 20 AGGATGTAGA CCAGTGCTGT CAAGCTCTCT CTCAAAGACT GGGAACACAA CCGTATTTCT 600  
 TCAATAAGCA GCCTACTGAA CTTGACGCAC TGGTATTTGG CCATCTATAC ACCATTCTTA 660  
 CCACACAATT GACAAATGAT GAACTTTCTG AGAAGGTGAA AACTATAGC AACCTCCTTG 720  
 25 CTTTCTGTAG GAGAATTGAA CAGCACTATT TTGAAGATCG TGGTAAAGC AGGCTGTCAT 780  
 AGAGTTATGT GTTAGTCTCA GGAGTCTTAA CTTTGTAAAT ATGTTTTACT TGAATGTTAC 840  
 30 ATTAGATATT GGTGTCAGAA TTTTAAAACC AAATTACTGC TTTTGTAAAC CTCAAATTAT 900  
 ATAATGTATC TTAGTATGT GCTTTATATT GTTATTTGTG TATACATTAA AATAATCTG 960  
 AATTATTTAA TCTGATATGT TGTATCTGT ATCTTGAAAT TTTTGTTCCT TTGAAACATG 1020  
 35 CATGCATTTA AAAATAAAGC TTAAACAACT GTAAAAA AAAA AAAA CTC 1073

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(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

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CAACCCCTGC CTTTTTTTGG TTTTCCATTT GCTTGGTAGA TCTTCCTCCA TCCCTTTATT 60  
 TTGAGCCTAT GTGTGTCTCT GCCCGTGAGA TGAGTCTCCT GAATACAGCA CACTTACTGG 120  
 TCTTGACTCT GTATCCAATT TGCCAGTCTG TGTCTTTCAT TTGGAGCATT TAGCCCATTT 180  
 ACATTTAAGG TKAATATTGT TATGTGTGAA TTTRATCYTR TCATTATGWT GTTAGCTGGT 240  
 TATTTTGCTT GTTAGTTGAT GCAGTTTCTT CCNGGCATCA ATGGTCTTTA CAANTTGGCA 300

## (2) INFORMATION FOR SEQ ID NO: 129:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GGCAGAGCCT GTCCCTGCTG CCCCTGCAAA AAAAACCCCC TCTGGTGTGA GCAGGATGGT 60  
TGGAGGTTAT GTGAGCTCCT TCTCCTTTCC TCCAGTTTCC TCTTCCCTTC TCCTCCCTGC 120  
CTCTTTTGCT TTTCCCTTTC TTCCTGGTAC CCCCTGCCCA TTCCTGTATT TTCTCCCATC 180  
GCCATTCTCC CCTCTCCAC TGTCCCTAAC CCGTTCAAAC TCTTTCCTCT TAAATGGMTG 240  
AGATTTTCTC TCACCAAGCA CACCCAGTA TTAATTAAAC TAGCTGCAA CAGGCAGCAA 300  
GTGGTCTACC ATGACAGATG GGTTTTGTGT GTGTGTGTGT GTGTGTAATT GTAATAAAAC 360  
ATATTGARTC ACTCAATAAA CACAGAGTGT CTACTACATG TATCARGCAC TATCATAGAT 420  
GCTAATTAAC GAAACTGAAA TGGCCAGGCC CTCACAGTGG CTCATGCCTA TAATCCCAGC 480  
ACTTTGGGAG GATGAGGCAG GAGGATCACT TGAGGCCGGG AGTTCAAGAC CAGCCTGGGC 540  
AACATAGTAA GACTCCATCT CTACAAAAA AAAATTTTTT TTATTATACT TTAAGTTTGT 600  
GGTTACATGT GCAGAACGTG TAGTTTTGTT ACATAGGTAT ATACGTGCCC TGGTAGTTTG 660  
CTGCACCCAT CAACCCATCA CCTACATTAG GTATTTCTCC TAATGTTACC CCTCTCCTAG 720  
CCCCCACCC CGTGACAGGC CCTGGTGTGT GATGTTCCCC TCCCTGTGTC CATGTGTTCT 780  
CATTGGTCAA CTCTCACCTA TGGAGTGAGA ACATGTGGTA TTTGGTTTTT TGATCTTGTG 840  
ATAGCTTGCT GAGAATGPKG GTTCCAGCT TTATCCACGT CCCTGCAAAG GGCATAAACT 900  
CATCCCTTTT TATGGCTGCA TAGTGTTCCTA TGGTGATATC GTGCCACATT TTCTTAATCT 960  
ATCATTGATG GACAAGTTTT GCTATTGTGA ATAGTGCCAC AATAACATA CGTGTGCGTG 1020  
TGTCTTTATA GCAGCATGAT TTATAATCCT TTGGGTATAT ACCCAGTAAT GGGATCACTG 1080  
AGTCAAATGG TATTTCTCGT TCTAGATCCG TAAGGAATTG CCACACTGTC TTCCACAATG 1140  
TTTGAACATA TTTACTCTCC CACCAACAGT GTAAAAGTGT TTCTATTTTT CCACAACCTC 1200  
TCCAACATCT GTTATTTCTT GACTTTTTAA TGAACGTCAT TCTAACTGGC GTGAGATGGT 1260  
ATCTCATTTG GGTGTT 1275

## (2) INFORMATION FOR SEQ ID NO: 130:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 472 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

10 CNGAAACCCC GTGAACCCCTC CCCGGGTAA AAAGCCCCC CTAAATGGGG GGAACGCTC 60  
ACACGTTATA AAAAGCACT AGAATGTTT GAAAGCGAGA AACAACAGCT GTGTAGGTA 120  
15 GCTAGCAGTT AGTGTGTAC AGAAGACAGA TATTTGTGCA TTTYTGCA TTCTAAGTTT 180  
GCTGCAATGA GCATGTATTA CTTTCATAGT TATAAACAC ATGCAAAATG CCCTTTTAAA 240  
ATGAAAAAAA ATCCATGAGT GTAAGTGATA TATATGCTTT GGAAAGCCTG GGACGGTCAT 300  
20 TGTTTACTCT CAATAGTATG TGTTCGCTT TGTCTTTTG AGACATTTT TTTAATCTG 360  
TTGATGACAA TAACCTGTTG ATAATATAAC TTGATAACAA ATAAATGAC TTATGATTGA 420  
25 AWMAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA NN 472

## 30 (2) INFORMATION FOR SEQ ID NO: 131:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1950 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

40 ACCTCTCAGA ATCTTCTCTC AGCAACCTGA GTCTTCGCGG TCCTCAGAG CGCCTCAGTG 60  
ACACCCCTGG ATCCTTCCAG TCACCTTCCC TGGAAATCTT GCTGTCCAGC TGCTCCCTGT 120  
GCCGTGCTG TNATTGCTG GTGTATGATG AGGAAATCAT GGCTGGCTGG GCACCTGATG 180  
45 ACTCTAACCT CAACACAACC TGCCCTTCT GCGCTGCCC CTTTNGCCC CTGCTCAGTG 240  
TCCAGACNT TGATTCCCGG CCCAGTGTC CCAGCCCCAA ATCTGCTGGT GCCAGTGCCA 300  
GCAAAGATGC TCCTGTCCCT GGTGTCCTG GCCCTGTGCT CAGTGACCGA AGCTCTGCCT 360  
TGCTCTGGAT GAGCCCCAGC TCTGCAACGG GCACATGGGG GGAGCCTCCC GGCGGGTTGA 420  
GAGTGGGGCA TGGGCATACC TGAGCCCCCT GGTGCTGCGT AAGGAGCTGG AGTCGCTGGT 480  
55 AGAGAACGAG GGCAGTGAGG TGCTGGCGTT GCCTGAACCT CCCTCTGCCC ACCCCATCAT 540  
CTTCTGGAAC CTTTGTGGT ATTTCCAACG GCTACGNTG CCCAGTATTC TACCAGGCCT 600  
60 GGTGCTGGCC TCCTGTGATG GGCCTTCGMA CTCCAGGCC CCATCTCCTT GGCTAACCCC 660

5 TGATCCAGCC TCTGTTTCAGG TACGGCTGCT GTGGGATGTA CTGACCCCTG ACCCCAATAG 720  
 CTGCCCACCT CTCTATGTGC TCTGGAGGGT CCACAGCCAG ATCCCCCAGC GGGTGGTATG 780  
 GCCAGGCCCT GTACCTGCAT CCCTTAGTTT GGCAGTGTG GAGTCAGTGC TGCGCCATGT 840  
 TGGACTCAAT GAAGTGCACA AGGCTGTGGG GCTCCTGCTG GAAACTCTAG GGCCCCCACC 900  
 10 CACTGGCCTG CACCTGCAGA GGGGAATCTA CCGTGAGATA TTATTCCTGA CAATGGCTGC 960  
 TCTGGGCAAG GACCACGTGG ACATAGTGGC CTTGATAAG AAGTACAAGT CTGCCTTTAA 1020  
 CAAGCTGGCC AGCAGCATGG GCAAGGAGGA GCTGAGGCAC CGGCGGGCGC AGATGCCCCAC 1080  
 15 TCCCAAGGCC ATTGACTGCC GAAAATGTTT TGGAGCACCT CCAGAATGCT AGAGACCTTA 1140  
 AGCTTCCCTC TCCAGCCTAG GGTGGGAAG TGAGGAAGAA GGGATTCTAG AGTTAAACTG 1200  
 20 CTTCCTGTT GCCTTCATGG AGTTGGAAC AGGCTGGGAA GGATGCCCAG TCAAAGGCTC 1260  
 CAAGCGAGGA CAACAGGAAG AGGGATCCAC TGTTACCAA AGTCCTGATT CCCCCATCAC 1320  
 CAACCTACCC AGTTTGTTCG TGCTGATGTT GGGGGAGATC TGGGGGGAGT TGGTACAGCT 1380  
 25 CTGTTCTTCC CTGTCTCTAT ACCGGGAAC CCCCTCCAGG GTACCCACAG ATCTGCATTG 1440  
 CCCTGGTCAT TTTAGAAGTT TTGTTTAA AAAACAACG GAAAGATGCA GAGCTACTGA 1500  
 30 GCCTTTGCCC TGAATGGGAG GTAGGGATGT CATTCTCCAC CAATAATGGT CCCTCTTCCC 1560  
 TGACGTGCT GAAGGAGCCC AAGGCTCTCC ATGCCCTTCT ACCTAAGTGT TTGTATTTTA 1620  
 TTTTAAATTA TTTATTCTGG AGCCACAGCC CCCTTGCTTA TGAGGTTCTT ATGGAGAGTG 1680  
 35 AGAAAGGGAA GGGAAATAGG GCACCATGGT CCGGTGGTTT GTAGTTCCTT CAAAGTCAGG 1740  
 CACTGGGAGC TAGAGGAGTC TCAAGCTCCC CTTAGGAAGA ACTGGTGCCC CCTCCAGTCC 1800  
 40 TAATTTTCT TGCCTGCCCC GCCTTGGGGA ATGCCCTACC CACCCAGGTC CTGACCTGTG 1860  
 CAATAAGGAT TGTTCCTGC GAAGTTTGT TGGATGTAAA TATAGTAAAA GCTGCTTCTG 1920  
 45 TCTTTTCAA AANAAAAAA AAAAAAACT 1950

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

TGGAAGATTT AAAATAGGTT TCATATTTCT CTTGAATATG AATATATAAG CTTGAATAAG 60

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	CTTGAGTCTT TATTATTATG AATTTTCCT TATTATTTCT ACCAATGCTT CTTATATTAA	120
	AGCCTGATCT TTTTCATATT AATATATGTA CATTAGCTGC CTGTGGATTA ACATTTCCAT	180
5	GAATGTATT TTTGCATTTT TGTATCTTAA ACTTTTGTG TCTTTATATA AGGTATGCTY	240
	CTTTAAGCA TGATATTTT AACCACAATA GTTGAAAGAC AATCTYCACC TTTTACTTGT	300
	ATATTTACAT GTAATGTAAT TTTTGATGCA TATTACGTCT TATTATTTAA CCAACCTATT	360
10	TTATTTTATC TAGGGCATTT TTCAGAAAGC CTTATTTTCT TGTATTAATC AAATATTTTT	420
	AYCATGTAT TTTCCCTAT TATTTAGKAA TACGKTACYC YAAATATATA TTGTGGSTAT	480
15	TTTCAGAAAT GCATATGCC TCCTTAATTT ATTAGAGGCT AACCTAAAT ATTACTTTTA	540
	CCACTTACTT GAAATCTCG GAATTTTAGA ACATTTATTG TTTTATGCAT TTTAATTCTA	600
	CTTGATTTTT TACTACTCCT AAACATTATT ATGTGTTTAG ACAAGCCAAA ATATATNTTG	660
20	TTATATCTT ATCTCCATTT TCTTCTGTA TTTTATGCC ACTATGTATG CTCAATTTCC	720
	TTCTATGTGA TGAACCTAAT TCAGTACTTT TGTTTTAA TCTGTGCAGG TAGCCTGGCC	780
25	ATTAAATTTT TATTTTGGT TTGCTGAAAA AATGTGTGTT ATTTCTATAT GCATACTTAT	840
	GCAATATGAA TCTAGTGG ACATATTTTT AGTATTTATA AATGTAAAGT CATTAATTKG	900
	GCTCTATCA TTTCTGTGA GAATCAATT GTCAGCCCAA TAGTTTTTCA TTTTAAATTA	960
30	CNGAATTTTT TCATGTCTCT GGTMTTAGGA	990

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(2) INFORMATION FOR SEQ ID NO: 133:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

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GTCTGATAAG CGACTGTGGT TATTCCTTA AAGTTTACTT CAGCACTAAC ACTAGTGCTT	60
CCGCTGGAGT TTGCAGTTTT CCAGCTTTAT ACAGGATTTT CCTTTGACTG GAAGAGTCAA	120
GGATATAGAG ACTCAGCAGT GACATTTATT GTACAACATC AAGGGGAATA GGATACTCAT	180
CAACTGGGA TTATCTTTAT CAAACATGG TCTTCTTTGA ATAAGAAAAA TACATAGTTG	240
GTTATTATGG ACTTAAACT GGTAAATG GATATCTGA TAAATATTT GCTGCTCTGT	300
AGAGTGTGGA AATCTGAGA ATATTAGCTT TACTCATCTT GAGCTTTGAG GATGTTCTCT	360
GTACGCCGAT GGTTCATAT TAACTAAAA AGCTGGGTAT TGTAATCTT CATTTATAAA	420
AACTCAGATG AGAAGAAAT TTTCTTTGAT GGTGAGACTG TTGTCTTAGT TCAGGAAATT	480

ATTTAATAAT CCTTTGTTAC CTGTGAATGA AGGAACCTTG TAATCTGAT TTATCGTAAA 540  
 ACATGAGCCT TTCCAGAGTC AGCTTAGACA CTGTTGTCGC AAATAGCCAT GCTTTGCCTT 600  
 5 ATGCCAAGGA GGGCCAGAGG GAGGGCCTAG TCTCCTCTG TTGCTGTACA TATATTGAAA 660  
 TGCTTTTTTT TTTTATTTTG CATTGTTAT CTATAATGAG CTTTCTGAGC CCTGATATTA 720  
 10 TGTGAGACAA ACAGGAGTTA TTGATGTTAT AACTCCCTT CCATTCAGGA TTTTCTGCTT 780  
 GGAGGGAAAT ATGTTGACCT TAGAGAATTG TGAATATTGT TGCAATCTT GAATATATTA 840  
 CCATGTGAAT AATAGAGACT GTGTTGCTCT CTAGTATAAG CTATATTTAT TTTTGATTCA 900  
 15 TTTGAATTAC TAGTTATAAC TGGAGAAAT TTGTTACCTC TATCCTGGCT TGCCTGACTG 960  
 GCTGTATAAT AGCAGCAGCC TCTTTTAGAG CATCTTAATG AAAACATGGA TGAAAGGAAT 1020  
 20 TAATGATGAT ATCTGCAGAC TGCCTAGAAA ATGGCTTTTG TTCCCAGCGT TAACATTTTC 1080  
 TTCTCAATCA CATTTCAATG TTTGTGGAGA GTGGCAGATT CACACCAGAA AACTAGGTG 1140  
 TTCATATCCA TAGCATGGAT GCAGAATAAG CAGTTGGGAG AGAAGCTTCT TCCTACCTGG 1200  
 25 TACTCCTCCC ATTCACCTCA GCCCAGCCCC AGACAGGCGT TAGCATTGAG TGTGGGCCCT 1260  
 CAGGCAGCCC TGAAGCCTGG CTGGGTCATC AGATGGGGGC AGCCTGTGAC GGCACCAGC 1320  
 30 GGCCTGATTC CAGGGAAGAG TTCCTGGAGG GTGTTGGCTG TTTTGTGTTAG CTCAGTTTTT 1380  
 TTCTGGGCTC CACCATTCCT AACTCCAGGT AGACAAGATA GATGTCACAC ACAACAATTT 1440  
 TAAAGTATTT TGCTTAGTGC ATTTTGTGTTA TGATTGCAGT GTTGTGTTCT TATTTAATAG 1500  
 35 GCTTTTTACT TCATTCTATT AAATTTTAGT GTTTAGAAGA GCGGGTACT GTCAGTGTG 1560  
 AAAATATGTA ATATTTTATA TGTATACCA TGTCATATAT ACTTGCAATA TCAGACCTTG 1620  
 40 CATTCATAT ACAATGCAAT TGAATCTTG CAGACCTGCA TTTTTCAGTG AACAATAAAA 1680  
 AGATTGTCTG GCACTCCAAA AAAAAAAAAA AAAAAAAAAA 1720

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(2) INFORMATION FOR SEQ ID NO: 134:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 705 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

GGCACGAGGC CATCTGGGCT CATTGAGCAG GAAATAATGG AAAAAGCTGC AATATCCAGG 60  
 60 TGTTTACTAC AATCTGGAGG CAAGATCTTT CCTCAGTATG TGCTGATGTT TGGGTTGCTT 120

386

GTGGAATCAC AGACACTCCT AGAGGAGAAT GCTGTTCAAG GAACAGAACG TACTCTTGGA 180  
TTAAATATAG CACCTTTTAT TAACCAGTTT CAGGTACCTA TACGTGTATT TTTGGACCTA 240  
5 TCCTCATTGC CCTGTATACC TTTAAGCAAG CCAGTGAAC TCTTAAGACT AGATTTAATG 300  
ACTCCGTATT TGAACACCTC TAACAGAGAA GTAAAGGTAT ACGTTTGTNA AATCTGGGAA 360  
GACTTGACTG CTATTCCATT TTGGGTATCA TATGTACCTT GATGAAGANG ATTAGGTTGG 420  
10 GATACTTCAA GTGAAGCCTC CCACTGGAAA CAAGCTGCAG TTGTTTITAGA TAATCCCATC 480  
CAGGTTGAAA TGGGAGAGGA ACTTGACTC AGCATTGAGC ATCACAAAAG CAATGTCAGC 540  
15 ATCACAGTAA AGCAATGAAG AGCAGTTTTC CAATGAAAAC TGTGTAAATA GAGCATCAAC 600  
AAGTACAAAA TTCTTGCTTT AATTAGTGGG GGTATATAAA AATTCCTTGT AATGGTCAAA 660  
TATTTTTTAA AATTGACATT AATAAGCAT ATTTTAAAAG TTTCT 705  
20

25 (2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

AGCACACACC TCCTTTAGTT GCTCCTAAGG TCATGTTCAA CATTCGTGGA GTGCATTTTC 60  
35 TGCTCAGGGA GCTTTCCAG ACCCGGAATG TTTGGTGCTC ACAGACYCTG GCAAGGATCG 120  
GTATTGCTGT TCCTCAGTTT TGCCTGGGGA AATGGAGGST CAGTGACGTT CAGTGACGTG 180  
40 CCCAGAGTCA TGCCATTGGC GGGTGGCCCA GKGMTCCAGG TCTCCAGCAC CCCTCGGCCC 240  
CCTCCTCACC AGGTCACATC ATCTCCTGGA TTAGAATCTG CTCACATAGT CTGTCCTGAA 300  
AGGAAAAAAA AAAAAAAAAA AAC 323  
45

50 (2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 582 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

GGACGGAATG GTGCAACCCT CCTWAMTTTT CTKGKGCTGT TGACAACAGA GGGAGGGAGG 60  
60



387

5 GAAAACATTT TTYGTGGGAG AATCCTACYT CTGCAGSGGA GCCCTTAAGC GATKGATTTT 120  
 GAATCTKGAC CCTTTACCAA CTAATTTTGA AGGAAGATAC CTTGGAAATA TTTGGCATTC 180  
 10 AGTGGGTTAC TGAACAGCA TTAGTGAATT CATCTAGAGA ACTCTTTCAT TTATTCAGGC 240  
 AACAACTGTA CAACTTGGAA ACCTTGTTAC AGTCCAGTTG TGATTTTGGG AARGTATCAA 300  
 CTCTACACTG CAAAGCAGAC AATATTAGGC AGCAGTGTGT ACTATTCTC CATTATGTTA 360  
 15 AAGTTTTCAT CTTACAGTAT CTGAAAGTAC AGAATGCTGA GAGTCATGTT CCTGTCCATC 420  
 CTTATGAGGC TTTGGAGGCT CAGCTTCCCT CAGTGTGAT TGATGAGCTT CATGGATTAC 480  
 TCTTGTATAT TGGACACCTA TCTGAACTTC CCAGTGTAA TATAGGAGCA TTTGTAAATC 540  
 AAAACCAGAT TAAGGTTTGA CTGGTTTCAT TTGATTTTGA AG 582

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(2) INFORMATION FOR SEQ ID NO: 137:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1021 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

TTCGGCAGAG CCCTTGCGCG CTCTTGAATA CCTGCKTTCT GTAGCGCTAG TTCTCTTCAA 60  
 35 GATTTGCTTA GTGTCATTC ATTTTCGGTTT CTTTCTCGC CATGTTTTC TGTCCGAATT 120  
 ACGGTTTCGT TGGTTCCTAT GACTCTCTA AAATGTTATC GTTTTTCATT TGTCTACTAA 180  
 TTTTCGTGCA TTGTTACTA CTGAGTTTCT TAATATCTGA CTGGCCTCCG CCCACGGGCT 240  
 40 CTGCAGANCA TAAATACTC AGGCTGATGG TAGTGAGAG ACTCTCCCTC CTTGATCAGC 300  
 GCAAACGTTG GTCTGAGGCT TGAGGGATGG AGCAACATTT TCTTGGCTGT GTGAAGCGGG 360  
 45 CTTGGGATTC CGCAGAGGTG GCGCCAGAGC CCCAGCCTCC ACCTATTGTG AGTTCAGAAG 420  
 ATCGTGGGCC GTGGCCTCTT CCTTTGTATC CAGTACTAGG AGAGTACTCA CTGGACAGCT 480  
 GTGATTTGGG ACTGCTTTCC AGCCCTTGCT GCGGCTGCC CGGAGTCTAC TGGCAAACG 540  
 50 GACTCTCTCC TGGAGTCCAG AGCACCTTGG AACCAAGTAC AGCGAAGCCC ACTGAGTTCA 600  
 GTTGGCCGGG GACACAGAAG CAGCAAGARG CACCCGTAGA AKARGTGGGG CAGGCAGARG 660  
 AACCCGACAG ACTCAGGCTC CRGCAGCTTC CCTGGAGCAG TCCTCTCCAT CCYTGGGACA 720  
 55 GACAGCAGGA CACCGAGGTC TGTGACAGCG GGTGCCTTTT GGAACGCCGC CATCCTCCTG 780  
 CCTCCAGCC GTGGCGCCAC CTCCCGGGTT TCTCAGACTG CCTGGAGTGG ATTCTTCGCG 840  
 60 TTGGTTTTCG CGGTTCTCT GACTCTGGG CGTGCTGTT ACGGATCTGT GGAGCTAAGC 900

	AGCCTTAGAT AGCAGCAGAA GGCTTTTGG ATTCTCCTCC TTGAAAAGAT TCTCAGTTAC	960
	CAAACGTCTC CACCTAGAAA ATAAAAATAC ATTAAGATGT TGANAAAAAA AAANAAAAAA	1020
5	A	1021
10	(2) INFORMATION FOR SEQ ID NO: 138:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 1777 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:	
	CGGAAGATGA TGGCTTCAAC AGATCCATTG ATGAAGTGAT ACTAAAAAAT ATTACTTGGT	60
	ATTGAGAAGC AGTTTTAACT GAAATCTCCT TGGGGAGTCT CCTGATCCTG GTGGTAATAA	120
25	GAACCATTCA ATACAACATG ACTAGGACAC GAGACAAGTA CTTTCACACA AATTGTTTGG	180
	CAGCTTTAGC AAATATGTCG GCACAGTTTC GTTCTCTCCA TCAGTATGCT GCCCAGAGGA	240
30	TCATCAGTTT ATTTTCTTTG CTGTCTAAAA AACACAACAA AGTTCTGGAA CAAGCCACAC	300
	AGTCCTTGAG AGGTTGCTG AGTTCTAATG ATGTTCTCTT ACCAGATTAT GCACAAGACC	360
	TAAATGTCAT TGAAGAAGTG ATTGGAATGA TGTTAGAGAT CATCAACTCC TGCCTGACAA	420
35	ATTCCCTTCA CCACAACCCA AACTTGGTAT ACGCCCTGCT TTACAAACGC GATCTCTTTG	480
	AACAATTTG AACTCATCCT TCATTTCAGG ATATAATGCA AAATATTGAT CTGGTGATCT	540
40	CCTTCTTTAG CTCAAGGTTG CTGCAAGCTG GGAGCTGAGC TGTCAGTGA ACGGGTCTG	600
	GAAATCATTA AGCAAGGCGT CGTTGCGCTG CCCAAAGACA GACTGAAGAA ATTTCCAGAA	660
	TTGAAATCA AATATGTGGA AGAGGAGCAG CCCGAGGAGT TTTTATCCC CTATGTCTGG	720
45	TCTCTTGTCT ACAACTCAGC AGTCGGCCTG TACTGGAATC CACAGGACAT CCAGCTGTTT	780
	ACCATGGATT CCGACTGAGG GCAGGATGCT CTCCCACCCG GACCCCTCCA GCCAAGCAGC	840
50	CCTTCAAGTT CTTTTATTTC TGGGTAACAG AAGTAGACAG ACAGGTTACT TGGTGTATCT	900
	TCTGTAAAG AGGATTGCAC GAGTGTGTTT TCCTCACACA CTTTGATTG GAGAATTGGT	960
	GCTAGTTGGC AATAGATAAC TCAGCGTAGA TAGTATTGCA AAAAGGGGAG GAAATACACA	1020
55	ACAATAATAA ATGTAAAAAC CTGCTATTCA ACATGCAGTT TTATTTTCGAR GCCAAAAATC	1080
	TAGAGCTTTC CCAAGATCCT GTTGCCTTAG GCACATNCAC ACTTCAACAG TGCACACTAT	1140
60	CCAACAGTGC AACTATTCA ACAGTGACA CTATTCAAAA GCGTAGACTA TTTTTTTGCA	1200

5 TGTTCAGAT ATTGTTTGT GTCTTATGTG TGTGTGAGAG AGAGAGATTC CTTTGACATT 1260  
AAGGAGCATC AATGAGAAAA GATGATGAGG CAGGAATTAA TAAAGAAATG AAGTCGTGTG 1320  
10 TGTPTGGTTG CCTGTCAGAG GGCACACAAT TTCATAAACA CCATGCCTGG ACAATTTGAT 1380  
ATTAATATTT AACACCTCTG CATCTTTTTC TTAATAAAGA ATATGGGCCA GATACAGTGG 1440  
CTCACATTTG TAATCCACGC ACTTTGGGGA GCCAAGTTAG CAGAATCCCT TGAGCACAGG 1500  
AATCTGAAAC CAGCTTGGGC AACATAGTGA GATCCCATCT NTACAAAAA CTTAAAAATT 1560  
AGCCAGGCAT GATGGCACAT TCCTGTAGTC CTAGCTACTC AGGAGGCTAA GGTAGGAGGA 1620  
15 TGCCTGAGC CCAGGAGTTC AAGGCTGCAG TGAGCTAAGN ACGTGCCAGT AACTCCAGC 1680  
CTGAGCCACA AAGTGAGACC CTGTCTCGCA AAAAAAAN TAAAAAGTC GGGGGGGGGC 1740  
CCGGTACCCA AATCGCCGGA TATGATCGTA AACAATC 1777  
20

25 (2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 643 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

35 TTTTTTTTT TTTTTTTTT TTTTTTTTT TTTTTTGGG AATGAGAAAA TAACTTTATT 60  
TTCATTGTGG GGAGCGGGCC GATGTCCAGC CTCAGAACTT CTGGAAGTGC TTCTTGGTGC 120  
CGGCAGCCTT GGTGACCTTG AGCAGTTGA AGCGCACTGT CTTGCTCAGA GGCCGGCACT 180  
40 CGCCCACTGT GACGATGTCA CCGATCTGGA CGTCCCTGAA GCAGGGGGAC AGGTGTACAG 240  
ACATGTTCTT GTGGCGCTTC TCGAAGCGGT TGTACTTGCG GATGTAGTGC AGATAGTCTC 300  
GGCGGATGAC AATGGTCTC TGCATCTTCA TCTTGGGTCA CCACGCCAGA GAGGATCCGC 360  
45 CCTCGAATGG ACACATTACC AGTGAAGGGG CATTTCTTGT CAATGTAGGT GCCCCTCAAT 420  
AGCCTCCTTG GGGTGTCTTT GAAGCCCAGA CCGATGTTCT TGTAGTAAC CCGCGGGAGC 480  
50 TTCTCCTTGC CAGTTTCTCC CAGCAGGACC CTCTTCTTGT TTTGAAAGAT GGTGGGCTGC 540  
TTTTGGTAGG CACGCTCAGT CTGAATGTCC GCCATCTTCT CGTGCCGMAY TCCTGCAGCC 600  
CGGGGGATCC ACTAGTTCTA GAGCGGCCGC ACCGCGGTGG AGC 643  
55

60 (2) INFORMATION FOR SEQ ID NO: 140:

390

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

GGCACGAGGA TGATAGACCT ACTGGAGGAA TACATGGTTT ACAGGAAGCA TACCTACATR 60  
AGGCTTGATG GCTCATCCAA GATCTCGGAG AGGCGAGACA TGGTTGCTGA TTTTCAGAAC 120  
AGGAATGACA TCTTTGTGTT CCTGTTAAGC ACACGAGCTG GAGGACTGGG TATCAATCTC 180  
ACTGCTGMAG ACACAGTGCA TTTTCTATGA TAGCGACTGG AACCCCACTG TGGACCAGCA 240  
GGCCATGGAC AGGGCCCACC GCTTAGGGCA GACAAAGCAG GTTACTGTGT ACCGGCTCAT 300  
CTGTAAAGGC ACCATTGAAG AACGCATTCT GCAAAGAGCC AAGGAGAAGA GTGAGATTCA 360  
GCGGATGGTG ATTTTCAGGTG GGAACCTCAA ACCAGATACC TTGAAACCCA AAGAGGTGGT 420  
TAGTCTTCTT CTAGACGACG AAGAGTTGGA GAAGAAACGT ATGTACTCTA AACCTCTATA 480  
CACTCCCCTC ACGTATCTGA GAATGGAAGA GGTACTTGGG TGTGTGCCAA GGGTTAGGCA 540  
AAGCCAGAGG CTGTATTTAG GGAAAGTATT TTTGTGCTCA TATTTTATAT AAAAACCCAA 600  
ACAAGAATGT GTTTGTAGGC CAGGCGTGGT GGCTCGCGCC TCTAGTCTCA GCATTTGCGG 660  
ARGCCAAAGT GGCAGATCA CCTGARGTCA GGARTTTGAG TTTGARACCA GCCTGGCCMA 720  
CGTTGTGAAA CCCACCTCT ACTARGARTA CSGAAAATG GTTGGGCATG GTGGCGGGCA 780  
CCTGTAATTC CAGCACTTTG GGAGGCTGGG GCAGAANAAT TGCTTGAGCC CAGGAGGTGG 840  
AGATTGCGGT GAGCCGAGAT YGTGCCATTG CAMTCCAGCC SGGGCAATAA GAGTGAAAYT 900  
CCATCTTTTA AAAACAAACA AAAACAAAAA ACACAAGACG GCTCACACCT GTAATCCCAG 960  
CACTTTGGGA RGCCGARGCA GGTGGATCAC GARGTCAGGA GTTCCAAGAC TAGCCTGGCC 1020  
AACCTGGTGA AGCCCCGTCT CTAATAAAAA TACMAATATT AGTCGGGCGT GGTGGTGGCC 1080  
ACGTGTAATC CCAGCTACTC GGGAGGCTGA GGCAGGAGAA TCCCTTGAAG CTAGGAGGCA 1140  
GAGGTTGCAG TGAGCCAGGA TCGTGCCATT GCACTCCAGC CTGGACAACA AGAGCAAGAT 1200  
TCCATCTCAA AAAAAAAAAA 1220

## (2) INFORMATION FOR SEQ ID NO: 141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

5 AATTTCGGCAC GAGCCAGGTT AGCCGGAAGG GCAGCTCTCC AGGCCCTGCC CACCCACAG 60  
 GGGGCTCCTT ATGCACAGCG GGGCGTCTCC TTGTGGCCAT AGAAACGGAA CTGGCTCTTT 120  
 TCAACAGTGC TGCAAGAGGA TGGTTATTTA ACCTGGCCC CCAAGGAGGA AAGGCACAGA 180  
 10 CYTTCCTCCC TCCTGGAACA TCCAAGGGCA CTGGATCCTC TGTGTCCCTC TGAGATGGGG 240  
 TGCCACTCCA GCAAGAGCAC CACGGTGGCA GCTGAGTCCC AGAAGCTTGA AGAAGAGYGC 300  
 GAGGGAAGAG AGCCAGGTCT GGAGACCGGC ACCCAGGCAG CAGACTGCAA GGATGCCCCG 360  
 15 CTGAAGGATG GAACCCCTGA GCCAAAGAGC TGAATGCCT CTCTCCAGAG TCGGACCCTC 420  
 ACCTCYTTCC TGGAAGTCCC TTTGGCCCCA GAACCATGAG ACAATCCCCA CCCTGAGAAG 480  
 20 CTCCGATCAC TGGGAGGAGA GAGAAAGCCT CCAGCTTTGG GATTCAGGCT TCAGAAGTTT 540  
 TTAGCAGCCT TTGCTCATTG GAGAGGTGGG GAAAGGATAA AGTTCTTATA AGGAAATCCC 600  
 TAATTTCCCC CAGCTCCTCC CCNCCNGAAG AAGGAACNAA AGAAAGTTCC TTCCACACGT 660  
 25 TTTGTTGGAA ACTTTTCCCT TGCCAACTTT CCTTGGATTG CCAGAACAAA GCCCTCCAGA 720  
 A 721  
 30

## (2) INFORMATION FOR SEQ ID NO: 142:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1468 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATGAATTAAT GTTTATAAAT GACTGTACTG AATTTAAAAC CGTACAGTTT CATTTGCATT 60  
 45 TTGACATTAC TTTATTATAC ATTTTGCAAT TAAAAGGCTG CACCAGTTGG CTMTCTTCT 120  
 GTTTTATTCT CAAATATAG AGATTCTGTG ATTTATTTGC CCTGTTTATG GATTAAAAG 180  
 AAAATCTTAA TATAAAGCAT TTCAATAGGA TGCATAGGTA TATTACGTTT TTTAAATGCT 240  
 50 TTAGATCTGT GATTCCTGAC TTACTATTTA TTTTATCCCC TTTAAGTCAG GGATGCTTTA 300  
 TTCTATTTTA AAGCACTTAT GAGTTACATG TTGTAATCAA GTTTCACAA TATATTTATC 360  
 55 TATATGAGGA ACCATAAAT GAATAGCTAA TTTTAAAAT GCCATTAAAA TGCATGAAAT 420  
 KCTTATTAAT ACCTTACTAT ACTATTTCTT CAAGGCAAGT AAATTGACCA TGRGAAAGR 480  
 ACACAGTTAT TAAACACTGT TGACAGGAAA ATTCTCCTTG ATAACATAGG ACAATTAATG 540  
 60

GAAAAAAAA TTCTCATTAT TTGCAAAGAA TGAACAAGTT AATGAACAAA CAACTAGAT 600  
 TTGGTATGTT TTCAGCTTTT GTATCATGTT TAATTGTTTA ATTTGGTTGA AAAACTGCAG 660  
 5 TTGAGAAATC AGATAGCAAT ATAGACATTC ACAGCAGCTC TGTGGATACC ATGTAATTGT 720  
 CAGGTAATTT CAGAATGTTG AAAATTATTC AGTGCAGCCC TCATAGTATC ATACTTGAAG 780  
 10 AAATTGATTA CAGTCCACT AAATTGTTGA AGATAAATTA TTTTAAAGG TTATGAAAAC 840  
 TAAGTTATAT TAATTCATAT GTTTGATTTT TAAATCCCAC CTCCTCAAGC TATCCAATTT 900  
 NCTGACTTTG AAAATAACCA TGAGAGATGC CACATTTCTC TCTGGGAAAC TACCACTCAA 960  
 15 AGAATAATTG TTAAAAATTA AGCTTTTAGG TATTAGAAGC TGTATAAAG TATAAAATTA 1020  
 AGATATAAGC AGATCACATG TAAATCATTC CTAAGCACA AGAAAAGAAT GTGCCTTGAT 1080  
 GTACATATAT TACTAAGTTG CCTCTCCCAG TTTACTTTAA AAATGGCTTT AAGGATAAAG 1140  
 20 AATAAATGTG ATAGCTGTGC ATGCATTATA TATTTGCATT TGCAAATTC CCATTGTTTT 1200  
 AACAGCTGTG TGGCTGACTT TCAATTTTAA GACGTGAATT GACATACAGC CCATAACTTT 1260  
 25 ATAATGGCTG CTCATTTATC TTATCTTTCA GTTAGTGGAA AAACATTTCA ACCTGACTAA 1320  
 AATTTGGAAT TGTGCTTTT ATGTTCCATC CTCGTGTGTT ACTAGATTTA GTTTAAAAAT 1380  
 TGTGTATGAC CATTAAATGA TGTCAATAAC ATGTAAATAA AAGATGTTGA ATCTTGTTGA 1440  
 30 AAAGCAWRRA AAAAAAAAAA AAACTCGA 1468

35

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

45

TGAATTTTTT GCCAACTTA GTAACCTCTGT TAAATATTTG GAGGATTTAA AGAACATCCC 60  
 AGTTTGAATT CATTTCAAAC TTTTAAATT TTTTGTACT ATGTTTGGTT TTATTTTCCT 120  
 50 TCTGTAATC TTTGTATTC RCTTATGCTC TCGTACATTG AGTACTTTTA TTCCAAACT 180  
 AGTGGGTTTT CTCTACTGGA AATTTTCAAT AAACCTGTCA TTATTGCTTA CTTTGATTAA 240  
 55 AAAAAAAAAA AAAAAAAAAA AAACCCNAG GGGGGGGCCG GGTNCCCAAT CCCCCCAA 300

60

(2) INFORMATION FOR SEQ ID NO: 144:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2243 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

10	TGCTCCCTT CCTGCAGATT GTGGACAGTA GTTCCTCAGC CTGCACCCTG GATTCTTCT	60
	TCCCCTTCCT AGCTCCATGG GACTCGCCCC AAGACTGTGG CTTCAAGGAC CACCAGCCCC	120
	TTACTCTTCA AGCCCTGACT GTGGAGTTGG TAGATGCCTC TGATCCTCAG TATTCTCTCT	180
15	GGCAATGTC CACGGCTTCT CCTTCTGGG AGCTGGCTCC ATAACCTGAT TTTCCCCAA	240
	CGTGTGCAA TCCCTGCTGC CCCTTAGCCA CCCAGGGTCT TGTGTGGGTA TGAGTGTAGA	300
20	GGATGGGGT ATGCCAGGCC TGGGCCGTCC CAGGCAGGCC CGCTGGACCC TGATGCTACT	360
	CCTATCCACT GCCATGTACG GTGCCCATGC CCCATTGCTG GCACTGTGCC ATGTGGACGG	420
	CCGAGTGCCC TTYCGGCCCT CCTCAGCCGT GCTGCTGACT GAGCTGACCA AGCTACTGTT	480
25	ATGCGCCTTC TCCCTTCTGG TAGGCTGGCA AGCATGGCCC CAGGGGCCCC CACCCTGGCG	540
	CCAGGCTGCT CCCTTCGCAC TATCAGCCCT GCTCTATGGC GCTAACAACA ACCTGGTGAT	600
30	CTATCTTCAG CGTTACATGG ACCCCAGCAC CTACCAGGTG CTGAGTAATC TCAAGATTGG	660
	AAGCACAGCT GTGCTCTACT GCCTCTGCCT CCGGCACCGC CTCTCTGTGC GTCAGGGGTT	720
	AGCGCTGCTG CTGCTGATGG CTGCGGGAGC CTGCTATGCA GCAGGGGGCC TTCAAGTTCC	780
35	CGGGAACACC CTTCCAGTC CCCCTCCAGC AGCTGCTGCC AGCCCCATGC CCCTGCATAT	840
	CACTCCGCTA GGCCTGCTGC TCCTCATTCT GTACTGCCTC ATCTCAGGCT TGTGTCAGT	900
40	GTACACAGAG CTGCTCATGA AGCGACAGNG GCTGCCCTTG GCACTTCAGA ACCTCTTCCT	960
	CTACACTTPT GGTGTGCTTC TGAATCTAGG TCTGCATGCT GCGGGCGGCT CTGGCCAGG	1020
	SCTCCTGGAA GGTTCCTCAG GATGGGCAGC ACTGCTGGTG CTGAGCCAGG CACTAAATGG	1080
45	ACTGCTCATG TCTGCTGTCA TGAAGCATGG CAGCAGCATC ACACGCCTCT TTGTGGTGTG	1140
	CTGCTCGCTG GTGGTCAACG CCGTGCTCTC AGCAGTCCTG CTACGGCTGC AGCTCACAGC	1200
50	CGCCTTCTTC CTGGCCACAT TGCTCATTTG CCTGGCCATG CGCCTGTACT ATGGCAGCCG	1260
	CTAGTCCCTG ACAACTTCCA CCTGATTCC GGACCTGTA GATGGGGCG CACCACCAGA	1320
	TCCCCCTCCC AGGCCTTCCT CCCTCTCCCA TCAGCAGCCC TGTAAACAAGT GCCTTGTGAG	1380
55	AAAAGCTGGA GAAGTGAGGG CAGCCAGGTT ATTCTCTGGA GGTGGTGGTA TGAAGGGGTA	1440
	CCCCTAGGAG ATGTGAAGTG TGGGTTTGGT TAAGGAAATG CTTACCATCC CCCACCCCA	1500
60	ACCAAGTTCT TCCAGACTAA AGAATTAAGG TAACATCAAT ACCTAGGCCT GAGAAATAAC	1560

CCCATCCTTG TTGGGCAGCT CCCTGCTTTG TCCTGCATGA ACAGAGTTGA TGAAAGTGGG 1620  
 GTGTGGGCAA CAAGTGGCTT TCCTTGCCTA CTTTAGTCAC CCAGCAGAGC CACTGGAGCT 1680  
 5 GGCTAGTCCA GCCCAGCCAT GGTGCATGAC TCTTCCATAA GGGATCCTCA CCCTTCCACT 1740  
 TTCATGCAAG AAGGCCCAGT TGCCACAGAT TATACAACCA TTACCCAAAC CACTCTGACA 1800  
 GTCTCCTCCA GTTCCAGCAA TGCCTAGAGA CATGCTCCCT GCCCTCTCCA CAGTGCTGCT 1860  
 10 CCCACACCT AGCCTTGTGTT CTGGAAACCC CAGAGAGGGC TGGGCTTGAC TCATCTCAGG 1920  
 GAATGTAGCC CCTGGGCCCT GGCTTAAGCC GACACTCCTG ACCTCTCTGT TCACCCTGAG 1980  
 15 GGCTGTCTTG AAGCCCGCTA CCCACTCTGA GGCTCCTAGG AGGTACCATG CTTCCCACTC 2040  
 TGGGGCCTGC CCCTGCCTAG CAGTCTCCCA GCTCCCAACA GCCTGGGGAA GCTCTGCACA 2100  
 GAGTGACCTG AGACCAGGTA CAGGAAACCT GTAGCTCAAT CAGTGTCTCT WTAAGTGCAT 2160  
 20 AAGCAATAAG ATCTTAATAA AGTCTTCTAG GCTGTAGGGT GGTTCCTACA ACCACAGCCA 2220  
 AAAAAAAAAA AAAAAAACTC GAG 2243

25

## (2) INFORMATION FOR SEQ ID NO: 145:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1082 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GCCAAGCTCT AATACGACTC ACTATAGGGA AAGCTGGTAC GCCTGCAGKT ACCGGTTCCG 60  
 40 GGAATTCCCG GGTGACCCA CGCGTCCGCT TCCGTGTGTC AAAATCCTCA CCTCCTTCAT 120  
 AACCATCTCC CACAATTAAT TCTTGACTAT ATAAATTTAT GGTTTGATAA TATTATCAAT 180  
 45 TTGTAATCAA TTGAGATTTC TTTAGTGCTT GCTTTTCTGT GACTCAACTG CCCAGACACC 240  
 TCATTGTACT TGAAACTGG AACANCTTGG GAATGCCATG GGGTTTGATA ATCTGCCAGG 300  
 GACATGAAGA GGCTCAGCTT CCTGGGACCA TGACTTTGGC TCAGCTGATC CTGNACATGG 360  
 50 GAGAACAACC ACATTTTCTT TTGTGTGTGC TTCTAGCAGC TGTTCGGGAG GACCKTGACC 420  
 CAAYAGTGT CCATGCTGT TTCTTGTAAT ATGCTCTCGG CTATGTAGCA GCTTTTGATT 480  
 CCTGCATAC CTTAGGCTGC TGCCCCATC CTGTCCCTTG TTTATAACAT TGAGAGGTTT 540  
 55 TCTAGGGCAC ATACTGAGTG AGAGCAGTGT TGAGAAGTCG GGGAAAATGG TGACTACTTT 600  
 TAGAGCAAGG CTGGGCATCA GCACCTGTCC AGCTCTACTT GTGTGATGTT TCAGGAACTC 660  
 60 AGCCCTTTT TCTGCCTAGG ATAAGGAGCT GAAAGATTAA CTTGGATCTY CTAATGGTCC 720



5 AAATCTTTTG GTCACAATAA AGAGTCTCCA AATTAGAGAC TGCATGTTAG TTCTGGATGG 780  
 APTTGGTGGC CTGACATGAT ACCCTGCCAG CTGTGAGGGG ACCCCGTTTT TAAGATGCAT 840  
 GGCCAAGCTC TCTGCAAATG GAAATGCTTA CACTGGGTGT TGGGGATGTT TGCTACCTCC 900  
 TGCTATTTTT GTGGTTTTGG TTCTCCCACT ATGCTAGGAC CCCTGGCCAG CATTGTGGCT 960  
 10 TGTGATGTCA GCCCCATTGA CTACCTTCTC ATGCTCTGAG GTACTACTGC CTCTGCAGCA 1020  
 CAAATTTCTA TTCTGTCAA TAAAGGAGA TGAAATATAA AAANAAAAA AAAAAACTCG 1080  
 NG 1082

20 (2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

30 CAAGCTGGTT TGAAACTAGG GGTGGGCTC GGCCGTCGTC GTTGTGTTGTC GCCGCATCCC 60  
 CGCTTCCGGG TTAGGCCGTT CCTGCCCCC CCCTCCTCTC CTCCTTTCGG ACCCATAGAT 120  
 CTCAGGCTCG GCTCCCCGCC CGCCGAGCC CACTGTTGAC CCGGCCCCGTA CTGCGGCCCC 180  
 35 GTGGCCACCA TGTCCCTGCA CGGCAAACGG AAGGAGATCT ACAAGTATGA AGCGCCCTGG 240  
 ACAGTCTACG CGATGAATG GAGTGTGCGG CCCGATAAGC GCTTTCGCTT GGCGCTGGGC 300  
 AGCTTCGTGG AGGAGTACAA CAACAAGGTT CAGCTTGTG GTTTAGATGA GGAGAGTTCA 360  
 40 GAGTTTATTT GCAGAAACAC CTTTGACCAC CCATACCCCA CCACAAAGCT CATGTGGATC 420  
 CCTGACACAA AAGGCGTCTA TCCAGACCTA CTGGCAACAA GCGGTGACTA TCTCCGTGTG 480  
 45 TGGAGGGTTG GTGAACAGA GACCAGGCTG GAGTGTGTC TAAACAATAA TAAGAACTCT 540  
 GATTCTGTG CTCCTTGAC CTCTTTGAC TGAATGAGG TGGATCCTTA TCTTTAGGT 600  
 ACCTCAAGCA TTGATACGAC ATGCACCATC TGGGGGCTGG AGACAGGGCA GGTGTTAGGG 660  
 50 CGAGTGAATC TCGTGTCTGG CCACGTGAAG ACCCAGCTGA TCGCCCATGA CAAAGAGGTC 720  
 TATGATATTG CATTTAGCCG GGCCGGGGT GGCAGGGACA TGTTCGCTC TGTGGGTGCT 780  
 55 GATGGCTCGG TCGGATGTT TGACCTCCGC CATCTAGAAC ACAGCACCAT CATTTACGAA 840  
 GACCCACAGC ATCACCCTACT GCTTCGCCTC TGCTGGAACA AGCAGGACCC TAACTACCTG 900  
 GCCACCATGG CCATGGATGG AATGGAGGTG GTGATTCTAG ATGTCCGGGT TCCTGCACAC 960  
 60

	CTGTSGCCAG GTTAAACAAC CATCGAGCAT GTGTCAATGG CATTGCTTGG GCCCCACATT	1020
	CATCCTGCCA CATCTGCACT GCAGCGGATG ACCACCAGGC TCTCATCTGG GACATCCAGC	1080
5	AAATGCCCCG AGCCATTGAG GACCCTATCC TGGCCTACAC AGCTGNAAGG WGAGATCAAC	1140
	AATGTGCAGT GGGCATCAAC TCAGCCCGAA YGTGCGCCAT CTGCTACAAC AACTGCCTGG	1200
	AGATACTCAG AGTGTAGTGT TGGTGGCGCT GTGCCCCACGA GGCAGGGGCT TTTGTATTTT	1260
10	CTGCCTCTGC CCCACCCCCA AAGTAAGAAG AAACATGTTT CCAGTGGCCA GTATGTCTTT	1320
	CATTGCTTTG CACCCACTGT TACCAGAAGC TGCTCTAGGA GTTCTTGCC AGTCACCCCA	1380
15	TCGCCCTCTG TGGCAGACTC AGTGCTGTGT GCGCCTCCT CAGCCAGGG CTGAGTTTAA	1440
	AGATTTTCTC TCCTTTCTC TTCTCCTTTG GTTCTCAAT TAAAAATGT GTGTATATTT	1500
	GTTTGTGAG CGTTGTGTG AGGAGCAGTT CACGCACTGG CTGTGTCTAT TCCTCTGCCC	1560
20	AGGTGTCTCT GTTTGCTGCC CAAKGYWKKT TTTCAATGCT CGTCCATGTC CATGTTCTGT	1620
	TTAGCACTWA CGTGGGAACA AATACCAATT TGTCTTTTCT CCTAGTATCA GTGTGTTTAA	1680
25	CAAATTTTAA CTTTGTATAT TTGTTATCTA TCAGGCTAAT TTTTTTATGA AAAGAATTTT	1740
	ACTCTCCTGC TTCATTTCTT TGTCTTATAG TCCTCCCTCT TTGCACCTTC TTCTCTTCCC	1800
	TCAGTGCTG GAGCTGGTAC TGGGCCCTG GCCCCATGAG CAGTTTGCCT TCTTGAGTCA	1860
30	CTGCCTGTGT AGTACATACC TGACCGGGAG TCCAAACCAC CTTGGTGCTC TGAAGTCCAC	1920
	TGACTCATCA CACCTTTCTT AGCCTGGCTC CTCTCAAGGG CATTCTGGGC TTGTAAACAG	1980
35	ACATAGGAAG CCTCTGTTTA CCCTGAAGCA CCACTGTCCA GCCCATTTGGT TCCCACTGGC	2040
	AGCATGGTAG AGCTGAGAGA AACAGGCTCT CAGGGTACCT GACTTGAGGG GAATCGTTTC	2100
	ATGAAGCTGA ACTTCAAGCA TATTTCCAGT ACATTCTTTC AGAGTCTGTT TTTCCATCCA	2160
40	AATATAAGCC CCAGGCCATT CCACCTAGTG TCTTTTCAAT GATAGGCAAG AATGATATCT	2220
	GAGTTGAACT TCGGTGCTTC TGTGTTTGA GTTTACTGTG CCTGGTGGTA TATTGGGCAT	2280
45	TCPTTGATT GAGTGTCTG AGGTGAGAGA GTCTTCCCGA GGCATCCTGT CTGTGCTTCC	2340
	AACCTGAAC AAGACCTTAC ATGAGAGATG GACTGATGGA CTGCGGCAAT CCTGGGCTGT	2400
	CAAGTGGATA GATAGTTAAA AAGCATTATA CTGTGGGTAA TGAAAAGGA GGAAAAAAA	2460
50	AGAAGGAAAA GGAATTATAG ACCCCAGGG TCAGCCAGTT AAGAGCTCTA CCCACACCTG	2520
	TCAACCCCTC TCTCCCCAG TTTAGTTCT GAGCAGTATT GGACTTGTAG CCTGCAGTTG	2580
55	TCTTTTGA CTGAGGCCGC AGTGTCTTTC TGTATGTGA ATGAGTTCCA TGGAGGGGCA	2640
	TATGTGTGAT TCCACCGTTA GATGAGCCCT TGGGGCAGGC AGTTTGGGAT GTGCTCTTGG	2700
60	GGGAAAGTTG GCTGTTTCT TCGCTCTGC TCCTACCCGA AGTTTAAAG TCCCTCTGAA	2760

	TTGCTCATCT GAGATTAGTA GAGTAGCAGG CCTGAAGGAT GATGGTTTGG TCCTCTTTGG	2820
	TTCTCACCTG CTTGAGAAGT AAAACAGTAA CTTTGTTCCT CTGGGCCCTT AAGCTTTTTT	2880
5	GGTTAAGTCT TCCTTTTCAG AAGTAGATGT CATTATATGC CAAAAGTCTA GCTCTTTGCT	2940
	TTACCATAACA GGGACCTGTC CCAAAGAAAA AGGCTCTTTT TTTAGCCAGC ATATTTCCCC	3000
	TTCTACCCCTT TTACTTTGTT GTTCTGATTT TAGGACTCTG GCTGGCCATG TGCTTGTTGGT	3060
10	TGCTCTCCTT GCATTTGCCA CTGGATTGTC ACTGCATCGT TTGGAGATAC AAAGCGAGCA	3120
	GTCTCTGGTC AGAACCTCC TCTGCTTTTC ATTGTGTTTG ATAATGGTTA CTGGGTCCTT	3180
15	CTCTCAAGGG TAGCAAGGCC AAGCTGATGG CTGCTGTGTT AGGAGGCCAT CAGTTCCTTC	3240
	CTGTGGAGAA GGGTCTGAAA TGGAAGTCAG TGGTAGAAGG GGCTGGTCTG CTGGGCAGGG	3300
	CTTACATCCA CTGAGTTCTA AGATTCCCTT CCTGATCTGC ACCTACGCCT GGTCTGTATG	3360
20	GTGGAATTTG TCAGCTGGAA CTCAGAAACA ACAACTTGAA AAAAAATAA TAATTAGAAC	3420
	ATATTGTCAT AAGATAGCTA TTTACTCTGG AAACCAACAA CTTTGTAGAT TTCCCTTGCC	3480
25	CTGTGGACGC CCAGCTCCTG TCATCCTTCC TTAGGTCCTG CAGTACAGTC TTCCCTGAA	3540
	TGCCACCGGG GACCCAGGGG GACTCCACCC CCTAAGCAA GCACACACAT ACTCACAGTT	3600
	GATGAGTTGC TGGTCTTTGA GTCCCAGTC TCTTACCCTC CCTTTACTCC ACCAGCCCGA	3660
30	CGACCCATGA CTGAGGAGGG GATTCTTACA GTCTCAGGAT TTAGAAAGTC TGTAAGCCAT	3720
	CCATGCTCCA GAAAGCACCG ATCTGTTGTA GTTGCAAAAA CAACTCTGTA ATTTGTTGAG	3780
35	GTCTCTAAAC TGACAGCCAG CGAGACTGGG TGGGAGGCC TGGATCTGTT CTCCCTGACT	3840
	GGGGGAGGAG CAGCCACTAG GACTTTAGCA GGAAGCCAC ATGGAGGCTC CGCCAGGCTG	3900
	TGGCCAGCT GGTGATGGCC CTTTGTCTCC TGGCAGCTG AGGCACAGCT GCCTGTATTG	3960
40	TCCTCATCTG TTCTGACTGA AGGATGGAGG TGCTGAATAA ATTAGGCCTC AGGCNTCTAC	4020
	CACCAGAGAG CTGGAGAATG GGTCCACGTC ATTCAAGGAC CTGAATTTTT TATGCTCAGG	4080
45	AGCATTGGAA TCCTCTTCTT CCAGGGAGGA ATTAGCCTGC AAGGTTAGGA CTTGAAGAGG	4140
	GAAGGTATTT AATAACTGGG CGAGGATGGG TGTGGTGGCT CACACCTGTA ATCCCAGCAT	4200
	TTTGGGAGGC TGAGGTGGCC AGATCCAAG GTCAGAAGAT CGAGACCATC CTGGCTAACA	4260
50	TGGTGAAACC CCATCTCTAC TAAAAATACA AAATTAAATT GGCCGGGCGT GAA	4313

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(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1183 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

5 GGCAGAGCCT CAAGCTGACT TGGATTATGT GGTCCCTCAA ATCTACCGAC ACATGCAGGA 60  
 GGAGTTCCGG GGCCGGTTAG AGAGGACCAA ATCTCAGGGT CCCCTGACTG TGGCTGCTTA 120  
 10 TCAKWWGGGG AGTGTCTACT CAGCTGCTAT GGTACAGGCC CTCACCCTGT TGGCCTTCCC 180  
 ACTTCTGCTG TTGCATGCGG AGCGCATCAG CCTGTGTGTC CTGCTTCTGT TTCTGCAGAG 240  
 CTTCTTCTC CTACATCTGC TTGCTGCTGG GATACCCGTC ACCACCCCTG GTCCTTTTAC 300  
 15 TGTGCCATGG CAGGCAGTCT CGGCTTGGGC CCTCATGGCC ACACAGACCT TCTACTCCAC 360  
 AGGCCACCAG CCTGTCTTTC CAGCCATCCA TTGGCATGCA GCCTTCGTGG GATTCCCAGA 420  
 20 GGGTCATGGC TCCTGTACTT GGCTGCCTGC TTGCTAGTG GGAGCCAACA CCTTTGCCTC 480  
 CCACCTCTC TTTGCAGTAG GTTGCCCACT GCTCCTGCTC TGGCCTTTC TGTGTGAGAG 540  
 TCAAGGCTG CGGAAGAGAC AGCAGCCCCC AGGGAATGAA GCTGATGCCA GAGTCAGACC 600  
 25 CGAGGAGGAA GAGGAGCCAC TGATGGAGAT GCGGCTCCGG GATGCGCCTC AGCACTTCTA 660  
 TGCAGCACTG CTGCAGCTGG GCCTCAAGTA CCTCTTTATC CTTGGTATTC AGATTCTGGC 720  
 30 CTGTGCCTTG GCAGCCTCCA TCCTTCGCAG GCATCTCATG GTCTGGAAAG TGTTTGCCCC 780  
 TAAGTTCATA TTTGAGGCTG TGGGCTTCAT TGTGAGCAGC GTGGGACTTC TCCTGGGCAT 840  
 AGCTTTGGTG ATGAGAGTGG ATGGTGCTGT GAGCTCCTGG TTCAGGCAGC TATTCTTGGC 900  
 35 CCAGCAGAGG TAGCCTAGTC TGTGATTACT GGCACCTGGC TACAGAGAGT GCTGGAGAAC 960  
 AGTGTAGCCT GGCCTGTACA GGTACTGGAT GATCTGCAAG ACAGGCTCAG CCATACTCTT 1020  
 40 ACTATCATGC AGCCAGGGGC CGCTGACATC TANGACTTCA TTATTWATR ATTCAGGACC 1080  
 ACAGTGGAGT ATGATCCCTA ACTCCTGATT TGGATGCATC TGAGGGACAA GGGGKCGGT 1140  
 45 STCCGAAGTG GAATAAAATA GGCGGGCGTG GTGACTTGCA CCT 1183

(2) INFORMATION FOR SEQ ID NO: 148:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 734 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

60 GAATTCGGCA GAGTGAAGCA TTAGAATGAT TCCAACACTG CTCTTCTGCA CCATGAGACC 60

AATCCAGGGC AAGATCCCAT CCCATCACAT CAGCCTACCT CCCTCCTGGC TGCTGGCCAK 120  
 GATGTCGCCA GCATTACCTT CCACTGCCTT TCTCCCTGGG AAGCAGCACA GCTGAGACTG 180  
 5 GGCACCAGGC CACCTCTGTT GGGACCCACA GGAAAGAGTG TGGCAGCAAC TGCMTGGCTG 240  
 ACCTTTCTAT CTTCTCTAGG CTCAGGTACT GCTCCTCCAT GCCCATGGYT GGGCCGTGGG 300  
 GAGAAGAAGC TCTCATACGC CTTCCCACTC CCTCTGGTTT ATAGGACTTC ACTCCCTAGC 360  
 10 CAACAGGAGA GGAGGCCTCC TGGGGTTTCC CCRRGGCAGT AGGTCAAACG ACCTCATCAC 420  
 AGTCTTCCTT CCTCTTCAAG CGTTTCATGT TGAACACAGC TCTCTCCRCT CCCTTGTGAT 480  
 15 TTCTGAGGGT CACCACTGCC ARCCTCAGGC AACATAGAGA GCCTCCTGTT CTTTCTATGC 540  
 TTGGTCTGAC TGAGCCTAAA GTTGAGAAAA TGGGTGCCAA GGCCAGTGCC AGTGTCTTGG 600  
 GGCCCTTTTG GCTCTCCCTC ACTCTCTGAG GCTCCAGCTG GTCCCTGGGAC ATGCAGCCAG 660  
 20 GACTGTGAGT CTGGGCASGT CCAAGGCCTG CACCTTCAAG AAGTGAATA AATGTGGCCT 720  
 TTGCTTCTAT TTAA 734

25

(2) INFORMATION FOR SEQ ID NO: 149:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GGCACAGTGG ACCCCAGACT CCCTCTCCGC CTTTCTCTGC CTGGGGAGAC CCACTGTGTG 60  
 40 CATGGCATCA CTGACTCCCA TACCTCTGGC TATCAAAGGT TTCTGCCATG GCCACCCTGG 120  
 AAGSAAACCA GAGGGAGGTA GACAGGGAGA TCAGGTCCCT TCTACTCTGG TTCCTGCTCT 180  
 GTGAAATTGT CTCAGGCTGG CTGTGTCCAG ARGGTCCCTG GTTCTCTCAR GGATGCCAAA 240  
 45 TCTACAAGAA TCTCTCCTCT TCCAGTTCCT ATAACCTCTC CTTCTTTTGG TCTCTTTAGA 300  
 CCTTGGAGTA GTAGCAGCCA GGTTCCTTCT ATCTCTGGGT TAGTGCAATTA TCTCTGGTGG 360  
 50 CTCCCTTACC CAGGACTTTG GGAATGGTCT TTTTGTAAATA CATCTCCTC AAATAATTCA 420  
 ATTTTGAGTG TTCTGTATGT ATCTGTCTGG GAGGTGTGTA TATACAAATC ACTGTGCCCC 480  
 TTTAGCAGAG AAGGAGACTG AAGCTCAGGG AGGTAAAGTG TCTTTCTCTA GGTGTAATTG 540  
 55 TGGAGAAAGT GGCTGACTGG GGAATTGAAT GAGGTCCCTA GTTTCATGCT CGGAGGGCAA 600  
 AGANGAATGT CCAATTGGCC TGAGATAAGC CTCTGGTAAA ATGTACTGTA CATAATAGGT 660  
 60 AATCAATAAA TGTTGGCTGA TGACAAACAT GTTTTCTTTG TTCATTAGTT ATAGTGATTA 720

	TGTTCTAAAT AACTCCMACA AGGAARTCAG CACATTTGGA ATATCAWTAT CTTTCCATGA	780
	TAATATCTTT CCMYGGAAAG AWAATGATAT TCCMAACTGG GAGTGTCCCW AGCARATCTG	840
5	ANTCTGTGTA TTGGCCCTGG GGTGGGCCAG CCCCTTAGAC TCTATGGTCT CATCTCTTT	900
	GTTTACAAAA TTGAGATAAG GCCTTATTCT CTCCCCACCC CACCCATCCA TATTGTTTIG	960
10	AGAATAAAAT GAGAGGATGT GTGTCAAGGG TGTATTTTGG CAATAGTCTC TGAGCCATTT	1020
	TCTGAGCACC TCCATACTGT TGACACTCAA GTAATATTTC ATCAGCATTC CATTCAAGNT	1080
	CCTCCCTTAA TGAGGTGTGC GATGTACAAG AGTYGTGAGG TGGCAAAGGA TGGGCTCCTG	1140
15	AGGAAACACT TAGGAAACTG GGCTTTCTGC CATTAAAAGA GACAAACCTT TGTGGTGACC	1200
	TAATTAAAGT TTTTAAATTT CAATTTGGAA AGTTAGCAAG CTAGCTCCTK TCCAGGWAAA	1260
20	ATAAGGAGTC AGTGCATGAC CTAACCGGTC CCGGGCTGCT TGCCATTCCA AACAACTGCA	1320
	GTAAGTTTAT CACNTTCTTT CAGGGACTGA GGTTCACAG CACAGACTTG GATAAGGAAG	1380
25	GATGTCCTAT GGGGTCACAT TGATG	1405

## (2) INFORMATION FOR SEQ ID NO: 150:

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## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2890 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

	TTATATGCTA CAGCTACAGT AATTCTTCT CCAAGCACAG AGGANCTTTC CCAGGATCAG	60
40	GGGGATCGCG CGTCACTTGA TGCTGCTGAC AGTGGTCGTG GGAGCTGGAC GTCATGCTCA	120
	AGTGGCTCCC ATGATAATAT ACAGACGATC CAGCACCAGA GAAGCTGGGA GACTCTTCCA	180
45	TTCGGGCATA CTCACTTGA TTATTCAGGG GATCCTGCAG GTTTATGGGC ATCAAGCAGC	240
	CATATGGACC AAATTATGTT TTCTGATCAT AGCACAAAGT ATAACAGGCA AAATCAAAGT	300
	AGAGAGAGCC TTGAACAAGC CCAGTCCCGA GCAAGCTGGG CGTCTTCCAC AGGTTACTGG	360
50	GGAGAAGACT CAGAAGGTGA CACAGGCACA ATAAAGCGGA GGGGTGGAAA GGATGTTTCC	420
	ATTGAAGCCG AAAGCAGTAG CCTAACGTCT GTGACTACGG AAGAAACCAA GCCTGTCCCC	480
55	ATGCCTGCCC ACATAGCTGT GGCATCAAGT ACTACAAAGG GGCTCATTGC ACGAAAGGAG	540
	GGCAGGTATC GAGAGCCCCC GCCCACCCTT CCCGGCTACA TTGGAATTCC CATTACTGAC	600
60	TTTCCAGAAG GGCACCTCCA TCCAGCCAGG AAACCGCCGG ACTACAACGT GGCCCTTCAG	660

	AGATCGCGGA TGGTCGCACG ATCCTCCGAC ACAGCTGGGC CTTTCATCCGT ACAGCAGCCA	720
	CATGGGCATC CCACCAGCAG CAGGCCTGTG AACAAACCTC AGTGGCATAA AYCGAACGAG	780
5	TC TGACCCGC GCCTCGCCCC YTATCAGTCC CAAGGGTTTT CCACCGAGGA GGATGAAGAT	840
	GAACAAGTTT CTGCTGTTTG AGGCACAGAC TTTTCTGGAA GCAGAGCGAG CCACCTGAAA	900
	GGAGAGCACA AGAAGACGTC CTGAGCATTG GAGCCTTGA ACTCACATTC TGAGGACGGT	960
10	GGACCAGTTT GCCTCCTTCC CTGCCTTAA AGCAGCATGG GGSTTCTTCT CCCCTTCTTC	1020
	CTTTCCTTCT TGCACTGTGAA ATACTGTGAA GAAATTGCCC TGGCACTTTT CAGACTTTGT	1080
15	TGCTTGAAAT GCACAGTGCA GCAATCTTCG AGCTCCCACT GTTGCTGCCT GCCACATCAC	1140
	ACAGTATCAT TCCAAATTCC AAGATCATCA CAACAAGATG ATTCACTCTG GCTGCACTTC	1200
	TCAATGCCTG GAAGGATTTT TTTTAATCTT CCTTTTAGAT TTCAATCCAG TCCTAGCACT	1260
20	TGATCTCATT GGGATAATGA GAAAAGCTAG CCATTGAACT ACTTGGGGCC TTTAACCCAC	1320
	CAAGGAAGAC AAAGAAAAC AATGAAATCC TTTGAGTACA GTGCTTGTC ACTTGTTTAC	1380
25	AATGTCCTCC TTTTAAAAA AAAAAATGA GTTTAAAGAT TTTGTTTACA GAGTAAATAT	1440
	ATATCCATT AATGATTACA GTATTATTTT AAACCTTAAG TAGGGTTGCC AGCCTGGTTT	1500
	CTGAAAACC AAATATGCCG GACAGGGTGT GGCCACACCA AGAAGACGGG AAGACCTGGC	1560
30	TTGTGACCCT GGCTTCCCAT GTCTTCTGG TCTCAGCCGC GAAGTGCCCT ATCCTGGAAG	1620
	TATGAAATGT TAGCCAATTA ATACCAAGAC ACCTCATCTG CTCCTTCCCC AGTGGATGGG	1680
35	GTTCTTCTGT AAAACTGTTT GCACATGGCC AGGGGAGGGA ACTAGGACCC TTGTGTCCTG	1740
	TCTGAGCCTT ATGGAGGCAG GACGGTGTCA TTGGCGGATG TGTCTGCTC CATGAGATG	1800
	GATGGCAAAC CCCATTTTTA AGTTATATTT CTTTGATTTT TGTTAATTTA GAGGTGTAGG	1860
40	TTTTGTTTTT TGTTTTTTTG TTTTTTTTTA AGAGAAACAT TTATAACTGG ATAGCATGCG	1920
	AGTGAAAGCA GCTTGGGATG TTGGAGCTAA TGCCAGCTGT TTATACTGCT CTTTCAAGAC	1980
45	AGCCTCCCTT TATGAAATG GCATTAGGGA ATAAACAAGC CTTTAAACGT GATAAAAGAT	2040
	CAAAAACCTG GTTAGACATG CCAGCCTTTG CAAGGCAGGT TAGTCACCAA AGACTAACCT	2100
	CCAAGTGGCT TTATGGACGC TGCATATAGA GAAGGCCTAA GTGTAGCAAC CATCTGCTCA	2160
50	CAGCTGCTAT TAACCTATA ATGACTGAAA TGACCCCTCC ACTCTATTTT TGTGTTGTTT	2220
	TGCACAGACT CCGGAAAAGT GAAGGCTGCC AATCTGAGTA GACTCAAAAT GTGAGGAACT	2280
55	GCTGGTCTTG GATTTTTTTT CCATTAAAT CAGCTGATCA TATTGATCAG TAGATAAAG	2340
	TAAATAGCTT CAAATTTTAA AAGTGGAATT GCAGTGTTTT TCACTGTAT CAAACAATGT	2400
60	CAGTGCTTTA TTAAATAATT CTCTTCTGTA TCATGGCATT TGTCTACTTG CTTATTACAT	2460

5 TGCAATTAT GCATTTGTAA TTTTACATGT AATATGCATT ATTTGCCAGT TTTATTATAT 2520  
 AGGCTATGGA CCTCATGTGC ATATAGAAAG ACAGAAATCT AGCTCTACCA CAAGTGCAC. 2580  
 10 AAATGTTATC TAAGCATTAA GTAATTGTAG AACATAGGAC TGCTAATCTC AGTTCGCTCT 2640  
 GTGATGTCAA GTGCAGAATG TACAATTAAC TGGTGATTTC CTCATACTTT TGATACTACT 2700  
 TGTACCTGTA TGTCTTTTAG AAAGACATTG GTGGAGTCTG TATCCCTTTT GTATTTTAA 2760  
 15 TACAATAATT GTACATATTG GTTATATTTT TGTGAAGAT GGTAGAAATG TACTATGTTT 2820  
 ATGCTTCTAC ATCCAGTTTG TACAAGCTGG AAAATAAATA AATATAACAT AAAAAAAAAA 2880  
 20 AAAAAAAAAA 2890

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

30 GAACCTTTCC ATCTGGCAA CCGGAACTC CATCCCCATT AAACCAACTC CCCCTTTTGG 60  
 TTTCCCCCCC AGNGGAATAG AATTTGGACN CCCATATAAA TCCAGGAAAC CACCTAAATT 120  
 CTTTAGTNGT TTGTGTTTGC AAGATCTAAG GTCATGGTAA ACATTAAGTT CTTAAATTTT 180  
 35 TTGGGAGGGA CCAAGTCACC TCTCCCTCTG AATTGTTTCNC CAATTTAAAA TTGGAGTAAG 240  
 GTTTTAAAAA GTCTNATTCC ATTGGAAGGG TNGTATTATT CATTTTGAGC CCAGAGGGGA 300  
 40 GAGGCACATT TTAAATATCA GAATTAGATT AGCTTTGAGT TTGTACAATT GGGAACATAA 360  
 TAGAATTTCA TAAATTATGT GTGCCTTGTT GGAAGTGCA ACTGCTTTA TGTCTGCTTG 420  
 TAAAAGTTTC AAAATATGTT TTCCTCAAA AAGGCAACGT TACTTCATTT GCTTGAATAT 480  
 45 TATGATAGGA ATGCTTACTG ATATTACTTG ATAGTCATAT ATAGCCTAGG AAATTTAACA 540  
 TATATATAAC TATAGCAGTA TTAATAATGA TAGTTGTACT TCTTTAAAAC ATTAAATTTG 600  
 50 AGGAAACTTT AATGCTGTCT CGTGACATT GCTTTACTAC AGTGAGGGGG AATATCCTTT 660  
 AGATTGAGCC TCAATTTACT GGTAGTAGT ATGTGAATC TGGTATAAAA ACGTAAACTA 720  
 GACAGTAGAG CCGATGAATT AAAATTGTAA ATTGCTACAT TGGCATTTTC TACCTCCTTT 780  
 55 TCTGTCAGAG TATTACTTTT TCCAGCATTT ATTCTTATTT GTGAGTAAAG AGGAAATGGG 840  
 AACCTGAGGT TAAAATGAC ATTTTGTGTT CATTGAGAAT TTAAGCAGTA GGTACAGGAG 900  
 60 AAGTGACTTG TCACATTAAT TTGGTGCCTA AATCTGTAAC TACAAGTTGT GATCGACATG 960



	TACAAAATGT CTAAGAAAGG TCATATGCTG AATATTTTAC TTTCCTGTA TAGTCTGCAT	1020
5	GATTTGTTTC ATAAACCCAG CTTATTTTCT CCAAAAAGCA AAATGGTCCT GTAATTTTTA	1080
	AAGTAAAATA AACGTGCCAT TTTGTCTGCA ATCTATAATT TCAGGAAGTT ATTGRAAGTT	1140
	CTGACTCAGG GCTTTTAAAC AGTTCAAGCA ATTGTCAGTT ATATTTTGGG AACTCCATCT	1200
10	GTGTAATTCT CCAGTGCCTT GAAAGAATTA TTAAGTTGGC AACACTATTA AAACTTTATA	1260
	AAAGATGGTC TTTAGTGCAC GTGTATCATT ATATACACGT TTTAAAGTCA TATTGCTTAG	1320
15	CTTGTAATA ATGATTCTGC ATGTGTGCTG GGTTCGGTA ATTCTTTAAA GGAAGTTTTC	1380
	TAGATTGCA CTTGATGTTT GTTTTTTAAA AACTGATTAT TTATGGCCGT GACACTGTTA	1440
	CCAGAAAAGT AATTCTAATT AAGTTATTAT GCAAAGTCAT CTATAAGTAG CATCTGGGAA	1500
20	GAGGAGATSG AGGCCACAGT TTGCTATTTT AGTATGAAAG GAGGATCTGT TTGGGAAACA	1560
	TAGATTGTCT TCCCCTCAAA TGAGGGGAAA AAAAAAGACC CTTTGTTCAG ATGGATTCTG	1620
25	TTGTAAAAA TTATTTTAA AGGAAATCAC AAATTGTATG TCATTCTTAA TGCTAGTCTT	1680
	ATAGAATAAA TCCATAAAAT TGTTTTATG TTCAGTATGT TTATGTCATT CTAAATGCAG	1740
	CAAATTCAAT GATAGCAGTT CAATTGACTC ATAGCAGTGT TTTGTATTTT TTCTAATTCT	1800
30	TTAGCTTTCA ATATTGGATT AAAGTCTTGT TTGTGAATAT AGTTTCCGTA TGGCAAATGA	1860
	TTTCTTGCTT ATTAGCTTTT GTTAAAGAAT GCTTAGTAAG AGCTAAGCTT TTAAAAGTAA	1920
35	TGCAAACATT TATCGTTAAT AAAACCTATG GTGTAATATC ATATAATGCT TTTCTTTGAT	1980
	CTTTGGAGAA TTATCTTTTT ATAGTAGTAT ACATGAATTT TGATTTTAA AGCATTTAAA	2040
	AACAAATCTC AATACATTAA AAAACCTGTT ATTGTTAAAA RGGAAATTAC CATGCCTTTA	2100
40	AGAAACAAGG ATGTACATCT TCAATTCAGC ATRAGTGTC ACATCTAGAA GGCTCTCATT	2160
	GCAGTTGTTT ACAGTTAAGG TACCTCTATC TAAAGGGCCA AAGAAGCATT TCATAYTTTA	2220
45	ACACCTCACA TTCTTTCAGG ATTAAGACAT ATGAAAATAG TCTGAATAGG ATAAATTTGG	2280
	ATAGGAAGTA ACTTAACCAG TCTGGGAAGA TTCAGGCTTT TTCTATKAAA AAGCTTATTC	2340
50	CTCTTCACAA CTCNGGTGGT AGGNTTTCAT TTTTCAAGAG GSTAGATATT TTAAAGCCA	2399

(2) INFORMATION FOR SEQ ID NO: 152:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 802 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

	CGTGCCTGTA GTAAGCTCAT CCCTGCCTTT GAGATGGTGA TCGTGCCAA GGACAATGTT	60
5	TACCACCTGG ACTGCTTTC ATGTCAGCTT TGTAATCAGA GATTNTGTGT TGGAGACAAA	120
	TTTTTCCTAA AGAATAACWT GAYCCTTTGC CARACGGACT ACGAGGAAGG TTTAATGAAA	180
	GAAGGTTATG CACCCCMGGT TCGCTGATCT ATCAACATCA CCCCATTAAG AATACAAAGC	240
10	ACTACATTCT TTTATCTTTT TTGCTCCACA TGTACATAAG AATTGACACA GGAACCTACT	300
	GAATAGCGTA GATATAGGAA GGCAGGATGG TTATATGGAA TAAAAGGCGG ACTGCATCTG	360
15	TATGTAGTGA AATTGCCCCA GTTCAGAGTT GAATGTTTAT TATTAAAGAA AAAAGTAATG	420
	TACATATGGC TGGATTTTTT TGCTTGCTAT TCGTTTTTGT GTCACCTGGC ATGAGATGTT	480
	TATTTTGGAC TATTGTATAT AATGTATTGT AATATTTGAA GCACAAATGT AATACAGTTT	540
20	TATTGTGTTA CCATTGTGT TCCATTGCT YCTTGTATT GTTGCATTTA GTACAATCAG	600
	TGTTTAAACT TACTGTATAT TTATGCTTTC TGTATTTACC AGCTATTTTA AATGAGCTGT	660
25	AACTTTCTAG TAAAGAATG AAAAGCAAAT CCTCACTAAA GGATACACAG GATAGGATAA	720
	AGCCAAGTCN CATCAACATT AAAAAATACT AAAANANAAA ACACAAAAAA AAAAAANCCC	780
30	GGGGGGGGCC CGGAACCCAT TC	802

## (2) INFORMATION FOR SEQ ID NO: 153:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: -461 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

45	CTAGGAGCAC CGAGCAGCTT GGCTAAAAGT AAGGGTGTG TGCTGATGGC CCTGTGCGCA	60
	CTGACCCGCG CTCTGCNCTC TCTGAACCTG GCGCCCCCGA CCGTCGCCGC CCCTGCCCCG	120
	AGTCTGTTCC CCGCCGCCCA GATGATGAAC AATGGCCTCC TCCAACAGCC CTCTGCCTTG	180
50	ATGTTGCTCC CCTGCCGCC AGTTCTTACT TCTGTGGCCC TTAATGCCAA CTTTGTGTCC	240
	TGGAAGAGTC GTACCAAGTA CACCATTACA CCAGTGAAGA TGAGGAAGTC TGGGGGCCGA	300
	GACCACACAG GTGGGAACAA GGACAGGGGG ATTTAAGCAG TCAAAGGAA AAACATGTTA	360
55	AGACCCTAGA CTTGTATATT GACACACTTG TACCTTGTA GGCAGAGGAA TGTAATTAAA	420
	AAGCACTTAT TTGGCWNAAA AAAAAAAAAA AAAAAAAAAA C	461

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## (2) INFORMATION FOR SEQ ID NO: 154:

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## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2388 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

	CCCCACGCGT CCGAAAGCGG AGAACGCTGG TGGGCCTGTT GTGGAGTACG CTTTGGACTG	60
15	AGAAGCATCG AGGCTATAGG ACGCAGCTGT TGCCATGACG GCCCAGGGGG GCTGGTGGCT	120
	AACCGAGGCC GGCCTTCAA GTGGCCATT GAGCTAAGCG GGCCTGGAGG AGGCAGCAGG	180
20	GGTCGAAGTG ACCGGGGCAG TGGCCAGGGA GACTCGCTCT ACCCAGTCGG TTAATTGGAC	240
	AAGCAAGTGC CTGATACCAG CGTGCAAGAG ACAGACCGGA TCCTGGTGA GAAGCGCTGC	300
	TGGGACATCG CCTTGGGTCC CCTCAAACAG ATTCCCATGA ATCTCTTCAT CATGTACATG	360
25	GCAGGCAATA CTATCTCCAT CTCCCTACT ATGATGGTGT GTATGATGGC CTGGCGACCC	420
	ATTCAGGCAC TTATGGCCAT TTCAGCCACT TTCAAGATGT TAGAAAGTTC AAGCCAGAAG	480
30	TTTCTTCAGG GTTGGTCTA TCTCATTGGG AACCTGATGG GTTTGGCATT GGCTGTTTAC	540
	AAGTGCCAGT CCATGGGACT GTTACCTACA CATGCATCGG ATTGGTTAGC CTTCAATTGAG	600
	CCCCCTGAGA GAATGGAGTT CAGTGGTGA GGACTGCTTT TGTGAACATG AGAAAGCAGC	660
35	GCCTGGTCCC TATGTATTTG GGTCTTATTT ACATCCTTCT TTAAGCCCAG TGGCTCCTCA	720
	GCATACTCTT AAACATAACA CTTATGTTAA AAAGAACCAA AAGACTCTTT TCTCCATGGT	780
40	GGGGTGACAG GTCCTAGAAG GACAATGTGC ATATTACGAC AAACACAAAG AAATATACC	840
	ATAACCCAAG GCTGAAAATA ATGTAGAAAA CTTTATTTTT GTTCCAGTA CAGAGCAAAA	900
	CAACAACAAA AAACATAAC TATGTAAACA AGAGAATAAC TGCTGCTAAA TCAAGAACTG	960
45	TTGCAGCATC TCCTTTCAAT AAATTAAATG GTTGAGAACA ATGCATAAAA AAAGTTGCAC	1020
	AAGTTCCTTA TTTTCCTTAA TATTTCATT CTATTTAATA CAAGCTGGGA CATAAAAATT	1080
50	CTGTTGGGGA TACCTGGGGG AAGATGTGAG AAATAATGC TGAATTCAGC TTATACATGA	1140
	TGAAAAGAAA AACCAGACAA AAGGAGCACA TAAATATGCA TACAGTGTA CTGTTATTAT	1200
	TTTAATACCC ACGATAAGGG ATTTTGTGTA GCATGTTTAG GGGGAACGAG GATTGGTGGG	1260
55	ATCCTTGGGG CCACAGGAAT CTGAGGCAAC GGAAGATATA TAGAGTGATC GTCCCCCTGC	1320
	CGAAGGAACC TGGCAYCTGT CAAGCAGATG CTGCAGTTCA AACTTCAGCT TTAAAGATAG	1380
60	ATAGCTATTG AAGGCAGAGG GTCAGCAGGA GGATGTGTAT TTCTAATCTA CCCTGGTAAA	1440

	GTCATAGGTA AGACTCAAAA GCGGGATCCTT ATTCAAAAGG CAGGTATTTT CTTTGTTC	1500
	TGTCTTGAAA TAGCCCCTTC CCCTAAGGTG CATTCTCTCA AGTTTTTCAGT ATTGCTTTAT	1560
5	TTGCAGTGAT TAAAGAGAT GAGAGACTTT GGAGACAGAC AACGTAAGCA ACACATACAC	1620
	ACATGAAATA CTCTAGACAG AGATGAATAT AAATCTGGCC TAATAACCAG TTTTCCATGT	1680
	AACAGTGATT TTGTGTTTCG GGCTGAAGCA GTGGTTATAT TAAAGCCAC TAATTCCTT	1740
10	ATCCCTTTAA AAGATTTTAA CAATTCTCCA ACCACAAACA GCACTTCTAA AACTAATTT	1800
	ACTTCTGCC CATAATTTGT TCTACATGGA AAAAAAAT ATTACTTTGG CCAGGGGTGT	1860
15	GTGTAAATGT GGCAGAATTC CTAGGCAGGC TGACCTTTAC AGTATGGGCC TTTAAGATAC	1920
	TGGATCCTGG TTGGGCAACA AGTGTACGC CTGAAGTTTC TGAAAACAAA TTAGAAGACT	1980
	GTTGGCTTGG CTAATCTCGT AGTTCAGGGC CAAGTTTCTG TAGTCAGAAT GAAGAATAAA	2040
20	ATTGAAAGAA AAAGGGGAA ATGCTTATAC TTGGCATTAA GTTGAATGCC TCAAGTCTTA	2100
	ACTATGGCTT TGTAGATGAG GCAAAAGATT TCTTAGTGGT AAAATTTCTT CAACAGGTCA	2160
25	ATGCCAATCT GTATGCCATT TTAGTAAAGT AGGTAAGGAG AGTAGCCGCT CAGTAACTTT	2220
	GGCACTAAAG AAAGAGTGTG GCTCTAGAAC TTCCAATCCC ATTGCTAGAT GTGCCCTTTA	2280
	AAAGATGGTC CAGTGCTTTC AGGGAAGGAT GTTTAGCCAG TTTTCCTAGT ATTTGTTCCT	2340
30	TAAGATTTTT TGACCTGTGC TTAATAAGAC GGACGCGTGG GTCGACCC	2388

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(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 642 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

45

	AAAACAGACC ATTTAAAAAC TCAGACAAGA TTATATTAA TATATTAATT ACTAAAAAGG	60
	CACAAGATTA CACTGAACAT ATTAGCTACT AAAAAGGCAC TGCTAAGACA TTCAAGCAAA	120
50	TAGCTATTAC ACACTACTGC AGATTTTACA GGTTCCTAAT TCTAACATAT GTTTGAAAAA	180
	TCCGTGAGTA TTCCAAAATA TATTTAATAA TGAATATCT GCATTAATAT ACCATCCATG	240
	TGTTTTTACC ATTTGCCTTA ATATTGAATA TACTGTTTAC CTCACACTAA AAAGAAAACC	300
55	AGAAGCCTTA TTTGTGATTT TGGGAGTGGG AGCTTCCATT TTTGTGTCAA AAATGAATCC	360
	TGATTCTTAT GGAAATCTCT GTTATTAAGA TATTTCAGA TGAGACAACA CTGAAGATCA	420
60	AATTGTGTTT AGTATCACTA TCTTCTCTCC TCGTTTCTCT CTTACTCCTC ATCCTCCAG	480

5 AATCTACCAG TTTATGGTAG AAAGATGGGA ACCTTATTG AATGTGTTTT TTTTTTCCA 540  
TGATGTCCAA TTTTGTGTG GGAAGGATT TGGATAAAAT TTTGTTTAA ATTTTGGTAG 600  
ATTTTTATCT ATACAAATTT AAATAAAATT ATGTTTTGTA AG 642

10

(2) INFORMATION FOR SEQ ID NO: 156:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

20 GCCGCTGCCC CTCCACGGAG TTGCTGATCA TCTGGGCTGT GATCCACAAA CCCGGTCTTT 60  
TGTCCTCCT AATATCAAAC AGTGGATTGC CTTGCTGCAG AGGGGAACT GCACGTTTAA 120  
25 AGAGAAAATA TCACGGGCCG CTTTCCACAA TGCAGTTGCT GTAGTCATCT ACAATAATAA 180  
ATCCAAAGAG GAGCCAGTTA CCATGACTCA TCCAGGCACT GAGCATATTA TTGCTGTCAT 240  
GATAACAGAA TTGAGGGGTA AGGATATTTT GAGTTATCTG GAGAAAAACA TCTCTGTACA 300  
30 AATGACAATA GCTGTTGGAA CTCGAATGCC ACCGAAGAAC TTCAGCCGTG GCTCTCTAGT 360  
CTTCGTGTCA ATATCCTTTA TTGTTTGTAT GATTATTTCT TCAGCATGGC TCATATTCTA 420  
35 CTTCAATCAG AAGATCAGGT ACACAAATGC ACGCGACAGG AACCAGCGTC GTCTCGGAGA 480  
TGCAGCCAAG AAAGCCATCA GTAAATTGAC AACCAGGACA GTAAAGAAGG GTGACAAGGA 540  
AACTGACCCA GACTTTGATC ATTGTGCAGT CTGCATAGAG AGCTATAAGC AGAATGATGT 600  
40 CGTCCGAATT CTCCCCTGCA AGCATGTTTT CCACAAATCC TCGGTGGATC CCTGGCTTAG 660  
TGAACATTGT ACCTGTCTTA TGTGCAAACT TAATATATTG AAGGCCCTGG GAATTGTGCC 720  
45 GAATTGCCA TGTACTGATA ACGTAGCATT CGATATGGAA AGGCTCACCA GAACCCAAGC 780  
TGTTAACCGA AGATCAGCCC TCGGCGACCT CGCCGCGAC AACTCCCTTG GCCTTGAGCC 840  
ACTTCGAACT TCGGGGATCT CACCTCTTCC TCAGGATGGG GAGCTCACTC CGAGAACAGG 900  
50 AGAAATCAAC ATTGCAGTAA CAAAAGAATG GTTTATTATT GCCAGTTTTG GCCTCCTCAG 960  
TGCCCTCACA CTCTGCTACA TGATCATCAG AGCCACAGCT AGCTTGAATG CTAATGAGGT 1020  
55 AGAATGGTTT TGAAGAAGAA AAAACCTGCT TTCTGACTGA TTTTGCCCTG AAGGAAAAAA 1080  
GAACCTATTT TTGTGCATCA TTTACCAATC ATGCCACACA AGCATTTATT TTTAGTACAT 1140  
TTTATTTTTT CATAAAATG CTAATGCCAA AGCTTTGTAT TAAAAGAAAT AAATAATAAA 1200  
60

ATAAAAAAAAA AAAAACCCCG GGGGGGGCCC GGTCCCAAT TGGCCCTATG G

1251

5

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 2127 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

15

CCGGCGGGAG AGGGAAGCTG CAGCGAGAGG CGCGGATCTC AGCGCGGGAG CAGTGCTTCT 60

GCGGCAGGCC CCTGAGGGAG GGAGCTGTCA GCCAGGGAAA ACCGAGAACA CCATCACCAT 120

20

GACAACCACT CACCAGCCTC AGGACAGATA CAAAGCTGTC TGGCTTATCT TCTTCATGCT 180

GGGTCTGGGA ACGCTGCTCC CGTGAATT TTTTCATGACG GCCACTCAGT ATTTACAAAA 240

25

CCGCCTGGAC ATGTCCAGA ATGTGTCCTT GGTCAGTCT GAACTGAGCA AGGACGCCCA 300

GGCGTCAGCG CNCCCTGCAG CACCCTTGCC TGAGCGGAAC TCTCTCAGTG CCATCTTCAA 360

CAATGTCATG ACCCTATGTG CCATGCTGCC CTTGCTGTTA TTCACCTACC TCAACTCCTT 420

30

CCTGCATCAG AGGATCCCC AGTCCGTACG GATCCTGGGC AGCCTGGTGG CCATCCTGCT 480

GGTGTTCCTG ATCACTGCCA TCCTGGTGAA GGTGCAGCTG GATGCTCTGC CCTTCTTTGT 540

35

CATCACCATG ATCAAGATCG TGCTCATTA TTTATTGGT GCCATCCTGC AGGGCAGCCT 600

GTTTGGTCTG GCTGGCCTTC TGCCTGCCAG CTRACACGGC CCCCATCATG AGTGGCCAGG 660

GCCTAGCAGG CTCTTTTGCC TCCGTGGCCA TGATCTGCGC TATTGCCAGT GGCTCGGAGC 720

40

TATCAGAAAG TGCCTTCGGC TACTTTATCA CAGCCTGTGC TGTKATCATT TTGACCATCA 780

TCTGTTACCT GGGCCTGCCC CGCCTGGAAT TCTACCGCTA CTACCAGCAG CTCAAGCTTG 840

45

AAGGACCCCG GGAGCAGGAG ACCAAGTTGG ACCTCATTAG CAAAGGAGAG GAGCCAAGAG 900

CAGGCAAAGA GGAATCTGGA GTTTCAGTCT CCAACTCTCA GCCCACCAT GAAAGCCACT 960

CTATCAAAGC CATCCTGAAA AATATCTCAG TCCTGGCTTT CTCTGTCTGC TTCATCTTCA 1020

50

CTATCACCAT TGGGATGTTT CCAGCCGTGA CTGTTGAGGT CAAGTCCAGC ATCGCAGGCA 1080

GCAGCACCTG GGAACGTTAC TTCATTCTCT TGTCCTGTTT CTTGACTTTC AATATCTTTG 1140

55

ACTGGTGGG CCGGAGCCTC ACAGCTGTAT TCATGTGGCC TGGGAAGGAC AGCCGCTGGC 1200

TGCCAAGCTG GNTGCTGGCC CGGCTGGTGT TTGTGCCACT GCTGCTGCTG TGCAACATTA 1260

AGCCCCGCCG CTACCTGACT GTGGTCTTCG AGCAGGATGC CTGGTTCATC TTCTTCATGG 1320

60

CTGCCTTTGC CTCTCCAAC GGCTACCTCG CCAGCCTCTG CATGTGCTTC GGGCCCAAGA 1380

AAGTGAAGCC AGCTGAGGCA GAGACCGCAG AGCCATCATG GCCTTCTTCC TGTGTCTGGG 1440  
 TCTGGCACTG GGGGCTGTTT TCTCCTTCCT GTTCCGGGCA ATTGTGTGAC AAAGGATGGA 1500  
 5 CAGAAGGACT GCCTGCCTCC CTCCTGTCT GCCTCTGCC CCTTCCTTCT GCCAGGGGTG 1560  
 ATCTGAGTG GTCTGGCGGT TTTTCTTCT AACTGACTTC TGCTTTCCAC GGCCTGTGCT 1620  
 10 GGGCCCGGAT CTCCAGGCCC TGGGGAGGGA GCCTCTGGAC GGACAGTGGG GACATTGTGG 1680  
 GTTTGGGGCT CAGAGTCGAG GGACGGGGTG TAGCCTCGGC ATTTGCTTGA GTTCTCCAC 1740  
 TCTTGCTCT GACTGATCCC TGCTTGTGCA GGCCAGTGA GGCTCTTGG CTTGGAGAAC 1800  
 15 ACGTGTGTCT CTGTGTATGT GTCTGTGTGT CTGCGTCCGT GTCTGTCAGA CTGTCTGCCT 1860  
 GTCTGGGGT GGCTAGGAGC TGGGTCTGAC CGTTGTATGG TTTGACCTGA TATACTCCAT 1920  
 20 TCTCCCTGC GCCTCCTCCT CTGTGTCTC TCCATGTCCC CCTCCCACT CCCCATGCCC 1980  
 AGTTCTTACC CATCATGCAC CCTGTACAGT TGCCACGTTA CTGCCTTTT TAAAAATATA 2040  
 TTTGACAGAA ACCAGGTGCC TTCAGAGGCT CTCTGATTTA AATAAACCTT TCTGTMTTT 2100  
 25 TTCTCCATGG AAAAAAAAAA AAAAAA 2127

30

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1625 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

40

CAAAAGATCT ATAATCAGGA CATGTATTAT GTAAGTTGGA CAANAAAAAT TCTTCCCCTT 60  
 TATGTCCACC CTTCTATGA TTGCAAGACA AAATTTCCCT CTTTACCTC ATCCCTATAA 120  
 45 CATGGGAGGC TGAGAAAAAT GAGGGGAGAT GGAACCAGAT ACAAGGAGAT CCAATAAGAG 180  
 AAGCTTATTT AAATATTGTG AAATAAAGGA AGAMCCAAAG CATTTTTTTA AGTGGGAAT 240  
 CCTTTTGAAC AGTTATTATT TATCCATATT ATTAAYAACA TCTTTTCTGA CAAAATCCAT 300  
 50 CAGATGAAGT GTAAATGGAT AATCTTTTAA TGGATCTAAA CCTAGAAAGT TTCCTTACT 360  
 GTTCATGTCC GTGTCCAGA ATTGTGAAAT GGTGTGTGGT TTTGCTTTCC AAGTTCTTCT 420  
 55 CTGCCTCCTC TTAATTCTCT AATCCATGT CTTACAGAAG AATGAGAAAT TTCTTTCTTA 480  
 CTTGAGTATC ATGCTCTAAA AAACCTGGCT TCAGTCACAG AAACGCTGGC TCTCTGTGC 540  
 TTATATTGAA GCCAACTGCC TTTAATTCTT GGGCCCTCTT ATATTTTAA GGTGCAAAAT 600  
 60

	TTGAAGTCTC AGTCACCAGA CACAGGTTCT ATACAATTAA TGATGAGCTG GAGAAGTAAT	660
	ATGTAGCTAA TTTTTCAAAA GCATTGAATA TACTTTCCGG AAAGAAAACA GAAATTAAAT	720
5	ATTGCCACAT CTGCCCAGAA TCCCATCTGA CACCTTAACT TTGTCAGGTT TCCTACAACT	780
	TGCTAATCAA GTTTTATACA TTCTAAATCT CCCAGTTTC TTTGGGGCTG GAAGATGCAA	840
	CTTCCATTTA ATAGAACTT TGAAATCTTG GGGTAAGGGA GCAGTGGGGG GACTAGGGAG	900
10	AAGGATAAGA AATAGAATTA TTGAAAAGCC CCCACCAGGG ACCTTCCTGG CCAGAATATG	960
	CAGAGTAATT CTGCTGGCT TCACCTTTGA AAGTCCCTCG AAATATGCA GATGAACTG	1020
15	AGTCTGTTTT TGATATTGTC AGATGTATTC TACCTTGAA GTCCCNACAC CTAACTGGA	1080
	ATTCTTGAT TTACATCTCC TCCACTGTCC CCCACACCAC CCCTCAATTC CTGCTGCCCC	1140
	TGCTAATGTT AAGCATTTTT CTCTTGTTAT CATCAGGTTT ACATTAAAAM CAGRTACTTA	1200
20	CAAACGACT TGAAGCACAG ATACTTTTAC GAATGTGATA AAATATTTTC TTAAGAAAAG	1260
	GAAAGAGGAT GTGGTCAAA TAAACACCG CATGGATGTT GATTGGTGAA TACTGGTGTA	1320
25	AGAAAAGGGA GCTCAGGAAT TTTTATTACT GTATTGTGAA ATGAGTTTGA AGGAATTTGT	1380
	AAATGCCACT GGTACATTTT TAAGGTGACA CATTGCTCC TTATAAAGTT ATTAAAAATT	1440
	ACAGGTAAG CTTAAATGAC GTTTGCCAGT AGTTTACTT TATATAATCA ATATTGATAT	1500
30	TGTTGCTGAA CTATGTAAT TTATGATGCA TTTTTCAGTC CCTTTTCAGA GCAAATGCTT	1560
	TTGCAATGGT AGTAATGTTT AGTTTAAATT GACTTAATAA ATTMTTACCT GAGCAAAAAA	1620
35	AAAAA	1625

40 (2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1687 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

50	CGGGGTCACC AGTTATTAGA GGAAGTAACA CAAGGGGATA TGAGTGCAGC AGACACATTT	60
	CTGTCCGATC TGCCAAGGA TGATATCTAT GTGTCAGATG TTGAGGACGA CGGTGATGAC	120
	ACATCTCTGG ATAGTGACCT GGATCCAGAG GAGCTGGCAG GAGTCAGGGG ACATCAGGGT	180
55	CTAAGGGACC AAAAGCGTAT GCGACTTACT GAAGTCAAG ATGATAAAGA GGAGGAGGAG	240
	GAGGAGAATC CACTGCTGGT ACCACTGGAG GAAAAGGCAG TACTGCAGGA AGAACAAGCC	300
60	AACCTGTGGT TCTCAAAGGG CAGCTTTGCT GGGNATCGAG GACGATGCCG ATGAAGGCCC	360



TGGAGATCAG TCAGGCCAG CTGTTATTG AGAACCGYG GAAGGGACGG CAGCAGCAGC 420  
AGAAGCAGCA GCTGCCACAG ACACCCCTT CTGTTTGAA GACTGAGATA ATGTCTCCCC 480  
5 TGTACCAAGA TGAAGCCCCT AAGGNAACAG AGGCTTCTTC GGGGACAGAA GCTGCCACTG 540  
GCCTTGAAGG GGAAGAAAAG GATGGCATCT CAGACAGTGA TAGCAGTACT AGCAKTGAGG 600  
10 AAGAAGAGAG CTGGGAACCC TCCGTGGTAA GAAGCGAASC GTGGGCCTAA AGTCAGATGA 660  
TGACGGGTTT GAGATAGTGC CTATTGAGGA CCCAGCGAAA CATCGGATAC TGGACCCCGA 720  
AGGCCTTGCT CTAGGTGCTG TTATTGCCTC TTCCAAAAG GCCAAGAGAG ACCTCATAGA 780  
15 TAACTCCTTC AACCGGTACA CATTTAATGA GGATGAGGGG GAGCTTCCGG AGTGGTTTGT 840  
GCAAGAGGAA AAGCAGCACC GGATACGACA GTGCCTGTT GGTAAAGAAG AGGTGGAGCA 900  
20 TTACCGGAAA CGCTGGCGGG AAATCAATGC ACGTCCCATC AAGAAGGTGG CTGAGGCTAA 960  
GGCTAGAAAG AAAAGGAGGA TGCTGAAGAG GCTGGAGCAG ACCAGGAAGA AGGCAGAAGC 1020  
CGTGGTGAAC ACAGTGGACA TCTNCAGAAC GAGAGAAAGT GGCACAGCTG CGAAGTCTCT 1080  
25 ACAAGAAGGC TGGGCTTGGC AAGGAGAAAC GCCATGTCAC CTACGTGTGA GCCAAAAAG 1140  
GTGTGGGCCG CAAAGTGGC CGGCCAGCTG GAGTCAGAGG TCATTTCAAG GTGGTGGACT 1200  
30 CAAGGATGAA GAAGGACCAA AGAGCACAGC AACGTAAGGA ACAAAAGAAA AAACACAAAC 1260  
GGAAGTAAGC AGAGCTGCCA GGCTCCCAGG AGAGCATGGG GACTAGGAGG AAGGGTGTGG 1320  
CATGGCTCAG TCTGGCCCCC TTGATTACCG GCCTAGCCCC TGCTCACATC ACAGCTGTCT 1380  
35 GAAGAACAGT GAGGTGGAGT GCCTAGAACT CCCGTGGTGG TCCTGAGCAG AGAGGAGGAT 1440  
GTCTCCTGTC CTGCTGAAG GTCTCCCATG AAAACACTGC TGAAGTGTGT TGACACTCAT 1500  
40 GACCCCTTTT TTAACCGTT AAAGGGAAGT TCGGTGTTGG AGCGATACTC AATGTAGTCA 1560  
GTCTACACCT GGACGTGTGG GCCACTTAAG CCCTCCCCAC CCCCATCCTA TTCCTRAATA 1620  
45 AAACCAGGAT AATGGAARAA AAAAAAAAAA AAAAAAAG GGGGGGCCN TAAAGGNCC 1680  
CANNTTT 1687

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(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1842 base pairs
- (B) TYPE: nucleic acid.
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

	GGATGACAGA TTGCGACANA GATTGTGTGAC CCTTCCTGCT GAACTTCAGA GGGAGCTGAA	60
	ANCAGCGTAT GATCAAAGAC AAAGGCAGGG CGAGAACAGC ACTCACCAGC AGTCAGCCAG	120
5	CGCATCTGTG CCCCAGAGAAT CCTTTACTTC ATCTAAAGGC AGCAGTGAAA GAAAAGAAAA	180
	GAAACAAGAA GAAAAAACC ATTGGTTCAC CAAAAAGGAT TCAGAGTCCT TTGAATAACA	240
10	AGCTGCTTAA CAGTCCTGCA AAAACTCTGC CAGGGCCTG TGGCAGTCCC CAGAAGTTAA	300
	TTGATGGGTT TCTAAACAT GAAGGACCTC CTGCAGAGAA ACCCCTGGAA GAACTCTCTG	360
	CTTCTACTTC AGGTGTGCCA GGCCTTTCTA GTTTGCAGTC TGACCCAGCT GGCTGTGTGA	420
15	GACCTCCAGC ACCCAATCTA GCTGGAGCTG TTGAATTCAA TGATGTGAAG ACCTTGCTCA	480
	GAGAATGGAT AACTACAATT TCAGATCCAA TGGAAGAAGA CATTCTCCAA GTTGTGAAAT	540
20	ACTGTACTGA TCTAATAGAA GAAAAAGATT TGAAAAAACT GGATCTAGTT ATAAAATACA	600
	TGAAAAGGCT GATGCAGCAA TCGGTGGAAT CGGTTTGGA TATGGCATT TACTTTATTC	660
	TTGACAATGT CCAGGTGGTT TTACAACAAA CTTATGGAAG CACATTAAAA GTTACATAAA	720
25	TATTACCAGA GAGCCTGATG CTCTCTGATA GCTGTGCCAT AAGTGCTTGT GAGGTATTGT	780
	CAAAGTGCAT GATAGTAATG CTCGGAGTTT TTATAATTTT AAATTTCTTT TAAAGCAAGT	840
30	GTTTGTGACA TTTCTTTTCA AAAAGTGCCA AATTTGTCAG TATGTCATGT AAATAATTGT	900
	GTTAATTATT TTACTGTAGC ATAGATTCTA TTTACAAAAT GTTTGTTTAT AAAGTTTAT	960
	GGATTTTAC AGTGAAGTGT TTACAGTTGT TTAATAAAGA ACTGTATGTA TATTGGTAC	1020
35	RGGCTCCTTT TKGTAAYCC TTAAAACTC AACTCTAGGA RGCAACTACT GTTTATTATA	1080
	CTAAARGGCT GAAAAACCCT CAGGCCAGAC TGCTAAGCTC TGAAATYCCT GAGAGGTCTC	1140
40	AGACCGGGAT TCTACTTGTT CCAAGAAAGG GTAAAGCTTC TAAACCATCT TATCTCTGTC	1200
	TCCAAGCATG AACACAGGAG CATGTYAAGA AAATCTTTAC TACTTTCTYC CATGCCGAGA	1260
	AATCTACATA TTTTGAATTA GAAACACCCT CACACCCACT TGAAGATTTT TTTCTGGGA	1320
45	ACATTATGTC CCGTAGATCA GAGGTGGTGT TGTCTTTTGT CTTCTACTGG CCATTGAGAA	1380
	ACTTTGATGA TAAAAAGAA CGGTATAGAT TTTTCAAACG TATATAAAAT ATTTTATGT	1440
50	TATATGTTAT GCCATAACTT TAAAATAAAA ATAGTTTAAA ATTCTATGCT AGTGGATATT	1500
	TGGAACTTTT TCCTCAAACA AACACCCAC ACTGACTTCA GCAAAACCCT AAAACTAGCT	1560
	ACAGATTACT ACTACGAATG AATCATYAAG TTTTGTGTCT GCAACAATTT AGAAGCACTA	1620
55	AGCCCAAATA TCAGGAAATG TGTGTATGAT GGAATTTTCT AGGACAAAAC AGATCAAGAT	1680
	TAAACAGGA TCAAGGATTA ATGGTATAAA AATGGTCTAC TAAACAGGA TCAAGGATTA	1740
60	AAACAGGATC AAGGATTAAT GGTATAAAAA TCTCTACTGG TTACCGGGTG GCNGGGCCAT	1800

ACAGGGTAGT GGTGGATGGA TAGTTTAGTT TGGNAAGGGT AA

1842

5

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 770 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

15

GGCACGAGCC CTATGCTGTT CTTGTGATAA TGAGTGAGTC TCACAAGATC TGGTGGTGTT 60

ATAGGCATCT GGCATTTCCC CTGCTGACGC TCATTCTCTA TCCTGCCACC CTGGAAGAA 120

20

GTGTCTCTG TCATGATTGT AAGTTTCCTG AGGCCTCCCC AGCTATGTAG AACTGTGAGC 180

CAATTAAACC TCTTTTCTCT ATAAATTATC CAGTCTTATA TATTTCTTCA TAGCAGTGTG 240

25

AGAACAGATA ATACCGTAAA TTGGTATCAC AGAGAGTGGG GTGTTGCTAT AAACACATCT 300

GAAAATGTTA AAGCAAATTT GGAAGTGGGT AACAGGCAAA GGCTGGAACA GTTKGAAGAA 360

CAGTTAAGAA GAAGACAGGA AAATATGAGA AATCTTGAAA CTTCTAGAG TCTTAAAGGT 420

30

CTCAGAAGAC ATGAAGATGT GGAAGCTTT GGAAGTCTCT AGAGACTTGT TTGAATGGCT 480

TTGACCAAAA TGCTGATAGT GATATGGACA ATGAAGTCCA GGCTGAGCTT ATCCAGACAG 540

35

ACATAAGAAG CTCGCTGGGA ACTTGAGTAA AGATCACTCT TGCTAGGCAA AGAGACTGGT 600

GGCCTTTTTT CCTCTGCCCT AGAGATCTGT GGAATCTGA ACCTGAGAGA GATGATTTAG 660

GGTATCTGGC AGAAGAAATA TCTAAGCGGC AAAACCTTCM AGAGGAAGCA GAGCATAAAC 720

40

GTTTGAAAAA TTTGCAGCCT GACNATGGGA GACCAAAGTT AAACCCAATT 770

45

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs

50

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

55

GAATTCGGCA CGAGCTGAGA GGCACAGGAG CAACAGCCAG TGCCCCCTGC AGAGGACCAC 60

TGGGGTCACA GACTTCARAC CTGATGACCT GGGCTCAGAT CCCAGCTCTG CACCTACCAG 120

60

CCGTGTGACA AGGTGTCTC TCTGAGCCTC AGTCACACAC TGCCTTAACG GTTGGGCCTC 180

ATGGAGCTGT TTGTGAAGGT TAAATGGGAA GACATAAAGC ACTTAGCCCA GAGCCAAGGA 240  
 CATGCTGAAT AGGATAATGG TGGCCTCCTT TGGCGCTGTG CTGGTGCAGG TGTGCCGAGG 300  
 5 AAYTGGGCAG GGGTGACAGA TACCTCTTCT AACCTAGTTC CTTTCCAAGA ACCTAATTGG 360  
 TGTCTCTCCC TCCCCCAGGC AATGGAAGG AGGAGGCTGG GCCCCAGCCC CAGAATACGG 420  
 GAGGTTTCTC ACCGTGGTAG GGAAATTGCT GGGTTGGGGG TGTGGGCAAC CACAGTGATC 480  
 10 GTCTCTCTGC AGGACGGATG AGGCTTTGCT GACAGAGGC 519

15

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 753 base pairs  
 20 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

GGCACGAGCG GCACGAGCAG CCAGTTGCTG ACTGGCACAT GGCCTCCAGC GTCCCGGCTG 60  
 GTGGGCACAC TAGAGCCGGA GGGATCTTCT TAATTGGTAA ATTGGATCTT GAAGCTTCAC 120  
 30 TGTTTAAATC TTTTCAGTGG CTTCCCTTTG TACTTAGAAA AAAATGCAAC TTCTTCTGCT 180  
 GGGACTCATC CGCTCACAGC CTTCCCTCC ACCCTCTCTC TGCCTCATGC TCTGCCCTG 240  
 CCTGCCATGC CTCCGATACT CACCTTTTGT ACCCCAGCAC CCGTGCCCTC TGCCCTCGA 300  
 35 TCTTTGCCTG GCTGGTGTCT CCTCACTCAG TGTTCAGGAC AAATGCTCCT GGCCCTACCC 360  
 CATCTAGCCA GTCTAGCCCG GTCTTCCCTG TCTTCCCTGT TTCATTATG GCTCTTATG 420  
 40 TTTGTTWACT TGTGTGCTGT TGACTTTTAA CTCTCTCAGT CCCCCTGGA ATGCAAGCGA 480  
 TCTCCCAAGC TCCTAGAATT GTTCTGCTCT CTTACAGGC CCTTAGCTG TGTGTGCTCG 540  
 TGCCGAATTC GGCACGAGG TATGTGCACT TGCTGGTATG TATGTAGGTG TTTGCTAACA 600  
 45 CATACGTGCA CACGCAGAAT GCTTCCAGG GACTGCACAG CCTCTAGTTC GCAGCCCCCA 660  
 CCCCTCCCTT TGSCCCTGCA CTCTCCCTC TCTGAGCTGC ATTGCGATGA AAGGGTGCAN 720  
 50 GGTTCCTGAN CCCGCNAGCG NCACCTCCTG GGA 753

55

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1400 base pairs  
 60 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

5	GGCACAGTTT ATTAATACCT ATTATGGGAA AGTCACTTTG GTTGGCATTG AAAATTACAT	60
	CATCTTTAAA GCAGTATTTG TCCCCAGATG GACTCATCAC TAGCAAAGAC TAGGTTTCATT	120
	GGAAGGCATA GGGTGAGAGA ATGGGAAGAT GRAGTGGAGG CGGGTTGTTA AAGTGCTGTC	180
10	AGTGAGTGAT TTTGTCTACT TGAATAATGG TCCATGTTTG GGGGCATATT GTGTTTCATA	240
	AGAAGTGAAA GGTATTTGCA AAGTAAGCTA CAAATGACCC ATAAATCTGT TAACAACAGT	300
15	CCTTAATATG CAAAGATGAA AAACAAGCAT TACTGCTACC CAAAGGGAAC TGGTGCTTGG	360
	TGATGTGCAG ATGGGGCTGT TGGTTAAGAG AGCTATTACA GTTTTTCTCT CTTAGGTTTC	420
	ATAGGAGGTA GTTACTGAGA TGAGATTGTT TTATCTTTTT GAATACAGAT CTCTGTCTTT	480
20	GAGTTAGTTC TGAGGATGGG AGTAATAAAG GAGTTTTTTG TTTTTTTGTT TGTTTGTTTG	540
	TTTTGGCTCC TTAGTAATAC TCCTCTGACA TTTATTTCTA TTATTCCTCA AAGAAAGGAA	600
25	ACCAACTGAA ATGTTTGCTT TAACAAACAT TTTAATAAGT TCTCTGGGTT TTTTTTCCC	660
	CTTTTAAAAA AATTAGCATA TACCATAGCA ATAAAAGAAC TAATGTTAAC TATTGTATGC	720
	TACAACTTAA GTGATTTTTT TAAAGAAGCA CAATGTCATT GRAAGTATTA TTGAAAAGGA	780
30	TCATAGTCAC ATTGAATTTG TGAAGGCCAA AGAAATTGAA GGGAGTGATA TTTTCATTTT	840
	ATGATATTCa CATATTTAGT AAATTTTGTG TACAAGAATA CCAGGCAGAG TGTTTTACCC	900
35	ATGGAAACAG GTTTCAGATT ACTTTGTTTT TACTGTTAGA GTCTCAAGTT TAGAAATGCT	960
	AACACTTAAA TCAGTTTTTT TCTCACTATA CTTGAAGATT GTTAATATTT TGATATCTTC	1020
	CTAGCTTGAT GGAATTTAAA CATATCTTCA GATCTGTGAC AGTGACAGCC AATAGGACTG	1080
40	ATAATATTAG CTTCAAACCA ATAATATCCA GGGTTAAAAT AAAAATCATA GTGAAAGTAC	1140
	GATTGTAAAA TTATGCTATA TTAACTTTTA AGTCGTGAAT AACTTGACAT CAAAATGTTA	1200
45	TGTAATTACC ATAAATAATG GCTAGCGAGA ACATCTTTGG AAATTCTCAA ATTACCTTTC	1260
	TTACTACACT GTTTCAGAA TGAATGTAGA AATGATCCTG TTAGCTTTCT GAATGTTCTG	1320
	TGGTTGAATG TGTTTTTGCT TAAATAAAGC TTTTGGTATT TGTTTAAATW ACAAAAAAAA	1380
50	AAAAAAAAAA AAAAATCTGA	1400

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(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2153 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

5	CAGGCCTCAG GGCCTCTGGT GGCTCTGGCC CAGACAGTAT TTGCAGTTCT TGTGCTATGG	60
	GTGGGAGTCT TCTTCCTCAA GTTTCGGCAG CTGTGCTGTG NCTGGATGGG CTGCTCCTCC	120
10	CAGGGCTCAA GGGCTGTGGT CCGCTCAGGG TCTCATTTCC CCAGGCCAAG TTCAAGGCAG	180
	CAGCCCTTTG TGAGGCGCTC TTGGCCCTGG GCTGGAGGGA GAACTTTAAG CTTTTTGTCT	240
15	CACAGGGACG TGGTATGGGC CCTGGGTGCA GGTGCCACACA TTCTGCTAAT GAGAGCTTTG	300
	TCTGATCAGT CCTGGGTCCA TCAGTTTGTC CATGTGTCCG GCTGCCAGCC CGTCCCTTGG	360
	GATCCTTCCC CTGGGGTGTA GCCTTGTTCA TTAGTATATA CTCATTCTTT CATGCTTTCC	420
20	TCAGCAGAAC ACTTCCACTT CTGAGGTGAG CTTTTGCCCC RTGCCCTTCC TCCACAGGTG	480
	TTGCCTTTTT ATAAAGACCT GATAGCAGAA TAAATGGTG TTTCCCTGTT GACCCAGCAC	540
25	CATTTCTGTG GGCCTAGAAT ATGCCCTCA ACCCTTAGAG TGGGCGAGTG AGGGCTTGAG	600
	GAGTGACCTT TCCTTCTCA TGGTTTAGT CATTTTGGCT GCCAGCCCTT AATGGCACAG	660
	ATCTGCTGCT TCTAACAGAT GGCCAGGAGG TGACACCGAT TTCAGCCATT GCCAAGGTA	720
30	GCACCCCTCT CTTTGAGCCT AGGCCACAC TGTTCAATTG CACTTTAGGC AAGTGCCTGT	780
	TTGGCTTTAA AGGTAAGCCT GCCAGCTGTG AGAAGCCTTG GTAACGTATG GACTCATTTT	840
35	CTGGTCTTA AAGATGCAGC CTCCTAAGGG CTCCTTGATG GATGCCATCT CTCCTAGCCC	900
	CCAGCCCTGG TGCCACTGGT GGGCAGGTTT CCATTCTTTG GGGCTGGGAG GGACAGCTTG	960
	CCTGTTTCTG GTCACAAAT ACAGTCTTCT CTCCTGTACC ATTCTGTGGC TTCAGCATGG	1020
40	GGCAGTAGC CTTTCATTAG TGTAGATAGT CATTCCTTGG TAGGGTGGAG GGTAAACAT	1080
	AGGGTCTGGA ACTGTTTGGG ACCTTTGGG GATGTCTGT GCCTCCAGA TTCTTGTATT	1140
45	CTGGGAGGAG AGGCTGCCGC ATTCTGCTGC TCCTCACAGC GAGCAAAGCT GCACCCACTT	1200
	ACATTGAGTA TTTTCTGGC ACTACAAAGA GTGGGAAGGC CTGGGATTTG CTGCTGCTCC	1260
	CTTAGAGCAG GGGCCCTTCT TTAGCAGCTT TGGACACCTG GAGACCCAGC CCTGTTATTT	1320
50	AATGGTAGTG GGCAAGTGTG TGTGCATACT GTCTGCCACT GCTTTCTCCC TGCCCCATGC	1380
	CAGAGAGCCC TGTCCCTGCC AGGCCAGCC TTCTTAGCCC CAACTTGGGA ACAAGTGCA	1440
55	ACATGGGATC ATGGGTTGGG GTGCTCAGGT GAGCCCTCTC TATAGTGCTT CCCTGGGCCA	1500
	AGCTGACACC AGCCCTGAG GGTGGGTGG GACGGGTGGT GCTTAAAAGA GGAAGGGGAC	1560
	CAGTGTAGCA ACTTGCCAGG GACCCACCCC CTCCCTCTCT GGGCCTGTGC AGTGAGCATG	1620
60	GGGATTCCCA TCAAGGGGCC TGGCACCTGT GCTAGTTACG TAGCCGCTGN TCACGCGCTC	1680

5 ACTCCTGACC ACATGCACGT TCCCTAGATG CAGACTGCTT TGAAC TTAA AGCTGTACAA 1740  
 TTTGGTTATG TTTGTGCTGA CTAAAAATAT ATTTTAATGA GGAAAAATA ATGGAGAACC 1800  
 CTGGAAGGA CCTGGTTCTT TTGCTTCTCG GGAACTGTA AGCCCTCGCG TTCTGGGAAT 1860  
 CGCTCTCTGC TGCTCTTTCC TGAAGCTAA GCCTGTCTCC ACCGCCGAG GCCTGCGCCG 1920  
 10 GTGCTCCCGC CGCAGTTGCG TTGCTTTGG ACCTTGCCTG CGGGGAGGG GGTGCTCGGT 1980  
 CCGAGCCCGC TCCTTTCTGT ACACCTAGCG CTGCCCGCCC CGCTTGTGTC TGAGGTCGTG 2040  
 TATGTCAAAA ATAAAGCCGC TAGAAACGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2100  
 15 AAAC TCGAGG GGGGGCCCGT ACCCAATTAA CCCNNTATGA TCTATAAAGC GTC 2153

20

(2) INFORMATION FOR SEQ ID NO: 166:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

30 GCCCACGCGT CCGCCACGC GTCCGGCGGT GCGGAGTATG GGGCGCTGAT GGCCATGGAG 60  
 GGCTACTGGC GCTTCCTGGC GCTGCTGGGG TCGGCACTGC TCGTCGGCTT CCTGTCCGGT 120  
 35 ATCTTCGCCC TCGTCTGGGT CCTCCACTAC CGAGAGGGGC TTGGCTGGGA TGGAGCGCA 180  
 CTAGAGTTTA ACTGGCACC AGTGCTCATG GTCACCGGCT TCGTCTTCAT CCAGGGCATC 240  
 40 GCCATCATCG TCTACAGACT GCCGTGGACC TGGAAATGCA GCAAGCTCCT GATGAAATCC 300  
 ATCCATGCAG GGTAAATGC AGTTGCTGCC ATTCTTGCAA TTATCTCTGT GGTGGCCGTG 360  
 TTTGAGAACC ACAATGTTAA CAATATAGCC AATATGTACA GTCTGCACAG CTGGGTTGGA 420  
 45 CTGATAGCTG TCATATGCTA TTGTTACAG CTCTTTTCAG GTTTTTCAGT CTTTCTGCTT 480  
 CCATGGGCTC CGCTTTCTCT CCGAGCATTT CTCATGCCCA TACATGTTTA TTCTGGAATT 540  
 50 GTCACTTTTG GAACAGTGAT TGCAACAGCA CTTATGGGAT TGACAGAGAA ACTGATTTTT 600  
 TCCCTGAGAG ATCCTGCATA CAGTACATTC CCGCCAGAAG GTGTTTTCGT AAATACGCTT 660  
 GGCCTTCTGA TCCTGGTGTT CGGGGCCCTC ATTTTITGGA TAGTCACCAG ACCGCAATGG 720  
 55 AAACGTCCTA AGGAGCCAAA TTCTACCATT CTTCATCCAA ATGGAGGCAC TGAACAGGGA 780  
 GCAAGAGGTT CCATGCCAGC CTACTCTGGC AACAACATGG ACAAATCAGA TTCAGAGTTA 840  
 AACAGTGAAG TAGCAGCAAG GAAAGAAAC TTAGCTCTGG ATGAGGCTGG GCAGAGATCT 900  
 60

ACCATGTAAG ATGTTGTAGA GATAGAGCCA TATAACGTCA CGTTTCAAAA CTAGCTCTAC 960  
AGTTTTGCTT CTCCTATTAG CCATATGATA ATTGGGCTAT GTAGTATCAA TATTIACCTT 1020  
5 AATCACAAG GATGGTTTCT TGAAATAATT TGTATTGATT GAGGCCTATG AACTGACCTG 1080  
AATTGGAAAG GATGTGATTA ATATAAATAA TAGCAGATAT AAATTGTGGT TATGTTACCT 1140  
TTATCTTGTT GAGGACCACA ACATTAGCAC GGTGCCTTGT GCAKAATAGA TACTCAATAT 1200  
10 GTGAATATGT GTCTACTAGT AGTTAATTGG ATAACTGGC AGCATCCCTG A 1251

15

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 882 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

GACSMCTAG AACTATGGTC CCCCGGGACT GCAGGAATTC GGCACAGCGG CTGCGGGCGC 60  
GAGGTGAGGG GCGCGAGGTT CCCAGCAGGA TGCCCCGGCT CTGCAGGAAG CTGAAGTGAG 120  
30 AGGCCCGGAG AGGGCCGAGC CCGCCCGGGG CAGGATGACC AAGGCCCGGC TGTTCGGGCT 180  
GTGGCTGGTG CTGGGGTCGG TGTTCATGAT CCTGCTGATC ATCGTGTACT GGGACAGCGC 240  
AGGCCCGCG CACTTCTACT TGCACACGTC CTTCTCTAGG CCGCACACGG GGCCCGCGCT 300  
35 GCCCACGCC GGGCCGAGCA GGGACAGGGA GCTCACGGCC GAYTCCGATG TCGACGAKTT 360  
TCTGGACAAK TTTCTCAGTG CTGGCGTGAA GCAGAGTGAC YTTCCAGAA AGGAGACGGA 420  
40 GCAGCCGCTT GCGCCGGGGA GCATGGAGGA GAGCGTGAGA RGCTACGACT GGTCCCCGCG 480  
CGAMGCCCGG CGCACCCAGA CCAGGGCCGG CAGCARGCGG ANCGGAGGAR CGTGCTGCGG 540  
GGCTTCTGCG CCAAYTCCAG CCTGGCCTTC CCCACCAAGG AGCGCGCATT CRACGACATC 600  
45 CCCAACTCGG AGCTGAGCCA CCTGATCGTG GACGACCGGC ACGGGGCCAT CTACTGCTAC 660  
GTGCCCCAAGG TGGCCTGCAC CAACTGGAAG CGCGTRATGA TCGTGCTGAG CGGAAGCTGT 720  
50 GCACCGCGTG CGCCTACCGC GACCCGYTGC GNTCCCGCGC GAGCACGTGC ACAACGCCAG 780  
CGCGCACTGA CTTCAACAAT TCTGGCGCGG CTACGGGAAG TCTCCCCAC CTCATGAAGT 840  
55 CAAGCTCAAG AATACACCAA TTCTTCTGTC GCGACCTTC TG 882

60 (2) INFORMATION FOR SEQ ID NO: 168:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1208 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

GGGAAACTCA AAAGGATGAT GGAATGGTTG ATGGAGCCAG AGCCTAGAAG TRAAGGGATA 60  
CAGAGTGAAG ATAGAGGTAT TTACGTATAT TTWAATATTA GCTTTGGAAT TACGTAGGGA 120  
TTCTTAAGAA AAGATCATGA CAGGACAGCC ACATTTGGTA AAATGTCAGG GCAGCCAGTG 180  
CATGGTCCTC CTGGGGCTCC TCAGTTGACG GGTTTAAATC ATTTCTGAT CCCCTGCC 240  
TGGTTTGAGG AATGCATACA GTACGTGAAA TGCCTGTGGT ATGAGTTGCA ATGGGCAATC 300  
AACCTGGGTA AATCCAAGAT TAATGATTAG TTCTAAAGAT CCAGTTGAAG TTCTAGAGTG 360  
GGAATTTTCC GTCAAGCARG TCAGCACAGC TTTATGCCTG TTCCTCTAAT AACGATAGGT 420  
AACAAATAGC TGTGKTWCA CAGCTAGGAR GATAACCAA TCTAGAGTTC TTGARTCTCA 480  
TTTAATAAAT AAKTATTATG AGTACCAACT GCATATTTCA GGCCTGCAAT TTGACTCTGT 540  
TAAATACTGA TYCCTTAKGA CMSCCACWTC AGAWAACMTT AATCTGTCTG ATCAATAAAC 600  
AGCTTGACTT AGAGRGGTAA AATAGCTTGC CACAGGTWAC CCAATTAGTA GGTAACAGCG 660  
ACAGAATAAC AGTCAGTTA AAATCTTAGA CTGGAGACTA ATTGCATAAG TTTGAATTTT 720  
AGTTCTGCTA TGTAAATTG GGTGAGTACC TTAATTYACC TGAGTCTCGG TCTTTATATC 780  
TGTAGAATGG AGCTAATGAT ATTACTTAAT TTGCTTTATG TGAGATTAAA TGTACTAATA 840  
TATGTAAATC ACTTACAACA GCATTTGACA TATTTGACAT ACTTAATATA TTTGCTACTA 900  
ATACTATTAG CAACAGCATT CTGATTTTCC AAGTTGAAAT TCAGTGTTTT CTMTTTTACT 960  
TTGCCATAAT TTACAATGTT GTGCTCTGTA AACCATAAAT TTCCCTGAGG TGTGTGTCAGG 1020  
TTAAAAAAA ATCACTATGG CCCCARNMA CTTGGAAAAT AGAAATGAGA CCAGCTTCAT 1080  
CTATATTCTT TACTGCAAAT AACTTAGAAT TGTAATAGGC TAATATGTAC TGGGACTTCC 1140  
AATTTGGGAA TATGACAAAA ATAATACTAT TTAGCTAAAA CATATACAGA ACTTATTTT 1200  
CCTCTGAA 1208

## (2) INFORMATION FOR SEQ ID NO: 169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1307 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5 GGCACGAGAG AAAAGAGGTT GAGAATGTTT TCTAGCAGGC AGAATGTGCA TACATGTTTT 60  
CATGARTGTC CTTTGGGTGC TGTTCCTTTT AAATCCTCTG TGCACAGGGC TCTGGCCTTT 120  
ARTAAACTGT TTTTCTGTCT TACGTCATGC TGACTGGGTG CTAGGGGCTG ATTACAAAGG 180  
10 GGAAGAGTTG AACAGACATC AGGGGCCGAT GAAACCAAAG GACTAGGAGT CAGGAGAACA 240  
AGTCAGGGAT TAGGAGACAG CGGTTTGGTT TATTGTTATC CAGCTGGAGG ACTCCTAGGG 300  
15 GCAGCAGCAG GAGGAATACC AGGGCCACGG AGGGGCAGGA GTCTCACAGT GGAGGGCAGA 360  
CTCTAACAGA TGCCAGCTGA ACGCTCGCTG GCCCTGGATG TCATACGAGT TGGGGACCAG 420  
AAATCTGGGC TCAGAGAACC CGTCCAGGGA GATTGAAGC CATGGGTTAT CTTCTAGAGT 480  
20 TGATACTGAT AATATAATTTT AATTTTATTT GATGTTTAAT ACCTTCTGAA ACAGGAGGGT 540  
AAGATCAGAT GGAAGCCCY TCTGTGAAG GATCTTGGA ACCTTGGTGG TTTTMTTTTT 600  
25 TTGGTTTTTT TTTTTTTGAT CGAGCTGTGG ACATCCTTCT TAATTGATT NTGAGGATTT 660  
GTTTAACTAA AAAGTTCCCA AACACAGAAA GGGCCTCCCC ACCTGCTTTG GGGAGCTGTC 720  
TGTSTGGA GTGCCAGGCA TCCSATGGA CCCATCACTG CCAGTGTCTG TGCCTCCAG 780  
30 AGGTCAGCCC TGTGCTGCC CTGGCTCTGT CTCCTCTGTG ACAGGGCAGA GCATTTCTGG 840  
TCAGTTCTC CATGGTCCT CCCACCCCTT GTAAAGTG ATGGACATGA TGAATTCAG 900  
35 TTGTCTCACC CTGATAGCCT GGGTGTGAT ATCACTTTA CCCGACTCA GACACAGGCG 960  
ACCTGAAGC AGTTCTCGGT GTGTAGAGT CACGTGACAG TCCCCACAGC CTCCCAGAT 1020  
AGCTGTGTGC CTGTGCGCTA CTGCTGTGCC ATTTTCCCA CTNNGCGTT TACTAAATG 1080  
40 CAGCTGATCT CTCTCTCTGT GCATCTGTA TCCATGTGA ACAATACATG TAGGTTCTTT 1140  
TTCCACGCAA TGTAAGAACA TGATATACTG TACGTTGAA AGCATTTACC TTATTTATAT 1200  
45 ACCTGAATGT TCCTACTACA CAAATAAACA TATATTAAAT WCTAAAAAA AAAAAAAAAA 1260  
CTGGAGGGG GGGCCGTAC CCAAATCGCC GGATAGTGAT CGTAAAC 1307

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## (2) INFORMATION FOR SEQ ID NO: 170:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

	GGCACGAGGT CGCCGCCGCG GCCGCCTGGA ATTGTGGGAG TTGTGTCTGC CACTCGGCTG	60
	CCGGAGGCGA AGGTCCCTGA CTATGGCTCC CCAGAGCCTG CCTTCATCTA GGATGGCTCC	120
5	TCTGGGCATG CTGCTTGGGC TGCTGATGGC CGCTGCTTC ACCTTCTGCC TCAGTCATCA	180
	GAACCTGAAG GAGTTTGCCC TGACCAACCC AGAGAAGAGC AGCACCAAAG AAACRGAGAG	240
	AAAAGAAACC AAAGCCGAGG AGGAGCTGGA TGCCGAAGTC CTGGAGGTGT TCCACCCGAC	300
10	GCATGAGTGG CAGGCCCTTC AGCCAGGGCA GGCTGTCCCT GCAGGATCCC ACGTACGGCT	360
	GAATCTTCAG ACTGGGGAAA GAGAGGCAAA ACTCCAATAT GAGGACAAGT TCCGAAATAA	420
15	TTTGAAAGGC AAAAGGCTGG ATATCAACAC CAACACCTAC ACATCTCAGG ATCTCAAGAG	480
	TGCACTGGCA AAATTC AAGG AGGGGCGAGA GATGGAGAGT TCAAAGGAAG ACAAGGCAAG	540
	GCAGGCTGAG GTAAAGCGGC TCTTCCGCCC CATTGAGGAA CTGAAGAAAG ACTTTGATGA	600
20	GCTGAATGTT GTCATTGAGA CTGACATGCA GATCATGGTA CGGCTGATCA ACAAGTTCAA	660
	TAGTTCACG TCCAGTTTGG AAGAGAAGAT TGCTGCGCTC TTGATCTTG AATATPATGT	720
25	CCATCAGATG GACAATGCGC AGGACCTGCT TTCCTTTGGT GGTCTTCAAG TGGTGATCAA	780
	TGGGCTGAAC AGCACAGAGC CCCTCGTGAA GGAGTATGCT GCCTTTGTGC TGGGCGCTGC	840
	CTTTTCCAGC AACCCCAAGG TCCAGGTGGA GGCCATCGAA GGGGAGCCC TGCAGAAGCT	900
30	GCTGGTCATC CTGGCCACGG AGCAGCCGCT CACTGCAAAG AAGAAGGTCC TGTTCGACT	960
	GTGCTCCCTG CTGCGCCACT TCCCCTATGC CCAGCGGCAG TTCCTGAAGC TCGGGGGGCT	1020
35	GCAGGTCTCTG AGGACCCTGG TGCAGGAGAA GGGCACGGAG GTGCTCGCCG TGCCCGTGGT	1080
	CACACTGCTC TACGACCTGG TCACGGAGAA GATGTTGCGC GAGGAGGAGG CTGAGCTGAC	1140
	CCAGGAGATG TCCCCAGAGA AGCTGCAGCA GTATCGCCAG GTACACCTCC TGCCAGGCCT	1200
40	GTGGGAACAG GGCTGGTGCG AGATCACGGC CCACCTCCTG GCGCTGCCCG AGCATGATGC	1260
	CCGTGAGAAG GTGCTGCAGA CACTGGGCGT CCTCCTGACC ACCTGCCGGG ACCGCTACCG	1320
45	TCAGGACCCC CAGCTCGGCA GGACACTGGC CAGCCTGCAG GCTGAGTACC AGGTGCTGGC	1380
	CAGCCTGGAG CTGCAGGATG GTGAGGACGA GGGCTACTTC CAGGAGCTGC TGGGCTCTGT	1440
	CAACAGCTTG CTGAAGGAGC TGAGATGAGG CCCACACCA GGA CTGGACT GGGATGCCGC	1500
50	TAGTGAGGCT GAGGGGTGCC AGCGTGGGTG GGCTTCTCAG GCAGGAGGAC ATCTTGCGAG	1560
	TGCTGGCTTG GCCATTAAAT GGAAACCTGA AGGCCAAAAA AAAAAAAAAA AAAAAAAAAA	1620
55	AAAA	1624

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2003 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

10	GGCAGAGCC AGCTTGCAGG AGGAATCGGT GAGGTCCTGT CCTGAGGCTG CTGTCCGGGG	60
	CCGGTGGCTG CCTCAAGGT CCCTCCCTA GCTGCTGCGG TTGCCATGTC TTCTTGCTG	120
15	TTCTGGCATC AGGCACCTGG ATTGAGTTGC ACAGCTTTGC TTTATCCGGG CTGTGTGCA	180
	GGGCCCCGGCT GGGCTCCCA TCTGCACATC CTGAGGACAG AAAAAGCTGG GTCTTGCTGT	240
	GCCCTCCCAG GCTTAGTGTT CCCTCCCTCA AAGACTGACA GCCATCGTTC TGCACGGGGC	300
20	TTTCTGCATG TGACGCCAGC TAAGCATAGT AAGAAGTCCA GCCTAGGAAG GGAAGGATTT	360
	TGGAGGTAGG TGGCTTTGGT GACACACTCA CTTCTTTCTC AGCCTCCAGG AACTATGGC	420
25	CTGTITTAAG AGACATCTTA TTTTCTAATA GGTGAATTCT CAGATGATAG GTGAACCTGA	480
	GTTCAGATA TACCAACTTC TGCTTGTAAT TCTTAAATGA CAAAGATTAC CTAGCTAAGA	540
	AACTTCCTAG GGAAGTAGGG AACCTATGTG TTCCTCAGT GTGGTTTCCT GAAGCCAGTG	600
30	ATATGGGGGT TAGGATAGGA AGAATTTCT CGGTAATGAT AAGGAGAATC TCTTGTTTCC	660
	TCCACCTGT GTTGTAAGA TAACTGACG ATATACAGGC ACATTATGTA AACATACACA	720
35	CGCAATGAAA CCGAAGCTTG GCGGCTGGG CGTGGTCTTG CAAAATGCTT CCAAAGCCAC	780
	CTTAGCCTGT TCTATTCAGC GGCAACCCCA AAGCACCTGT TAAGACTCCT GACCCCAAG	840
	TGGCATGCAG CCCCCATGCC CACCGGGACC TGGTCAGCAC AGATCTTGAT GACTTCCCTT	900
40	TCTAGGGCAG ACTGGGAGGG TATCCAGGAA TCGGCCCTG CCCCACGGGC GTTTTCATGC	960
	TGTACAGTGA CCTAAAGTTG GTAAGATGTC ATAATGGACC AGTCCATGTG ATTTCAATAT	1020
45	ATACAACTCC ACCAGACCCC TCCAACCCAT ATAACACCCC ACCCCTGTTT GCTTCCTGTA	1080
	TGGTGATATC ATATGTAACA TTTACTCCTG TTTCTGCTGA TTGTTTTTTT AATGTTTTGG	1140
	TTTGTTTTTG ACATCAGCTG TAATCATTCG TGTGCTGTGT TTTTATTAC CTTGGTAGG	1200
50	TATTAGACTT GCACTTTTTT AAAAAAGGT TTCTGCATCG TGGAAGCATT TGACCCAGAG	1260
	TGGAACGCGT GGCCTATGCA GGTGGATTCC TTCAGGTCTT TCTTTGGTT CTTGAGCAT	1320
55	CTTTGCTTTC ATTGCTCTCC CGTCTTGGT TCTCCAGTTC AAATTATGTC AAAGTAAAGG	1380
	ATCTTTGAGT AGGTTCTGTC TGAAAGGTGT GGCCTTTATA TTTGATCCAC ACACGTGGT	1440
	CTTTTAACCG TGCTGAGCAG AAAACAAAAC AGGTTAAGAA GAGCCGGGTG GCAGCTGACA	1500
60	GAGGAAGCCG CTCAAATACC TTCACAATAA ATAGTGGCAA TATATATATA GTTTAAGAAG	1560

5 GCTCTCCATT TGGCATCGTT TAATTTATAT GTTATGTTCT AAGCACAGCT CTCCTCTCCT 1620  
ATTTTCATCC TGCAAGCAAC TCAAAATATT TAAAATAAAG TTTACATTGT AGTTATTTTC 1680  
AAATCTTTGC TTGATAAGTA TTAAGAAATA TTGGACTTGC TGCCGTAATT TAAAGCTCTG 1740  
TTGATTTTGT TTCCGTTTGG ATTTTGGGG GAGGGGAGCA CTGTGTTTAT GCTGGAATAT 1800  
10 GAAGTCTGAG ACCTTCCGGT GCTGGGAACA CACAAGAGTT GTTGAAAGTT GACAAGCAGA 1860  
CTGCGCATGT CTCTGATGCT TTGTATCATT CTTGAGCAAT CGCTCGGTCC GTGGACAATA 1920  
AACAGTATTA TCAAAGAGAA AAAAAAAAAA AAAAACTCG NGGGGGGGCC CGGTACCCAA 1980  
15 TTCGCCCTAT AGTGAGCCNA TTC 2003

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(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 786 base pairs ✓  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

30 GGCACAGCGG CACGAGAAGA CTTTGGTGTT TAAGAGATTA ATGTGTTAGC CAGAACAAC 60  
CATTTCTCTA CCMGTGTGTA GTCCATTTAT CTTTAAAGAT TTTCTATTGG AATAATTTTG 120  
35 AAATTACTTT CTTAGTTTTC TTCATTAAAA ACTAAGAAAA TGCTTTGTTT ATTATGAATT 180  
GCTATTTCTC TTGATTATTA TTCCTGGAGA AAGTCTATCA GACGTAATTC TTCTGATTG 240  
CTTCTAGGCT AGAGGAAAAT GTGAAAGATG ACAAATGAAA ATTTCAAAGG TTGTCAGTAG 300  
40 TATGACTTCT TTTATCGTTT GTCATTATCA CAAATATATC AACATAGGAC TTTTAAAAGA 360  
TATTTTGTAC ATATTGGGCC TTAGTAGGAT TTTGCATGAA TTTTMTTTTT CTTTATGCC 420  
45 CAGAGAGAAA GAGCAAAGAA ATAACCAAGG GTGATGTACT CGTATGAAG GTTTACCAA 480  
TAAGGACTGC TTTTATTATG AACTATAGTC TATATTCTAA GTAAATCAAT TTTCTATTA 540  
TGTGTTTTTT GTTCTGCAG GCAAGATCTC TGAACTTTAT GCAGAGGGTT CTTTAAAAA 600  
50 AACAAAGTTG AATTTTTTTA TTTCTGGAA TATTTTTTTT CATTGATTTC TCCCAAGTAG 660  
AGCAGATTCA AATCTCCTTT GTACCCTATG TCTTTTTTGT TTTGCTATTA GCTCAGTATT 720  
55 CGGTTTCTAC ATTTTCCTTT CCTAGAACCA GTCAATAAAT GACAAAAAA AAAAAAAAAA 780  
ACTCGA 786

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## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1758 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

10 GGGACGAGCC CTGCCACCT CCTGCAGCCT CTGCGCCCC GCCGAGCTGG CGGATGGAGC 60  
 TCGCACGGG GAGCGTGGG AGCCAGGCGG TGGCGCGGAG GATGGATGGG GACAGCCGAG 120  
 15 ATGGCGGCGG CGGCAAGGAC GCCACCGGT CGGAGGACTA CGAGAACCTG CCGACTAGCG 180  
 CCTCCGTGTC CACCCACATG ACAGCAGGAG CGATGGCCGG GATCCTGGAG CACTCGGTCA 240  
 20 TGTACCCGGT GGA CTGGTG AAGACACGAA TGCAGAGTTT GAGTCCAGAT CCCAAAGCCC 300  
 AGTACACAAG TATCTACGGA GCCCTCAAGA AAATCATGCG GACCGAAGCT TCTGGAGGCC 360  
 CTGCGAGGC GTCAACGTCA TGATCATGGG TGCAGGGCCR GCCCATGCCA TGTATTTTGC 420  
 25 CTGCTATGAA AACATGAAAA GGACTTTAAA TGACGTTTTC CACCACCAAG GAAACAGCCA 480  
 CCTAGCCAAC GGTATTTTGA AAGCGTTTGT CTGGAGTTAG AAAGTTCTCT TCTTCAACAC 540  
 30 GTCCCTCCCC AGGGTGTTC TCCCTGTGAC CCAGCCGCCT CGACTTGGG CCGCTTGCTC 600  
 ACGAATAAAG AACTCAGAGT TGTGTGTGCA ATGCACACCC AGACACACGC ACGCACACAC 660  
 ACGCGCGCGC ACACACATGC TTTTCTCTGT TCCCTCCGC TTTCTGAAGC CTGGGGAGAA 720  
 35 ATCAGTGACA GAGGTGTTTT GGTTTTATTG TTATGTGGGT TTTCTTTTGT ATTTTMTTTG 780  
 TTTGTTTTGT TTTTAAACAT TCAAAAGCAA TTAATGATCA GACATAGGAG AAACCTGAA 840  
 40 TAGAAACAAA ACTTTTGAAT GCTGGATTCA AAAAAAAAAA AAAGTTATCT GGACAGCTTC 900  
 TTTGAGACTA TTTAAAACT GGTACAACAG GTCTCTACAA CGCCAAGATC TAACTAAGCT 960  
 TTAAAAGGTC AAGAAGTTTT ATGGCTGACA AAGGACTCGC GCAACGCAGA AGGCCTTTCC 1020  
 45 CACCTTAAGC TTCCGGGGAT CTGGGAATTT TACCCCAATT CTCTTCTGTT TGTCTGAGTC 1080  
 TCATCTCTCT GCAAGCAAGG GCTGAAATCA TTTTGTGTTG TTGTTTTGAG GGAGAGAGGC 1140  
 50 GGGGTGGGGG GGTGCAAATC TGCCAGCAGC TCTTACGTAA GGCATGTTTT ATTGGGGAGG 1200  
 GCTGAGCTTT TATTTTCTCC TCTCCAGTGG GGTGCGCTT TATGTCTTCT TGTTTGGGTT 1260  
 TGGAAATGGA ATATGGATAG CAGCATAAAG TACTTTTATT TTGACAAAAT TCATTTTTTT 1320  
 55 CAACAATGGA GACATAGATT TGACCCACAA TAACTTCTCC CCTCTCTTT TACTCTGCT 1380  
 CAAAAGCAT CTCTCTCCC ATTACCCAAC CTGGTCATA AGTGTGCCTG GCTGGTTTGC 1440  
 60 AGATATTTGT TCTGCTTGT AAAAATTGGC CATTAGTGCA TTTATTGAGA TGATCTCTAA 1500

AGAGCTATGC CCTGACCTAC CCCTGATTCT ATGACATTGG GGCCCTTCTT TTGCTGAAAC 1560  
5 TGCCTTACGT AATGGTTTTA CTCCTTGAAA GAGATTGAC GGAATCCATT TTATGCCAAG 1620  
TGCTGCCCTG CACTGTTTCT GCAATATGTG GTGTATGCTG TGGTGATCTT GCTGGGAATG 1680  
ATTATAAGTG TGTGTGTGGT GGGGGAGTGG GTATTACATG CATTGCTGAA GAGTCAAAAA 1740  
10 AAAAAAAAAA AAACTCGA 1758

15 (2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 888 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

25 CTGTTAGAAT GCCCAGTTTA CCTGGATGGC AACCCAACAG TGCTCCTGCC CACCTGCCCC 60  
TCAATCCTCC TAGAATTCAG CCCCCAATTG CCCAGTTACC AATAAAAACT TGTACACCAG 120  
30 CCCAGGGAC AGTCTCAAAT GCAAATCCAC AGAGTGASMC ACCACCTCGG GTAGAATTG 180  
ATGACAACAA TCCCTTTAGT GAAAGTTTTC AAGAACGGGA ACGTAAGGAA CGTTTACGAG 240  
AACAGCAAGA GAGACAACGG ATCCAATCA TGCAGGAGGT AGATAGACAA AGAGCTTTGC 300  
35 AGCAGAGGAT GGAAATGGAG CAGCATGGTA TGGTGGGCTC TGAGATAAGT AGTAGTAGGA 360  
CATCTGTGTC CCAGATTCCT TTCTACAGTT CCGACTTACC TTGTGATTTT ATGCAACCTC 420  
TAGGACCCCT TCAGCAGTCT CCACAACACC AACAGCAAAT GGGGCAGGTT TTACAGCAGC 480  
40 AGAATATACA ACAAGGATCA ATTAATTCAC CCTCCACCCA AACTTTTCATG CAGACTAATG 540  
AGCGAGGCAG GTAGGCCCTC CTTCATTTGT TCTGATTC AATCAATCC CTGTTGGAAG 600  
45 CCCAAATTTT TCTTCTGTGA AGCAGGGACA TGGAAATCTT TCTGGGACCA GCTTCCAGCA 660  
GTCCCCAGTG AGGCCTTCTT TTACACCTGC TTTACCAGCA GCACCTCCAG TAGCTAATAG 720  
50 CAGTCTCCCA TGTGGCCAAG ATTCTACTAT AACCCATGGA CACAGTTATC CGGGATCAAC 780  
CCAATCGCTC ATTCAGTTGT ATTCTGATAT AATCCCAGAG GAAAAAGGGN AAAAAAARA 840  
AMAARAARA ARAAAGGAGA TGATGATGCA GAATTCCACC AAGGCTCC 888

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(2) INFORMATION FOR SEQ ID NO: 175:

- 60 (i) SEQUENCE CHARACTERISTICS:

426

(A) LENGTH: 2379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

	GGCAGAGCTA GTGTGGACTC CATCCCCCTG GAGTGGGATC ACGNCTATGA CCTCAGTCGG	60
10	GACCTGGAGT CTGCAATGTC CAGAGCTCTG CCCTCTGAGG ATGAAGAAGG TCAGGATGAC	120
	AAAGATTTCT ACCTCCGGGG AGCTGTTGSC TTATCAGGGG ACCACAGTGC CCTAGAGTCA	180
15	CAGATCCGAC AACTGGGCAA AGCCTGGATG ATAGCCGCTT TCAGATACAG CAAACCGAAA	240
	ATATCATTCG CAGCAAACT CCCACGGGGC CGGAGCTAGA CACCAGCTAC AAAGGCTACA	300
	TGAAACTGCT GGGCGAATGC AGTAGCAGTA TAGACTCCGT GAAGAGACTG GAGCACAAAC	360
20	TGAAGGAGGA AGAGGAGAGC CTTCTGGCT TTGTTAACCT GCATAGTACC GAAACCCAAA	420
	CGGCTGGTGT GATTGACCGA TGGGAGCTTC TCCAGGCCCA GGCATTGAGC AAGGAGTTGA	480
25	GGATGAAGCA GAACCTCCAG AAGTGGCAGC AGTTTAACTC AGACTTGAAC AGCATCTGGG	540
	CCTGGCTGGG GGACACGGAG GAGGAGTTGG AACAGCTCCA GCGTCTGGAA CTCAGCACTG	600
	ACATCCAGAC CATCGAGCTC CAGATCAAAA AGCTCAAGGA GCTCCAGAAA GCTGTGGACC	660
30	ACCGCAAAGC CATCATCTC TCCATCAATC TCTGCAGCCC TGAGTTCACC CAGGCTGACA	720
	GCAAGGAGAG CCGGGACCTG CAGGATCGCT TGTSGCAGAT GAATGGGCGC TGGGACCGAG	780
35	TGTGCTCTCT GCTGGAGGAG TGGCGGGGCC TGCTGCAGGA TGCCCTGATG CAGTGCCAGG	840
	GTTTCCATGA AATGAGCCAT GGTTCGCTTC TTATGCTGGA GAACATTGAC AGAAGGAAAA	900
	ATGAAATGTT CCCTATTGAT TCTAACCTTG ATGCAGAGAT ACTTCAGGAC CATCACAAC	960
40	AGCTTATGCA AATAAAGCAT GAGCTGTTGG AATCCCAACT CAGAGTAGCC TCTTTGCAAG	1020
	ACATGTCTTG CCAACTACTG GTGAATGCTG AAGGAACAGA CTGTTTAGAA GCCAAAGAAA	1080
45	AAGTCCATGT TATTGGAAAT CGGCTCAAAC TTCTCTTGAA GGAGGTCAGT CGTCATATCA	1140
	AGGAACTGGA GAAGTTATTA GACGTGTCAA GTAGTCAGCA GGATTGTCT TCCTGGTCTT	1200
	CTGCTGATGA ACTGGACACC TCAGGGTCTG TGAGTCCAY ATCAGGAAGG AGCACCACAA	1260
50	ACAGACAGAA AACGCCACGA GGCAAGTGTA GTCTCTCACA GCCTGGACCC TCTGTCAGCA	1320
	GTCCACATAG CAGGTCCACA AAAGTGGCT CCGATTCTC CTTTCTGAG CCARGGCCAG	1380
55	GTGGGTCCGG CCGCGGCTTC CTGTTTCAGAG TCCTCGAGC AGCTCTTCCC CTTTCAGCTC	1440
	TCCTGCTCCT CCTCATCGGG CTTGCCTGCC TTGTACCAAT GTCAGAGGAA GACTACAGCT	1500
	GTGCCCTCTC CAACAACCTT GCCCGGTCAT TCCACCCCAT GCTCAGATAC ACGAATGGCC	1560
60	CTCTCCACT CTGAACTAAG CAGATGCCAT CTGCAGAAGT GCTGGTAGCA TAAGGAGGAT	1620



5 CGGGTCATAA GCAATCCCAA ACTACCAACA AGAGGACCTT GATCTTGGCG AAAGCCMTCG 1680  
 GTGTGGCAGC TTTAGCCTCC TCCAGATCAC ATGTGTGCAA ATTATGGCTT CAGAGGTGGA 1740  
 AGATAAACAG TGACGGGGGA ACAAACAGAC AACAAGAAGG TTTGGAAGAA ATCTGGTTTG 1800  
 AGACTCTGAA CCTTAGCACT AAGGAGATTG AGTAAGGACC TCCAAAGTTC CCCGGACTCA 1860  
 10 TGAATTCTGG GCCCTTGGCC NATTCTGTGC ACAGCCAAGG ACTTCAGTAG ACCATCTGGG 1920  
 CAGCTTTCCC ATGGTGCTGC TCCAACCATC AGATAAATGA CCTCCCAAG CACCATGTCA 1980  
 GTGTCGTACA ATCTACCAAC CAACCAGTGC TGAAGAGATT TTAGAACCTT GTAACATACA 2040  
 15 ATTTTAAAGA GCTTATATGG CAGCTTCCTT TTTACCTTGT TTTCTTTGG GGCATGATGT 2100  
 TTTAACCTTT GCTTTAGAAG CACAAGCTGT AAATCTAAAA GGCACCTTTT TTTAGAGGTA 2160  
 20 TAAAGAAAAA CTAGATGTAA TAAATAAGAT CATGGAAGGC TTTATGTGAA AAAAGTTGAA 2220  
 TGTATAGTA AAAAAAAG ATATTATGT ATGTACAGTT TGCTAAAGCC AAGTTTGT 2280  
 TGTATTGATT TCTTGCATT TATTATAGAT ATTATAAAT AAAAAAAAAA AAAAAAAC 2340  
 25 TCGAGGGGGG GCCCGGTACC CAATCGCCC TATAGTGAG 2379

30

(2) INFORMATION FOR SEQ ID NO: 176:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

GCGCCTTAC GATGCCGCG GTCAGTGGTC CAGGTCCCTT ATTCTGCCTT CTCCTCCTGC 60  
 TCCTGGACCC CCACAGCCCT GAGACGGGT GTCTCTCTCT ACGCAGGTTT GAGTACAAGC 120  
 45 TCAGCTTCAA AGGCCCAAG CTGGCATTGC CTGGGGCTGG AATACCCTTC TGGAGCCATC 180  
 ATGGAGGTGA GGGGCAGGG TGGGACCGC TATGCCCAGG GTCCCTCAA GTGCTGGAGG 240  
 GGCTGTRACT TGGTGGGGAG TGGGTCTGTC ACAGCCATCC TCTGTCCAGG GTGGGGCAAG 300  
 50 GCCTGGGACA GTGCCAGGCA CCCCAGGACC CCTTCCAGGC TTGTCTCTCT CTCCACCGCC 360  
 TCAACACCCC CCACCCCTGC CCAAGCTGTT TCTCTCTGTC CTCTCTNNTT CCCTGCCCCA 420  
 55 GGACTTCTCT CTCTCTCTCT GCCTCTCCTT GGACCCCTGC CCTTCTCTTA CCTCTGACCT 480  
 GTGAACACAC AGACACATGC TCACACACTA AGTCCCARGC ACACMSAAG GCAATGTGGA 540  
 CCAGCACAAA CCTCCACTCT CCCGGCTCCA TCCCARCGG CCTGTGGCTG GCCATGAAAA 600  
 60

CTGGGGGCTA CCTGGAGGGA AGCATCCTCA TCCCAGGTGA GTGGGCACCA GCCCTTCCCT 660  
 GTATGTGTGT TGTGGGTGGA AGCAGGCATG AGAGCATCTT AGCCCATAGG TTGTATTCA 720  
 5 GGGACTTCCA AACCCAGACC TACAAAGAGT GTGTCTTCTA CCAGATCTTG TTCAAAAAG 780  
 GGTTTGTGAT GATGGAATA CACGATAGAG GGAGTGAGCA AGAACAATGA GGATTAGAGT 840  
 GGAGCGTGAA ATAGTCTAGG AGCATGGCTT CCAAAACATA TGCTGTGAGG TCTGTCCACC 900  
 10 TGAGAGTTGG GCCATGGATT TAATTCTGAG CCTCTTAGCA GGCAAAGCAA AGACAGAAAG 960  
 CAGATCGGCT GTGGATTCT GTCTATAAAA TGTGAGTTCT TGGCCGGGTG CGGTGGCTCA 1020  
 15 CGCCTGTAAT CCCGGCGCTT TGGGAGGCCA GGGCGGATGG GTCCCGAGGT CAGGAGGTTG 1080  
 GAAACCATCC TGGCCGAAT GGTGAAGCCC TGACTCTACT AGAAGTGCAA AGATTGGCTG 1140  
 GGTGTGGTGG CGTGCCTG TGGTCCCAGC TTCTCGGGAG GCTGAGGCGG GAGAGTTGCT 1200  
 20 TGGGCCTGGG AGGCCGAGGT TGGGTGAGC TGAGATCCTG CCATTGCACT TCAGCCTGGG 1260  
 CACAGAGCCA GACTCTGGCT CAAAAA AAAA AAAA ACTCGAGGGG GGCCCGTACC 1320  
 25 CAATTCGCG NATATGATCG TAAACAAT 1348

30 (2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1502 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

40 CTCAAATAA ATAAATAAAT AAAAATTTGT ATTCCATTGA TTTGGGTAGA CACCAGGAAT 60  
 GTGCATTTCT AACAAGCTTT CCAGGCGATC CTATAGTAAG TCATCTGTGG ACTACTTTAA 120  
 GAAACTCTTC TATAGAGAAT GGAGTTGGAT TAATAATAGG TGATTTTSTA CACTGGACTG 180  
 45 ATTCACAAGA ACCTAAACAG TAGTCCATGA AGCTGCTCAT CTGTGGTAAC TATTTGGCCC 240  
 CGTCTCACTC TGAAAGCAGC AGGAGATGTT GTTTACTTTG TTTCTATCCC CTTTGTCTGG 300  
 50 AGATTAATTT TGAATGAAA GTTTTCTCT CTATGCCATT CTGGTTCTT TTCCAAAGCC 360  
 TCATACAAGA GGATTAGGTC ACAATGCATG CATTAACCTT TAAAGAATG CGATATTGAT 420  
 ACCGATGCTT ACTTTTTTTT TTTTNACTA CTTGTTTTAT TCCTCCAGN AAAGTATAGC 480  
 55 CCGCCTTTCT ATAGCATAGT TCTCTTTAGG TGGAATGATT CCTATAAGAT TTCTCATTAT 540  
 TAAATCATGC ATTTTTCAAG ATGGAATCAA TMTTTGATTT AATCTAAGCT GATATCTCA 600  
 60 TTTGTTAGAA GAACAACCTA CATGCTAGAG AGAGAGGAGG AAATATACCC ACGACCACAC 660

AGCCAGTTAG TATCCAGTTG GTGCTGGACT CCAGCCAGGT GTCCTGCCTC ATGGTAGTTA 720  
 AATGATATAT AGAAAAGGTA AATTTTTTAAA GAAATATTTA TTAATATATT CCTATAAAAC 780  
 5 ATTTTAAAGG TAACCACATA AAAATGGTTA ATTTTTCAT TCCAAAGTAA ATGCTAAGCA 840  
 TGTTTATTAA TGAAGCAGTA CTTCTGATTA GTATATGACA TTCTGAAGTT AATTAAACTC 900  
 10 ATTGCACTAA ATGTGTCTTC CTTGGTATAG TGGAGGATTT GAGGATTGGA ATATAGAGTA 960  
 GAGTGCTTGC TTAAGCCTGG GAGCCCATCT TTATAGCTAT TTGATGTAAG AAAAGAGACA 1020  
 TGNCCATTT CTAACTATA TAAGGTGAGT GTGTCTATTC CCAGCAGATA TAAAGGAAAA 1080  
 15 AGGAAACTTT TTTGATTCCC ACCTTCCCAG CCTCACCTAG CCATCTTCCA GCCTCAAATA 1140  
 TAGAGATGTT AGTGCAAGGT CCTGGGCTCT AGGTGATCAT TTCATAAGTC CTTTACAGAT 1200  
 20 AAAGAAAAAG TAGTGTGTTG ATGTTTGTGTT TTAAGTAACC CCAAACAAA TTTATATTGT 1260  
 ATTCAGCAAA ATTGGAATTC AGGTGTTTAA TTTTGAACA TGAAGTGCCT GCTGTTTTAA 1320  
 GCATTGACTT GTATAAAAAG AATTGCATGT CTCCAGTAAG CTTATGGGTT TTCTCATTTT 1380  
 25 TAGGTATATG GCTTTTAATC ATGTAAAGTG AACATTAGT TTTCTTGCAT TTTATTACAG 1440  
 GTTCTTTGTT GCAATAAAGA TGCTGCTGAA ATTAATTGAA AAAAAAAAAA AAAAAAACTC 1500  
 30 GA 1502

35 (2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1637 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

45 ATTTTCTAGC CCACAAGGAC TGAAGTTCAG ATCCAAAAGT TCACTTGCTA ATTATCTTCA 60  
 CAAAAATGGA GAGACTTCTC TTAAGCCAGA AGATTTTGAT TTTACTGTAC TTTCTAAAAG 120  
 GGGTATCAAG TCAAGATATA AAGACTGCAG CATGGCAGCC CTGACATCCC ATCTACAAAA 180  
 50 CCAAAGTAAC AATTCAAACCT GGAACCTCAG GACCCGAAGC AAGTGCAAAA AGGATGTGTT 240  
 TATGCCGCCA AGTAGTAGTT CAGAGTTGCA GGAGAGCAGA GGACTCTCTA ACTTTACTTC 300  
 55 CACTCATTTG CTTTGTAAAG AAGATGAGGG TGTGATGAT GTTAACTTCA GAAAGGTTAG 360  
 AAAGCCCAAA GGAAAGGTGA CTATTTTGAA AGGAATCCCA ATTAAGAAAA CTAAAAAAGG 420  
 ATGTAGGAAG AGCTGTTTCTG GTTTGTTCM AAGTGATAGC AAAAGAGAAT CTGTGTGTAA 480  
 60

TAAAGCAGAT GCTGAAAGTG AACCTGTTGC ACAAAAAAGT CAGCTTGATA GAACTGTCTG 540  
 CATTTCTGAT GCTGGAGCAT GTGGTGAGAC CCTCAGTGTG ACCAGTGAAG AAAACAGCCT 600  
 5 TGTAACAAAA AAAGAAAGAT CATTGAGTTC AGGATCAAAT TTTTGTCTG AACAAAAAC 660  
 TTCTGGCATC ATAAACAAAT TTTGTTTCAGC CAAAGACTCA GAACACAACG AGAAGTATGA 720  
 GGATACCTTT TTAGAATCTG AAGAAATCGG AACAAAAGTA GAAGTTGTGG AAAGGAAAGA 780  
 10 ACATTTGCAT ACTGACATTT TAAAACGTGG CTCTGAAATG GACAACAACCT GCTCACCAAC 840  
 CAGGAAAGAC TTCACTGAAG ATACCATCCC ACGGAACACA GATAGAAAGA AGGAAAACAA 900  
 15 GCCTGTATTT TTGCAGCAAA TATAACAAAG AAGTCTTTAG CCCCCACGA CGTAAAGCCT 960  
 TTAAGAAATG GACACCTCCT CGGTACCTTT TTAATCTCGT TCAAGAAACA CTTTTTCATG 1020  
 ATCCATGGAA GCTTCTCATC GCTACTATAT TTCTCAATCG GACCTCAGGC AAAATGGCAA 1080  
 20 TACCTGTGCT TTGGAAGTTT CTGGAGAAGT ATCCTTCAGC TGAGGTAGCA AGAACCGCAG 1140  
 ACTGGAGAGA TGTGTCAGAA CTTCTTAAAC CTCTTGGTCT CTACGATCTT CGGGCAAAAA 1200  
 25 CCATGTCAA GTTCTCAGAT GAATACCTGA CAAAGCAGTG GAAGTATCCA ATTGAGCTTC 1260  
 ATGGGATTGG TGCACCCTGA AGACCACAAA TTAATAAAT ATCATGACTG GCTTTGGGAA 1320  
 AATCATGAAA AATTAAAGTCT ATCTTAACT CTGCAGCTTT CAAGCTCATC TGTATGCAT 1380  
 30 AGCTTTGCAC TTCAAAAAG CTTAATTAAG TACAACCAAC CACCTTTCCA GCCATAGAGA 1440  
 TTTTAATTAG CCCAACTAGA AGCCTAGTGT GTGTGCTTTC TTAATGTGTG TGCCAATGGT 1500  
 35 GGATCTTTC TACTGAATGT GTTTGAACAT GTTTTGAGAT TTTTAAAAA TAAATTATTA 1560  
 TTTGACAACA ATCCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1620  
 40 AAAAAAAAAA AAAAAA 1637

## (2) INFORMATION FOR SEQ ID NO: 179:

45

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2911 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

55 GGTGGTTTTT GTTCTGCAAT AGGCGGCTTA GAGGGAGGGG CTTTTTCGCC TATACCTACT 60  
 GTAGCTTCTC CACGTATGGA CCCTAAAGGC TACTGCTGCT ACTACGGGGC TAGACAGTTA 120  
 CTGTCTCAGC TCTAGGATGT GCGTCTTCC ACTAGAAGCT CTTCTGAGGG AGGTAATTAA 180  
 60 AAAACAGTGG AATGGAAAA CAGTGCTGTA GTCATCCTGT AATATGCTCC TTGTCAACAA 240

	TGTATACATT CCTGCTAGGT GCCATATTCA TTGCTTTAAG CTCAAGTCGC ATCTTACTAG	300
	TGAAGTATTC TGCCAATGAA GAAAACAAGT ATGATTATCT TCCAACTACT GTGAATGTGT	360
5	GCTCAGAACT GGTGAAGCTA GTTTTCTGTG TGCTTGTGTC ATTCTGTGTT ATAAAGAAAG	420
	ATCATCAAAG TAGAAATTTG AAATATGCTT CCTGGAAGGA ATTCTCTGAT TTCATGAAGT	480
10	GGTCCATTCC TGCCTTTCTT TATTTCTCTG ATAACCTGAT TGTCTTCTAT GTCCTGTCCT	540
	ATCTTCAACC AGCCATGGCT GTTATCTTCT CAAATTTTAG CATTATAACA ACAGCTCTTC	600
	TATTCAGGAT AGTGCTGAAG ANCGTCTAA ACTGGATCCA GTGGGCTTCC CTCCTGACTT	660
15	TATTTTTGTC TATTGTGGCC TTGACTGCCG GGAATAAAC TTACAGCAC AACTTGGCAG	720
	GACGTGGATT TCATCAGAT GCCTTTTTCA GCCCTTCCAA TTCCTGCCTT CTTTTCAGAA	780
20	ATGAGTGTCC CAGAAAAGAC AATTGTACAG CAAAGGAATG GACTTTTCCT GAAGCTAAAT	840
	GGAACACCAC AGCCAGAGTT TTCAGTCACA TCCGTCTTGG CATGGGGCAT GTTCTTATTA	900
	TAGTCCAGTG TTTTATTTCT TCAATGGCTA ATATCTATAA TGAAAAGATA CTGAAGGAAG	960
25	GGAACCAGCT CACTGAARGC ATCTTCATAC AGAACAGCAA ACTCTATTTT TTTGGCATT	1020
	TGTTTAATGG GCTGACTCTG GGCCTTCAGA GGAGTAACCG TGATCAGATT AAGAACTGTG	1080
30	GATTTTTTTA TGCCACAGT GCATTTTCAG TAGCCCTTAT TTTTGTAAT GCATTCCAGG	1140
	GCCTTTCAGT GGCTTTCATT CTGAAGTTC TGGATAACAT GTTCCATGTC TTGATGGCCC	1200
	AGGTTACCAC TGTCATTATC ACAACAGTGT CTGTCTGGT CTTTGACTTC AGGCCCTCCC	1260
35	TGGAATTTTT CTTGGAAGCC CCATCAGTCC TTCTCTCTAT ATTTATTTAT AATGCCAGCA	1320
	AGCCTCAAGT TCCGAATAC GCACCTAGGC AAGAAAGGAT CCGAGATCTA AGTGGCAATC	1380
40	TTTGGGAGCG TTCCAGTGGG GATGGAGAAG AACTAGAAAG ACTTACCAA CCAGAGTG	1440
	ATGAGTCAGA TGAAGATACT TTCTAACTGG TACCCACATA GTTTGCAGCT CTCTGAACC	1500
	TTATTTTCAC ATTTTCAGTG TTTGTAATAT TTATCTTTT ACTTTGATAA ACCAGAAATG	1560
45	TTCTAAATC CTAATATTCT TTGCATATAT CTAGCTACTC CCTAAATGGT TCCATCCAAG	1620
	GCTTAGAGTA CCCAAAGGCT AAGAAATCT AAAGAACTGA TACAGGAGTA ACAATATGAA	1680
50	GAATTCATTA ATATCTCAGT ACTTGATAAA TCAGAAAGTT ATATGTGCAG ATTATTTTCC	1740
	TTGGCCTTCA AGCTTCCAAA AAACCTGTAA TAATCATGTT AGCTATAGCT TGTATATACA	1800
	CATAGAGATC AATTTGCCAA ATATTCACAA TCATGTAGTT CTAGTTTACA TGCCAAAGTC	1860
55	TTCCCTTTTT AACATTATAA AAGCTAGGTT GTCTCTTGAA TTTTGAGGCC CTAGAGATAG	1920
	TCATTTTGCA AGTAAAGAGC AACGGGACCC TTTCTAAAA CGTTGGTTGA AGGACCTAAA	1980
60	TACCTGGCCA TACCATAGAT TTGGGATGAT GTAGTCTGTG CTAAATATTT TGCTGAAGAA	2040

GCAGTTTCTC AGACACAACA TCTCAGAATT TTAATTTTGA GAAATTCATG GGAAATTGGA 2100  
TTTTTGTAAT AATCTTTTGA TGTTTTAAAC ATTGGTTCCC TAGTCACCAT AGTTACCACT 2160  
5 TGTATTTTAA GTCATTTTAA CAAGCCACGG TGGGGCTTTT TTCTCCTCAG TTTGAGGAGA 2220  
AAAATCTTGA TGTCATTACT CCTGAATTAT TACATTTTGG AGAATAAGAG GGCATTTTAT 2280  
10 TTTATTAGTT ACTAATTCAA GCTGTGACTA TTGTATATCT TTCCAAGAGT TGAAATGCTG 2340  
GCTTCAGAAT CATAACAGAT TGTCAGTGAA GCTGATGCCT AGGAACTTTT AAAGGGATCC 2400  
TTTCAAAAGG ATCACTTAGC AAACACATGT TGACTTTTAA CTGATGTATG AATATTAAATA 2460  
15 CTCTAAAAAT AGAAAGACCA GTAATATATA AGTCACTTTA CAGTGCTACT TCACACTTAA 2520  
AAGTGCATGG TATTTTTCAT GGTATTTTGC ATGCAGCCAG TTAAGTCTCG TAGATAGAGA 2580  
20 AGTCAGGTGA TAGATGATAT TAAAAATTAG CAAACAAAAG TGAAGTCTC AGGGTCATGC 2640  
AGCTGGGTGA TGATAGAAGA GTGGGCTTTA ACTGGCAGGC CTGTATGTTT ACAGACTACC 2700  
ATACTGTAAA TATGAGCTTT ATGGTGTCT TCTCAGAAAC TTATACATTT CTGCTCTCCT 2760  
25 TTCTCCTAAG TTTCATGCAG ATGAATATAA GGTAATATAC TATTATATAA TTCATTTGTG 2820  
ATATCCACAA TAATATGACT GGCAAGAATT GGTGGAATT TGTAATTAAA ATAATTATTA 2880  
30 AACCTAAAAA AAAAAAAAAA AAAAAGCTGA G 2911

35 (2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 519 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

45 GGCACGAGCC CCAGGCCAGC CAGGCCAGG CCTACTTTGG CCACCCTTAA ATTAGAATGT 60  
GGGGTCAGGG GTCACAGAAA AGCCATTTCT CTGACCTAGT GTTTGGCGTC CGGGAACTCT 120  
GTGCCCCAACC TTCAGACCCT GGCAGTCCTC ACTGAGGCCA TTGGCCCAGA GCCCCCATC 180  
50 CCCCAGARACC CCGGGAGGCC GCCTGTGACC ACGTCCACAC CTGCCACACC CTCTGCCGGG 240  
CCCCAGCCCC TCCCAACCGG GACCGTGTCT GTCCCTGGGG GTCCCTGCCCC ACCTTGCTTT 300  
55 GGGGAGGCAT GGGCCCTCCT CCTCCACCC TGCCGGCCGT CACTCACCTC TTGCTTCTGG 360  
TCCCCAGGC CTAGCCCTTG GAAGGAGACA GGAGTCTAGG GAGGCTGAAG CCCACTCCCG 420  
GGGAGGCCCG TGCTCTCCA GCCCCAGGA CAGCAAGGAA AAGAGAAGAG AGCAGAGCAT 480  
60

TTCATGGCTC TAATAAAAAA AAAAAAAAAA AAAACTCGA

519

5

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 968 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

15

TCCCCCTGGG GCCGGA AAAA GCGGGGTGG CCTGNCCATT GGTINTCCAT GCCCCCCGCC 60

CATGCCCCAG TACTAGCCTG CAGTCCCAAT GTAGCCCTC CCTCYTCCMA GAGCCCYTCM 120

20 AACCGCCCCG STCANTTGTG ATTTCAGGAG GATTTGATGA AGATGTTAAA GCGAAAGTGG 180

AGAACCTTCT CGGGATTTC AGCCTGGA AAACGGACCC TGTTAGGCAA GCACCTGCA 240

25 GCCCTCCCTG TCCCTTCTT CCCCTCCCCT TCYCCCGCCC GTGGAGACAG CTGTTYTCAG 300

CAGGGCTCTC CGCAGGGAGG GGGCCGGCTC CTTCCCTGGC AGCAACATCC TTGCCCTTGT 360

CACACAAGTC AGCCTCCATC TGCGCAGCTC TGTGGATGCG CTGCTGGAGG GCAACAGGTA 420

30 TGTCACTGGC TGGTTCAGCC CCTACCACCG CCAGCGGAAG CTCATCCACC CGGTCATGGT 480

TCAGCACATC CAGCCCGCAG CGCTCAGCCT CTTGGCACAG TGGAGCACCC TCGTGCAGGA 540

35 GCTGGAGGCT GCCCTGCAGC TGGCTTTCTA CCCGGATGCC GTGGAGGAGT GGCTGGAGGA 600

AAACGTGCAC CCCAGCCTGC AGCGGCTGCA ARCTCTGCTG CAGGACCTCA GCGAGGTGTC 660

TGCCCCCCCG CTGCCACCCA CCAGCCCTGG CAGGGACGTT GCTCAGGACC CCTGAGGGGA 720

40 GAGCTCATGC CAGGGGGCTC CTGCTGGAGG CTGGGGGGGC TCTGCWYTKY CWWWITGCCT 780

GGGCAATACG GCCCACGTGG GCGTCGTGCC CTCTGGCCCA GCAGTGTCTT GCCCACTC 840

45 AGTTCCTGAG GGCCCTGGG AGCCCCCTGG GGAGAGACTA GAAAACACAG AAGGAAGCAG 900

CACAGGGAGA CCCGCTTTGT GATCTGCATG TGTGACACTG ATTCTTTGGA AATAAAGAGT 960

GGAAGCTG 968

50

(2) INFORMATION FOR SEQ ID NO: 182:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

TGTAAGAGTT ATCAGTAATC CTAATCTTT TCCTGGGTTT TCCTTTTGTC ACTTATTAAT 60  
 5 CAGTTTTTGA AAGGACGAAT GAATTTAGAG ATGTACTCTG GAGCAGTATC ATGTTAAACC 120  
 AGGGGTATAT TAGAAAAATC ATCCTCATAA TCATTCTGGG AAGTTTTTCC TCCCCAAAAA 180  
 AAGCCATCCT GATGGGTTTT CAAAACCAGA AAAAGCTCT TAATGAGGAA CAGACCACTG 240  
 10 GAGTACCCAT GAGCATCTCA GGAAACTGA GACCTCGAG AAGCCTTGAT TTCGTGCAAC 300  
 CCCCAGGTT TCAGAGCCAG CAGCCAGTG CTGTGGTTGA CAGACGTGGT TTTKTGGRGA 360  
 15 AAGCAGCCAG AGGCCAGGAA TTTTCAGAGT CGTGAGTCAC GRTYTCCAC CCAAGATTAG 420  
 AGCAGAGATT AGCCATACCT AGATTTGGTA AAATCATTCT GTCTAAGCAA TGGAGGTGTG 480  
 TGCAMACGTG CAGTGCCTGT TCACAGGGGA TGCAGGCAGA TCSYGGGTTT AGGATGGGGR 540  
 20 AGGCCACCGC ACCCCCYTTC AYTGCTCTGC ACCTGCTCCC TCACGTGGAC ACTGTCCACA 600  
 ACTGTGGCTC TCACAGGACA GTTGCCCAAG GAGCTCATAT CTTATTGGAG ATAGGGGGTC 660  
 25 GTACAGGTGA CATTCATGAG CAGTGTGAGC CGGGTGACAT GGGGGTGTA ACCCAGCATC 720  
 TGTCCAGGAG CTCCTCTGC AGCGGCTCTG GCAGGTGGCC TGAGGCTCCT TTTTGAGAGA 780  
 GAACTGTTTG GCCTTCCTGT CTCCTCTCCT CTGATCTGTT CTTTCTTGGA ACACCACCCA 840  
 30 AGAACGTCAC CTCCTCCATC AGATGTGAG CTCCTGGAGG GCAGGAGCTG TGTCTTCTA 900  
 TTCATCTTCC TATCCCCAGA ACCTGCACA GATCCTGGAA TGTGGTAGGT GCTCAGTAAA 960  
 35 TGTGTGTGA ATAAATGAAT GAATGAATGA ACAAATGAAT GAATTTGCTT ACTTCAAGGC 1020  
 AAAAGAACCA TGAAACTGTA TTTTGAGTTT CTATGTTATA GCAGTCAGCA AATCCTATTA 1080  
 40 AATACTTTGT GTTTCGAAGC AAAAAAAAAA AAAAAAAAAA AACTCGA 1128

## (2) INFORMATION FOR SEQ ID NO: 183:

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

CCGCGGCGTC TGACCTCATG GCGTAGAGCC TAGCAACAGC GCAGGCTCCC AGCCGAGTCC 60  
 55 GTTATGGCCG CTGCCGTCCC GAAGAGGATG AGGGGGCCAG CACAAGCGAA ACTGCTGCCC 120  
 GGGTGGGCCA TCCAAGCCCT TGTGGGGTTG GCGCGGCCGC TGGTCTTGGC GCTCCTGCTT 180  
 60 GTGTCCGCGC CTCTATCCAG TGTGTATCA CGGACTGATT CACCGAGCCC AACCGTACTC 240



	AACTCACATA TTTCTACCCC AAATGTGAAT GCTTTAACAC ATGAAAACCA AACCAAACCT	300
	TCTATTTCCC AAATCAGCAC CACCCTCCCT CCCACGACGA GTACCAAGAA AAGTGGAGGA	360
5	GCATCTGTGG TCCCTCATCC CTCGCCTACT CCTCTGTCTC AAGAGGAAGC TGATAACAAT	420
	GAAGATCCTA GTATAGAGGA GGAGGATCTT CTCATGCTGA ACAGTTCTCC ATCCACAGCC	480
10	AAAGACACTC TAGACAATGG CGATTATGGA GAACCAGACT ATGACTGGAC CACGGGCCCC	540
	AGGGACGACG ACGAGTCTGA TGACACCTTG GAAGAAAACA GGGGTTACAT GGAAATGAA	600
	CAGTCAGTGA AATCTTTTAA GATGCCATCC TCAAATATAG AAGAGGAAGA CAGCCATTTT	660
15	TTTTTTCATC TTATTATTTT TGCTTTTTCG ATTGCTGTTG TTTACATTAC ATATCACAAC	720
	AAAAGGAAGA TTTTCTTCTT GGTTCAAAGC AGGAAATGGC GTGATGGCCT TTGTTCCAA	780
20	ACAGTGAAT ACCATCGCCT AGATCAGAAT GTTAATGAGG CAATGCCTTC TTTGAAGATT	840
	ACCAATGATT ATATTTTTTA AAGCACTGTG ATTTGAATTT GCTTATGTAA TTTTATTTGC	900
	TTGACTTTTT ATATGATATT GTGCAAATGT TTGCCATAGG CAATTGGTAC TTAAATGAGA	960
25	GGTGAGTCTC TCTTTTGCCT TGGTGCTTTG GAAATTAAAT GTCACAAACG AGTATATAAT	1020
	TTTTTATCTG TACTTTTAGA GCTGAGTTTA ATCAGGTGTC CAAAATGTGA GTTAAACATT	1080
30	ACCTTATATT TACACTGTTA GTTTTTATTG TTTTAGATTT ATTATGCTTC TTCTGGAAGT	1140
	ATTAGTGATG CTACTTTTAA AAGATCCCAA ACTTGTAAT AAATTCTGAC ATATCTGTTA	1200
	CTGCTGACTC ACATTCATTC TCCGCCATTC AAATACTATT TTTTATCCAC ATTTTTTTTT	1260
35	GTCCCAAAC TGTAATGTAC AAGGATATGT GTGATAATGC TTGGGATTTG AGTAATATTT	1320
	TTTTTCTTC CAAGAAACT GCTTTGGATA TTTTAGATA ATTTAAACAT AATTAGGAT	1380
40	AATGATATTG CTCAATCTGA CCACAATTTT AGGTAAAACA TTAAATGTGT CAGAAATCTT	1440
	GGCAACAGAG ACTCTGCAGC TTGCAGTGA CATAGATAAA ATGTTACAGA GATACTATTT	1500
	TTTGGTTGG AATTACTATA TTAAATTTAG AAGCAGAAAC TGGTAAATG TTAAATACAT	1560
45	GTACAATTGC TTTTAGTTAG CAATTGATTG TAGCATGGGT TCCTCCAAGG TTCAAGCAA	1620
	TGGGCAGAGT TTAAATTTAT ATCAGATTCT TTTACTTCGT TTATTATTTT ACAGTAAATT	1680
50	TGAATAAATC TTAGGGGTCA TTATCACTTA AATAATACTG TACCTAGGTC TTCAAATTA	1740
	AAATTTATACC TGAATGAAGT TGTTTGTATA CATAAAGGAT ATTTGTGTAC AATTACCTTT	1800
	TTTCCCCAC ACTTGTTTTC TTGTTTTTGG TTTTATATGG CAACTGGAAA GTATTTACTA	1860
55	TGGGATTCAT TTAGTCTGT CTTTCTATCA TAAAGAATTG ATCAATATGT AAATATGTGA	1920
	TTTGAACCAT GGTGACTTA CAAGTGTCAC TACAGCTTTT TAGAAAACAT AGCCCTAATA	1980
60	TATGTTAAGC AGGACCCGGG TGAGCCAGTG GGCTTGCCT TTATGTAGAG CTGGAAGAAG	2040

5 GCGGTCCATC CTGTCTCTTG GCGGACAGT GTACTTTCCT AATAGGGAAG GGAAGCACAA 2100  
TGGAAATACC CCTGAACCGT TTTATTGCAG TAATTTTTTT CATATCTGAA ACTATTATTT 2160  
AATATTTTGA ATAAGATTTT AAAAAATAAA TGGCAAAGAT ATAAATCTAA AAAAAAAAAA 2220  
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 2276

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(2) INFORMATION FOR SEQ ID NO: 184:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TCCAAGCTAC GCCACTCGG CTGGGCGGTT GGGAGCGGA GTGCAGAGCG TGGTCGTGGC 60  
GGCGGCGGTG AGAAGAGCGA GGCGKAGGAG GGGGTGCCAT GGCCGGGCAG CAGTTCCAGT 120  
ACGATGACAG TGGGAACACC TTCTTCTACT TCCTCACCTC CTTCTGTTGG CTCATCGTGA 180  
TCCCGGCGAC ATACTACCTC TGGCCCCGAG ATCAGAATGC CGAGCAAATT CGATTAAAGA 240  
ATATCAGAAA AGTATATGGA AGGTGTATGT GGTACGTTTA CGGTATTATA AACCCAGGCC 300  
AAATATTATT CCTACAGTAA AGAAAATAGT TCTGCTTGCA GGATGGGCAT TGTCTTATT 360  
CCTTGCAAT AAAGTTTCCA AACAGACCG AGAATACCAA GAATACAATC CTTATGAAGT 420  
ATTAAATTG GATCCTGGAG CCAQAGTAGC AGAAATTAAA AAACAATATC GTTTGCTGTC 480  
ACTTAAATAT CATCCAGATA AAGGAGGTGA TGAGGTTATG TTCATGAGGA TAGCAAAAGC 540  
TTATGCTGCT TTAACGGATG AAGAGTCCCG GAAAATTGG GAAGAATTG GAAATCCAGA 600  
TGGGCCTCAA GCCACAAGCT TTGGAATTGC CCTGCCAGCT TGGATAGTTG ACCAGAAAAA 660  
TTCAATTCTG GTTTTACTTG TATATGGATT GGCATTATG GTTATCCTTC CAGTTGTTGT 720  
GGGCTCTTGG TGGTATCGCT CAATACGCTA TAGTGGAGAC CAGATTCTAA TACGSACAAC 780  
ACAGATTAT ACATACTTTG TTTATAAAAC CCGAAATATG GATATGAAAC GTCTTATCAT 840  
GGTTTTGGST GGAGCTTCTG AATTGATCC TCAGTATAAT AAAGATGCCA CAAGCAGACC 900  
AACGGATAAT ATTCTAATAC CACAGCTAAT CAGAGAAATT GGCAGCATT AATTAAAGAA 960  
GAATGAGCCT CCACTTACCT GCCCATATAG CCTGAAGGCC AGAGTTCTTT TACTGTCTCA 1020  
TCTTGCTAGA ATGAAAATTC CTGAGACCCT TGAAGAAGAT CAGCAATTCA TGCTAAAAAA 1080  
GTGTCTGCC CTACTTCAAG AAATGGTTAA TGTAATCTGC CAACTAATAG TAATGGCCCG 1140

60

GAACCGTGAA GAAAGGGAGT TTCGTGCTCC AACTTTGGCA TCCCTAGAAA ACTGCATGAA 1200  
GCTTTCTCAG ATGGCCGTTT AGGGACTTCA GCAATTTAAG TCTCCCCTTC TGCAGCTCCC 1260  
5 TCATATTGAA GAGGACAATC TTAGACGGGT TTCTAATCAT AAGAAGTATA AAATTAAAAC 1320  
TATCCAGGAT TTGGTGAGTT TAAAAGAATC AGATCGTCAC ACTCTACTGC ACTTCCTTGA 1380  
AGATGAAAAA TATGAAGAGG TTATGGCTGT CTTGGGAGT TTTCCATATG TGACCATGGA 1440  
10 TATAAAATCA CAGGTGTTAG ATGATGAAGA TAGCAACAAC ATCACAGTAG GATCCTTAGT 1500  
TACAGTGTG GTTAAGTTGA CAAGGCAAAC AATGGCTGAA GTATTTGAAA AGGAGCAGTC 1560  
15 CATCTGTGCT GCAGAGGAAC AGCCAGCAGA AGATGGGCAG GGTGAACTA ACAAGAACAG 1620  
GACAAAAGGA GGATGGCAAC AGAAGAGTAA AGGACCCAAG AAAACTGCTA AATCAAAAAA 1680  
AAAGAAACCT TTAAAAAATA AACCTACACC TGTGCTATTA CCACAGTCAA AGCAACAGAA 1740  
20 ACAAAGCAG GCAATGGAG TCGTTGGGAA TGAAGCTGCA GTAAAGGAAG ATGAAGAAGA 1800  
AGTTTCAGAT AAGGGCAGTG ATTCTGAAGA AGAAGAAACC AATAGAGATT CCCAAAGTGA 1860  
25 GAAAGATGAT GGTAGTGACA GAGACTCTGA TAGAGAGCAA GATGAAAAAC AAAACAAAGA 1920  
TGATGAAGCA GAGTGGCAAG AATTACAACA AAGCATAACG CGAAAAGAGA GAGCTCTATT 1980  
GGAAACCAAA TCAAAAATAA CACATCCTGT GTATAGCCTT TACTTTCTTG AGGAAAAACA 2040  
30 AGAATGGTGG TGGCTTTACA TTGCAGATAG GAAGGAGCAG ACATTAATAT CCATGCCATA 2100  
TCATGTGTGT ACGCTGAAAG ATACAGAGGA GGTAGAGCTG AAGTTTCCTG CACCAGGCAA 2160  
35 GCCTGGAAAT TATCAGTATA CTGTGTTTCT GAGATCAGAC TCCTATATGG GTTTGGATCA 2220  
GATTAAACCA TTGGAAGTTK GGAAGTTCAT GAGGCTGAAG CCTGTGCCAG AAAATCACCC 2280  
ACAGTGGGAT ACAGCAATAG AGGGGGATGA AGACCAGGAG GACAGTGAGG GCTTTGAAGA 2340  
40 TAGCTTTGAG GGAGGAAGAG GGAGGGAGGA AGGAAGGTGG TGGACTTAAG GCAGTTACTC 2400  
TGGAATGGGA CCCACAGTGT TTTGCACCAT ATTTTGGCAA TTTTMTTTCG CCGTTMTTNG 2460  
45 GAAGTGTMTT CCNTNANCC CAGGAACCAT TACAGAACCG 2500

50 (2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1337 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

60 CTTCCGGTTC TCCGGGCAGC TGCCACTGCT GTAGCTTCTG CCACCTGCCA CGACCGGGCC 60

TCTCCCTGGC GTTTGGTCAC CTCTGCTTCA TTCTCCACCG CGCCTATGGT CCCTCTTGGA 120  
GCCAGCGTGG CGGGCCTGGC GGCTCCCGGG TGGTGAGAGA GCGGTCCGGG AACGATGAAG 180  
5 GCCTCGCAGT GCTGCTGCTG TCTCAGCCAC CTCTTGGCTT CCGTCCCTCT CCTGCTGTG 240  
CTGCCTGAAC TAAGCGGGYC CCTGGMAGTC CTGCTGCAGG CAGCCGAGGC CGCGCCAGGT 300  
10 CTTGGGCCTC CTGACCCTAG ACCACGGACA TTACCGCCGC TGCCACCGGG CCCTACCCCT 360  
GCCCAGCAGC CGGGCCGTGG TCTGGCTGAA GCTGCGGGGC CGCGGGGCTC CGAGGGAGGC 420  
AATGGCAGCA ACCCTGTGGC CGGGCTTGAG ACGGACGATC ACGGAGGGAA GGCCGGGGAA 480  
15 GGCTCGGTGG GTGGCGGCCT TGCTGTGAGC CCAACCCCTG GCGACAAGCC CATGACCCAG 540  
CGGGCCCTGA CCGTGTGAT GGTGGTGAGC GCGCGGTGC TGGTGTACTT CGTGGTCAGG 600  
20 ACGGTCAGGA TGAGAAGAAG AAACCGAAAG ACTAGGAGAT ATGGAGTTT GGACACTAAC 660  
ATAGAAAATA TGAATGAC ACCTTTAGAA CAGGATGATG AGGATGATGA CAACACGTTG 720  
TTTGATGCCA ATCATCTCG AAGATAAGAA TGTGCCTTTT GATGAAAGAA CTTTATCTTT 780  
25 CTACAATGAA GAGTGGAATT TCTATGTTTA AGGAATAAGA AGCCACTATA TCAATGTTGG 840  
GGGGTATTT AAGTTACATA TATTTTAACA ACCTTTAATT TGCTGTTGCA ATAAATACCG 900  
30 TATCCTTTTA TTATATCTTT ATATGTATAG AAGTACTCTR TTAATGGGCT CAGAGATGTT 960  
GGGGATAAAG TATACTGTAA TAATTTATCT GTTTGAAAAT TACTATAAAA CCGTGTTTTC 1020  
TGATCGGTTT TTGTTTCTG CTTACCATAT GATTGTAAAT TGTTTTATGT ATTAATCAGT 1080  
35 TAATGCTAAT TATTTTGCT GATGTCATAT GTTAAAGAGC TATAAATTCC AACAACCAAC 1140  
TGGTGTGTAA AAATAATTAA AAATTCCTT TACTGAAAGG TATTTCCCAT TTTGTGGGG 1200  
40 AAAAGAAGCC AAATTTATTA CTTTGTGTTG GGGTTTTTAA AATATTAAGA AATGTCTAAG 1260  
TTATTGTTTG CAAAACAATA AATATGATTT TAAATCTCT TAAAAAATA AAAAAAAC 1320  
CCGGGGGGGG GCCCGGN 1337  
45

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GGCAGGAGCC TGGACGAGC AGCCACCGCC GCGTCCCTCT CTCCACGAGG CTGCCGGCTT 60

60

AGGACCCCCA GCTCCGACAT GTCGCCCTCT GGTGCGCTGT GTCTTCTCAC CATCGTTGGC 120  
CTGATTCTCC CCACCAGAGG ACAGACGTTG AAAGATACCA CGTCCAGTTC TTCAGCAGAC 180  
5 TCAACTATCA TGGACATTCA GGTCCCGACA CGAGCCCCAG ATGCAGTCTA CACAGAACTC 240  
CAGCCCACCT CTCCAACCCC AACCTGGCCT GCTGATGAAA CACCACAACC CCAGACCCAG 300  
ACCCAGCAAC TGAAGGAAC GGATGGGCTT CTAGTGACAG ATCCAGAGAC ACACAAGAGC 360  
10 ACCAAAGCAG CTCATCCAC TGATGACACC ACGACGCTCT CTGAGAGACC ATCCCAAGC 420  
ACAGACGTCC AGACAGACCC CCAGACCCTC AAGCCATCTG GTTTTCATGA GGATGACCCC 480  
15 TTCTTCTATG ATGAACACAC CCTCCGAAA CGGGGGCTGT TGGTCGCAGC TGTGCTGTTT 540  
ATCACAGGCA TCATCATCCT CACCAGTGGC AAGTGCAGGC AGCTGTCCCG GTTATGCCGG 600  
AATCATTGCA GGTGAGTCCA TCAGAAACAG GAGCTGACAA CCYGTGGGC ACCCGAAGAC 660  
20 CAAGCCCCCT GCCAGCTCAC CGTGCCGAGC CTCCTGCATC CCCTCGAAGA GCCTGGCCAG 720  
AGAGGGAAGA CACAGATGAT GAAGCTGGAG CCAGGGCTGC CGGTCCGAGT CTCCTACCTC 780  
25 CCCCACCCT GCCCGCCCT GAAGGCTACC TGGCGCCTTG GGGGCTGTCC CTCAAGTTAT 840  
CTCCTCTGYT AAGACAAAA GTAAAGCACT GTGGTCTTTG CAAAAA AAAA AAAAAA 900  
AAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 941  
30 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA

35 (2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GAATTCGGCA CGAGGCAGCT TGTGCTTTAA AGGAGGTGTT CAAAGCATGT CTGAGCAGAG 60  
45 ACTTTTGGGC TCTGTTTAA TTAATACTTT AAAATAATTC ATATTTAAAA TATCARATGT 120  
TTCCATAAAG AGGAGGATGT TTAATGCCT CCAGACTACA TTCCTTTTTA TTSCTTGATT 180  
50 TTACCTGGGA GTCCAAAGTT CAATTCCCAT AAAGCAAGCG TTTTATTGT CACTTTCAAT 240  
ATACATCCGA TTGCCATGCT TAAGATGCAA TATGGGCTGC GGAAATAGGT TAACCCACAG 300  
GCTCCAGGG CCCAGTGTAG AAGGTGAGAG ATTCGTGTAA AATGATTCAA ATAAAAGGAA 360  
55 GACCCTGGCC GGGTGCCGTA RCTCAGCCT GTAATCCAG CACTTTGGGA GGCCGAAGCG 420  
AGTGGATGAC GAGGTTAGGA GTTGGAGACC AGCCTGGCCA ACATCGTGAA ACCCGTCTC 480  
60 TACTAAAAAT AAAAAATTA GCCGGGCATG GTGGCAGGCA CCTGTAATCC TAGCTAGTTG 540

GGAGGCTGAG GCAGGAGAAT CGTTTGAATC TGGGAGTTGG AGGTTGTCAG TGAGCTGAGA 600  
TCGCGCCACA GCACTCCAGC CTGGGTGACA GGGTGAGACT CTGTCTCAAA NAGA 654

5

(2) INFORMATION FOR SEQ ID NO: 188:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1848 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

20

GAAACTGGAC CGGAGAACCG GAGCGAAGCG AAGCGGAAGC CCGGAATGAG GCCGGACTGG 60

AAAGCCGGAG CGGGGCCAGG CGGGCCTCCC CAAAAGCCTG CCCCTTCATC CCAGCGGAAA 120

CCGCCGGCCC GGCCGAGCGC GCGGCCGCT GCGATTGCAG TCGCGGCGGC GGAGGAAGAG 180

25

AGACGGCTCC GGCAGCGGAA CCGCCTGAGG CTGGAGGAGG ACAAACCGGC CGTGGAGCGG 240

TGCTTGGAGG AGCTGGTCTT CGGCGACGTC GAGAACGACG AGGACGCGTT GCTGCGGCGT 300

30

CTGCGAGGCC CGAGGGTTCA AGAACATGAA GACTCGGGTG ACTCAGAAGT GGAGAATGAA 360

GCAAAAGGTA ATTTTCCACC TCAAAAGAAG CCAATTGGG TGGATGAAGA AGATGAAGAT 420

GAGGAAATGG TTGACATGAT GAACAATCGG TTTCGGAAGG ATATGATGAA AAATGCTAGT 480

35

GAAAGTAAAC TTTCGAAAGA CAACCTTAAA AAGAGACTTA AAGAAGAATT CCAACATGCC 540

ATGGGAGGAG TACCTGCCTG GGCAGAGACT ACTAAGCGGA AAACATCTTC AGATGATGAA 600

40

AGTGAAGAGG ATGAAGATGA TTTGTTGCAA AGGACTGGGA ATTTTCATATC CACATCAACT 660

TCTCTTCCAA GAGGCATCTT GAAGATGAAG AACTGCCAGC ATGCGAATGC TGAACGTCCT 720

ACTGTTGCTC GGATCTCCAT CTGTGCAGTT CCATCCCGGT GCACAGATTG TGATGGTTGC 780

45

TGGGATTAGA TAATGCTGTA TCACTATTTC AGGTTGATGG GAAAACAAAT CCTAAAATTC 840

AGAGCATCTA TTTGGAAAGG TTTCCAATCT TTAAGGCTTG TTTTAGTGCT AATGGGGAAG 900

50

AAGTTTTAGC CACGAGTACC CACAGCAAGG TTCCTTATGT CTATGACATG CTGGCTGGAA 960

AGTTAATTC TGTGCATCAA GTGAGAGGTT TGAAAGAGAA GATAGTGAGG AGCTTTGAAG 1020

TCTCCCCAGA TGGGTCCTTC TTGCTCATAA ATGGCATTGC TGGATATTG CATTTGCTAG 1080

55

CAATGAAGAC CAAAGAACTG ATTGGAAGCA TGAAAATTAA TGAAGGGTT GCAGCATCCA 1140

CATTCTCTTC AGATAGTAAG AAAGTATACG CCTCTTCGGG GGATGGAGAA GTTTATGTTT 1200

60

GGGATGTGAA CTCAAGGAAG TGCCTTAACA GATTTGTTGA TGAAGGCAGT TTATATGGAT 1260

TAAGCATTC CACATCTAGG AATGGACAGT ATGTTGCTTG TGGTTCTAAT TGTGGAGTGG 1320  
 TAAATATATA CAATCAAGAT TCTTGCTCTCC AAGAAACAAA CCCAAAGCCA ATAAAAGCTA 1380  
 5 TAATGAACCT GGTACAGGT GTTACTTCTC TGACCTTCAA TCCTACTACA GAAATCTTGG 1440  
 CAATTGCTTC AGAAAAATG AAAGAAGCAG TCAGATTGGT TCATCTTCCT TCCTGTACAG 1500  
 TATTTTCAAA CTTCCAGTC ATTAAAAATA AGAATATTTC TCATGTTTAT ACCATGGATT 1560  
 10 TTTCTCCGAG AAGTGGATAC TTTGCCTTGG GGAATGAAAA GGGCAAGGCC CTGATGTATA 1620  
 GGTGACCA TTACTCAGAC TTCTAAAGAG ACTATTGAA GTCCAGTTGA GTCACAAGAG 1680  
 15 AAGCCTGTCT TGATATATCA TCTCAGAAAC TTTCTGAAT ATGTGATAAT ATATGGAAAA 1740  
 TGATTTATAG ATCCAGCTGT GCTTAAGAGC CAGTAATGTC TTAATAAACA TGTGGCAGCT 1800  
 TTTGTTTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACTCGA 1848  
 20

(2) INFORMATION FOR SEQ ID NO: 189:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

AAAAAAACC CAGGGGAACN TTGGGGGCCG CTTTNNNTTC CCCCTCCAGG CCATTGGGGA 60  
 35 ATTCTTCAAG TTAATCCTGC TTGCTCTTG GCCAACAGGG CTTGTAGGGG GGAGAGACCC 120  
 AGGATCATCA AGGGGTTTGA GTGCAAGCCT CACTCCCAGC CCTGGCAGGC AGCCCTGTTC 180  
 40 GAGAAGACGC GGCTACTCTG TGGGGCGACG CTCATCGCCC CCAGATGGCT CCTGACAGCA 240  
 GCCCACTGCC TCAAGCCCCG CTACATAGTT CACCTGGGGC AGCACAACCT CCAGAAGGAG 300  
 GAGGGCTGTG AGCAGACCCG GACAGCCACT GAGTCCTTCC CCCACCCCGG CTTCAACAAC 360  
 45 AGCCTCCCCA ACAAAGACCA CCGCAATGAC ATCATGCTGG TGAAGATGGC ATCGCCAGTC 420  
 TCCATCACCT GGGCTGTGCG ACCCCTCACC CTCTCCTCAC GCTGTGTAC TGCTGGCACC 480  
 50 AGCTGYCTCA TTTCCGGCTG GGGCAGMACG TCCAGCCCCC AGTTACGCCT GCCTCACACC 540  
 TTGSGATGCG CCAACATCAC CATCATTGAG CACCAGAAGT GTGAGAAGCG CTACCCCGGC 600  
 AACATCACAG ACACCATGGT GTGTGCCAGC GTGCAGGAAG GGGGCAAGGA CTCCTGCCAG 660  
 55 GGTGACTCCG GGGGCCCTCT GGTCTGTAAC CAGTCTCTTC AAGGCATTAT CTCCTGGGGC 720  
 CAGGATCCGT GTGCGATCAC CCGAAAGCCT GGTGTCTACA CGAAAGTCTG CAAATATGTG 780  
 60 GACTGGATCC AGGAGACGAT GAAGAACAAT TAGACTGGAC CCACCCACCA CAGCCCATCA 840

CCCTCCATTT CCACTTGGTG TTTGGTTCCT GTTCACTCTG TTAATAAGAA ACCCTAAGCC 900  
AAGACCCCTCT ACGAACATTCT TTTGGGCCTC CTGGACTACA GGAGATGCTG TCACTTAATA 960  
5 ATCAACCTGG GGTTCGAAAT CAGTGAGACC TGGATTCAAA TTCTGCCTTG AAATATTGTG 1020  
ACTCTGGGAA TGACAACACC TGGTTTGTTC TCTGTTGTAT CCCCAGCCCC AAAGACAGCT 1080  
10 CCTGGCCATA TATCAAGGTT TCAATAAATA TTTGCTAAAT GAAAAAATAA AAAAAAAAAA 1140  
ACTCGA 1146

15

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 906 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ACTCCCTCAC CCAGGTCCCA GCCCTGGGAA CCACCTACCG TGAGCCCTTT TGCAGATATA 60  
GACTCATTTT ATCCTCAGAT GGTCCCTTCAA GGTAGGTACT TTAGTCCCAT TTTAGAGATG 120  
30 AGACGATTGA GGCCAGAGGG GTGNNGTAACT TTGCCTGGGG GCTCACGAGC ACAAAGGAG 180  
CCGAGGCAGG ATCTGACCCT TGTCTCTTGG CCTCACTGCC CTCACCTTGC CATGACCCGA 240  
35 AGTTATGTCC CTACAAAGCA ATGCATGGTC CAAGGYTCTT TTTATTGTAT TTTTATTTTT 300  
AAGGGTCTTG TTCAAACTG GTGTGAGCTC TGAGGAGTCC TGAACCCCTG GTGCAGCATC 360  
CTAGCATCCT GGGAGTCTT TTCTGCCCAC ACTGAGCTGG GCTCCTCGAG GGGTGGGGCT 420  
40 GCTGTCCCTG GAAGCCTGGC AGCAGCACTG TATCGGGTTG GCTGAAGCTG ARC GCCGTGG 480  
GGTGCAGGGC TCCMGAATC CCCGTTTGGC TGAAGGGGTT CCCTGTAGCC MGGGATGTTT 540  
45 ATGAGGTCTC TCTGATGCCC CAGGCGCAGG ACATGTGTGC GGGTGGAGAA AAGCAGGCCC 600  
TTTCAGTGCC AGCTCCACTC AATTTCTATG TGGACCAAGA ACGATAAACT TAAAAAATTT 660  
TTTTTCCTAA GGTATCTTCA GAATATGGTG TATTTTATG TGGAAAAGAA AAGTTATGAA 720  
50 GGCAGCTGTT ACTTTAAGAG AAAATTCATT AAAAGTCTC GAGGTATGAA GATGACGGCG 780  
TGCTTCTCAA TCATTTTGGC ATAACCTGAT TGTGGCTGTA ATTTTTTTTT TTTTTTTTGT 840  
55 CAAGCATGTC AGACAATAAA GTCTTTGTAA AAAGRGAAA AAAAAAAAAA AAAAAAAAAA 900  
ACTCGA 906

60



## (2) INFORMATION FOR SEQ ID NO: 191:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1941 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

CTTCAGCTGA AGCCCAGGGA CCCCTTTTCC ACCCTGGGCC CCAATGCCGT CCTTTCCCGG 60  
CAGAGACTGG TCTTGAAAC CCTCAGCAA CTCAGCATCC AGGACAACAA TGTGGACCTG 120  
15 ATTCTGGCCA CACCCCCCTT CAGCCGCCTG GAGAAGTGT ATAGCACTAT GGTGCGCTTC 180  
CTCAGTGACC GAAAGAAGCC GGTGTGCCG AGATGGCTGT GGTACTGCTG GCCAACCTGG 240  
20 CTCAGGGGGA CAGCCTGGCA GCTCGTGCCA TTGCACTGCA GAAGGGCAGT ATCGGCAACC 300  
TCCTGGGCTT CCTAGAGGAC AGCCTTGCCG CCACACAGTT CCAGCAGAGC CAGGCCAGCC 360  
TCCTCCACAT GCAGAAGCCA CCCTTTGAGC CAAYTAGTGT GGACATGATG CGGCGGGCTG 420  
25 CCGCGCGCT GCTTGCTTG GCCAAGGTGG ACGAGAACCA CTCAGAGTTT ACTCTGTACG 480  
AATCAGGCT GTTGGACATC TCGGTATCAC CGTTGATGAA CTCAKTGGTT TCACAAGTCA 540  
30 TTTGTGATGT ACTGTTTTTG NATTGCCAG TCATGACAGC CGTGGGACAC CTCACCCCCC 600  
CGTGTGTGTG TCGGTGTGTG GAGAACTTAG AAAGTACTG TTGCCCTTTA TTTATGCAA 660  
ACCACCTCAG AATCCAGTTT ACCCTGTGCT GTCCAGCTTC TCCCTTGGGA AAAAGTCTCT 720  
35 CCTGTTTCTC TCTCTCTCT CCACCTCCCC TCCCTCCATC ACCTCACGCC TTTCTGTTC 780  
TTGTCTCAC CTTACTCCCC TCAGGACCTT ACCCCACCCT CTTTGAAAAG ACAAGCTCT 840  
40 GCCTACATAG AAGACTTTTT TTATTTTAAC CAAAGTTACT GTTGTTTACA GTGAGTTTGG 900  
GGAAAAAAA TAAATAAAA ATGGCTTTCC CAGTCCTTGC ATCAACGGGA TGCCACATTT 960  
45 CATAACTGTT TTTAATGGTA AAAAAAATA AAAAAAATAC AAAAAAAT TCTGAAGGAC 1020  
AAAAAAGGTG ACTGCTGAAC TGTGTGTGGT TTATTGTGT ACATTCACAA TCTGCAGGA 1080  
GCCAAGAAGT TCGCAGTTGT GAACAGACCC TGTTCCTGAG AGAGGCCTGT GCAGTAGAGT 1140  
50 GTAGACCCCT TCATGTACTG TACTGTACAC CTGATACTGT AACATACTG TAATAATAAT 1200  
GTCTCACATG GAAACAGAAA ACGCTGGGTC AGCAGCAAGC TGTAGTTTTT AAAAATGTTT 1260  
TTAGTTAAAC GTTGAGGAGA AAAAAAATA AGGCTTTTCC CCCAAAGTAT CATGTGTGAA 1320  
55 CCTACAACAC CCTGACCTCT TTCTCTCTC CTGATTGTA TGAATAACCC TGAGATCACC 1380  
TCTTAGAACT GGTTTTAACC TTTAGCTGCA GCGNCTACGT CNAWCGNIGT GTATATATAT 1440  
60 GACGKTGTAC ATTGCACATA CCCTTGGATC CCCACAGTTK GGTCTCTCTC CCAGCTACCC 1500

CTTTATAGTA TGACGAGTTA ACAAGTTGGT GACCTGCACA AAGCGAGACA CAGCTATTTA 1560  
ATCTCTTGCC CAGATATCGC CCCTCTTGGT GCGATGCTGT ACAGGTCTCT GTAAAAAGTC 1620  
5 CTTGCTGTCT CAGCAGCCAA TCAACTTATA GTTTATTTTT TTCTGGGTTT TTGTTTTGTT 1680  
TTGTTTTCTT TCTAATCGAG GTGTGAAAAA GTTCTAGGTT CAGTTGAAGT TCTGATGAAG 1740  
10 AAACACAATT GAGATTTTTT CAGTGATAAA ATCTGCATAT TTGTATTTC ACAAATGTAGC 1800  
TAAAACTTGA TGTAAATCC TCCTTTTTTT CCTTTTTTGG CTTAATGAAT ATCATTATAT 1860  
CAGTATGAAA TCTTTATACT ATATGTTCCA CGTGTTAAGA ATAAATGTAC ATTAAATCTT 1920  
15 GGTAAGACTT TAAAAA AAAA A 1941

20

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 2118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

30

AAATAATAAT AANAATAAAT AAAAATWAAG TGCTTAKTGT AACTCAGCGG ACAGGGCTCC 60  
CAGCTGCTCT GGCACGTGGG ACACCYTCCA CCCTGCACAC AACAGGCATG CAAAGAGGAC 120  
35 TGGATATGGT GGGGTAGAGT GCTTCTGGTG TGTTCACTTT AAGAAAACAT CTGCCAAGAG 180  
AGAAGAGTGC CCAGGAAAGA CCAGGAAAAT ACAAGTACAT GGCTGCTTCA TACCATATAC 240  
CCCAATTCTT TAAAGCAGCA AAAGGCACTT TTTTTTTCAG GCCAGAGTGA ATCTAAAACA 300  
40 AACCTGGCTT TGCTTACAGG GAAGCTGTCC CAGAAGGACT GAGTGATGCC TCTTGTTCCT 360  
TAAGGTCTGG AGAGTCTTTG CAAGTTTCCA ACGACATTTC CAACCAGGTG GGAGAGACCA 420  
45 GCAGTTGACG AGACAAGTCA GACCCAAAAA ACGACGCCAA GGTAGTGAGT GGGTGCCTAT 480  
TTGGGAGTAG GATGATTGTA GGAAACAGG AAGAAAAACC GGTGAGAAAG TGGCACTTTG 540  
GAAGTGGAAA GCTGTTTGCA AATAGCAACT CTGGCTAAAG CGAAAATGTT AATCAAGTAG 600  
50 AAAGTAAAT TCAGGATCTT AGAAGCTCAT CCTTCTGATG AGAACTATTT TTTTTCCGT 660  
GAAGGAATA TTATTACTTT AAAAGTGAGG GTAATTTACA TATGGGGTGT ATATATTCTA 720  
AAAATAGTAA TAAAGTACC TTTTATAAGC AATGTTGTGT GGCTGTAGA AGAAAGCAGG 780  
GAGGAAAAAA AGGCAGGCAA AACTAGTCTA GGTCTAGGCC CTAAAAATGA GCTTCCTTCC 840  
CACTTGACTG GAAACGCCCA TGTGATTCTT AGGCTGAAAA TAGGTAGGAT TTAACGAGTA 900  
60

ACCTAGTTCC CTTCTGTCTC TGATTTCTGA TCAGCTGATG GAGCTGCTAG TAAGAGGGGC 960  
CGATCATGCT CCCAGACGAG TCCTTTGGCC TCTTGCTCTC CATCCCAAGC CTGACTCCTT 1020  
5 CAGCAGCAGC CCCCTCCTTC TGTGTCCATC TGATGCAGGC AAGCAGGAGC AGTAAGAGGG 1080  
CATCCCATGT TCCAGTTCAC CTTCTATGGG GTGACTARGA GGTTCCTGGT AACTAGGGCA 1140  
GCCCARGCCC AGCAGGTTGC AAAAGCAGCT GCAAGCTTCA GAAACCCACT TCCTCCAACA 1200  
10 CCAGGGAGGT GGCAGAGAGC CCATCCAAA GCCCACTGGG AGAGGCATAA GATTCTGTGC 1260  
CAGGCCCCCA GGTCCCCTCT GTGTCAGGTA GGCTCTGCTA CTGGCCTCTG AAGTAAAGGC 1320  
15 AAANACAAAC GGCAGGGCA GGGTGGCAGG AATAAAAAAC TCTGGACAGA AACCCTTTTA 1380  
ATAAAGGAAA TTCCACCCCT CCCAATCCTT CCATGGAAGG GTGAGACCTT AATGTGATGT 1440  
AAGAGGAAGG TCTTCTCTGG CTTTCAGGGA AACAGCTGCA GCTGAAACTT AGGGGCCCAT 1500  
20 TCCAGGGCAC TTTTCACCAC AGCCAGTGCA GCCGCTCAA GTGCCACTGT CAGCCCCATC 1560  
ACTGCCAATT TCACAAAGCG GTTGGTCCTT GGCTTGGTCA GGACATCTTT TGTTCGATCT 1620  
25 TCAGGCCGCA GAAGTCCCCG AANACCGTG CCGCAGCACC ATATCAGGCC TCTGCTGGGC 1680  
TGATGCCAGC TCAAAGTCTT TGAAAGTAGA GGCTGCCGTC CTCTCAGCTT GCTGTTGGGC 1740  
AGCGGCCTCC CGAGCAAGTT CGGATGGGGG AAAGTGAACA AAAAGGTCTC CTSTCTGCTG 1800  
30 ATCAGTGTCT CATAGGGCAA GTCCTGAGGG ATCTGGGACA ACAGGTGGTG GACCGAGGCC 1860  
ATGTCACAGT CACAGTCCAG GACTTCCTGC TCGCGATACA ACACAATCAC GGCTGCAAAG 1920  
35 TAAATCGGCA TCACTGGGTG GCAGGCCAGG AAGAATCAT ATAACCGCAC GACGTGCCTG 1980  
AAGTCAGACA GGACATGCCC AAACCAGGTG ATGAGCCAGC TGAGGGCAA GATGGTCCCT 2040  
ACCTCAGCAC TCTGCATGAA GTCATGGAGC TCTGGATTCA CCTGGTCAAT GATGGGCATC 2100  
40 AGATAGTTTA ATATATGC 2118

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(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

55

CCGGGTTTCG CTCTGTGTCA GCAGCCGGGC GCGCTCGGG CGGGACATGG CAGCCTGTAC 60  
AGCCCGGCGG CCTGGCCGTG GGCAGCCGCT GGTGGTCCCG GTCGCTGACT GNGGCCCGGT 120  
60 GGCCAAGGCC GCTCTGTGCG CGGCCGNAGC TGGAGCCTTC TCGCCAGCGT CGACCACGAC 180

5 GACGCGGAGG CACCTCTCGT CCCGAAACCG ACCAGAGGGC AAAGTGTGG AGACAGTTGG 240  
TGTTGTTGAG GTGCCAAAAC AGAATGGAAA ATATGAGACC GGGCAGCTTT TCCTTCATAG 300  
CATTTTGGC TACCGAGGTG TCGTCCTGTT TCCCTGGCAG GCCAGACTGT RTGACCGGGA 360  
TGTTGCTTCT GCAGCTCCAG AAAAAGCAGA GAACCCTGCT GGCCATGGCT CCAAGGAGGT 420  
10 GAAAGGCAAA ACTCACACTT ACTATCAGGT GCTGATTGAT GCTCGTGA CTGACATAT 480  
ATCTCAGAGA TCTCAGACAG AAGCTGTGAC CTTCTTGGCT AACCATGATG ACAGTCGGGC 540  
CCTCTATGCC ATCCCAGGCT TGGACTATGT CAGCCATGAA GACATCCTCC CCTACACCTC 600  
15 CACTGATCAG GTTCCCATCC AACATGAACT CTTTGAAAGA TTTCTTCTGT ATGACCAGAC 660  
AAAAGCACCT CCTTTTGTGG CTCGGGAGAC GCTAAGGGCC TGGCAAGAGA AGAATCACCC 720  
20 CTGGCTGGAG CTCTCCGATG TTCATCGGGA AACAACTGAG AACATACGTG TCACTGTCAT 780  
CCCCTTCTAC ATGGGCATGA GGAAGCCCA GAATTCCTAC GTGTACTGGT GCGCTACTG 840  
TATCCGTTTG GAGAACCCTG ACAGTGATGT GGTACAGCTC CGGGAGCGGC ACTGGAGGAT 900  
25 ATTCAGTCTC TCTGGCACCT TGGAGACAGT GCGAGGCCGA GGGGTAGTGG GCAGGGAACC 960  
AGTGTATCC AAGGAGCAGC CTGCGTTCCA GTATAGCAGC CACGTCTCGC TGCAGGCTTC 1020  
30 CAGTGGGCAC ATGTGGGGCA CGTTCGCTT TGAAAGACCT GATGGCTCCC ACTTTGATGT 1080  
TCGGATTCTT CCTTCTCTCC TGGAAAGCAA TAAAGATGAG AAGACACCAC CTCAGGCCT 1140  
TCACTGGTAG GCCAGCTGAG GCCCCAAGTG CCCAGGCTTG GTCACCGGGA AGAACAACCTC 1200  
35 TCATCCACA ATTGCTGCAG AACTCTCTC TCCCCATCAT GGGCCACAGT GGGTCTCTTA 1260  
ATTTGATGT GGGTTCTTT TTGTGGGAG GGGTGGTATA ACTTTCTTC AGAAGACCCA 1320  
40 TGTGGGACAC CTCCAAGGCT GGCCTCCTCA TAAGCCCTGC CTACACCATG TTCCAGTAAA 1380  
CCTCTCCACC AAGGAACTGT GTTCAGCTGC CACAGGCTG GAGGAGTTTC CTGGCCTGTC 1440  
ACGTGAGGTT TGATCAGTAA ACCAGTGCAS GYTTGGCCAA AAAAAAAAAA AAAAAAAAAA 1500  
45 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAACCTCGA 1538

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(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1098 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

	AGACCCCTGTC TCAAATAATA ATAATAATAA TAATCTTATT TTGGAGAATA AAGAGACCTS	60
	TGGATTGAG GTGCCATTG GGTAGAAAGA AAAGACGTTT ACACCGAGAA ATAGTCTGTG	120
5	TTGCCCTGAA GGAGCAGAGG GATGCATCGC TGGAGGTGAC CTACAGTTGA AGAAGACTCA	180
	TTATGACAGA CCTGTCTCTT CTTCCTGTG GAAAGTGTTC CCTCTGCTGC TACTGCTCAT	240
10	GAGACTCTTC CCCCTCCCTG TCCCAGGGAA CCAAAGGGCT TTNCTACCAC ACCCTTTCTT	300
	NGCCCCCGC CTCCCATGTC TGCTGTGCCT TTGTACTCAG CAATTCTTNG TTTGCTCCCA	360
	TTATCTTCCA GCCGATACA GAGTGAATAG TTAACCACAC TTAGGTCAA TAGGATCTAA	420
15	ATTTTGTTC CTGCTCCNGT GTAAAGAGGC CAGTGTGTGT GTGTGCAAG CAGCCTTGA	480
	ATAGTAACTC TTCTCATTTG TTTGGGATCT GGCCAMCAAG TTCCAGAATG ATACACGGAT	540
	CAGTGAGAA GTTCATCAGG CTCTCGGACC TTAGGGCTGT TGGAGAAGGC TTCAGCAGCA	600
20	GAAGTATGG TKAWKGYTCG TGTCTCCAT CCTCACTTT CTTTGCTTCG ATCATAACA	660
	AGAATACATT TGAAGGGCA AAAAATGAAC ACTGTTGTTC ATTGCAGCCG TGTMTTGTGA	720
25	CACAGATGCA CAGTCTGCTG TGAAGACCTT CTCTCAAGTG GSATYTGGGA GTCCATGCCA	780
	GATCATGGTG CTTCATGAGA GACTGACAGC TATCAGGGGT TGTGGCACTT AGTGAGGACT	840
30	CTCTCCCCC AGTGTGTGCT GATGACACAT ACACACCTGA CAATAGCTTG AGTCTTCTCT	900
	GTTCCTTTTA CTCTGTAGCC AACATACACA TGATTTAAAA CCCTTTCTAA ATATCTATCA	960
	TGGTTCATCC TTGTCCAAAT GCAGAGTCAG AGCTATTTGT ACTTCATTAT TATTTCCAAG	1020
35	GCGAATAGTT GGCTTTCTTT TTGCAAAAAT AATTAAAGTT TTTGTATGTT GCAAAAAAAA	1080
	AAAAAAAAA CTACGTAG	1098

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(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1001 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

	GAATTCGGCA CGAGATAGCT TGATCTCAT CCCAGTAAAA CCATTATTT ATAACATATC	60
	AACGTATTGA CAAGTTGAA GAGCAAGATT GTTCTGAGGT GAGATGCAAA TTTCAAAGGG	120
55	GTGAGCACTA ATTGTTCCAG TGATTGTTTA TTTATTGGCT AGGACATAAT TACTCTCTTT	180
	GAGGTTACAC ATCTGCCTCC AGGTTCTGT GTGCTTGTC CCTTGGGATC AGGCCAGGGC	240
60	AGACTGTGAT CACTGAGATT CAACTCCCA GARTAAATCAG CAAGAGCTTT CTAGAGACCA	300

AGGCCAGGCC TGATCCCTGA GGGATGCATG AGAAGGCTTG GAATCTCAT TCTGCTATGGT 360  
 GGCTCTCTCT TGATCTTCTT GGAGTAGCAA AAACAGCAAT GTGGGCCCAA TGGTGTGGCC 420  
 5 TAAATGATCA CAAAGGTAAA TGAGTAAAGG GCTCAGCAGA TGAGTAAGGA GCCTTGTCTT 480  
 GAGAAATTAG CACTGGGCTC TGCATTGAGA AACATGTGAT AAGCATTGCC CATTGCACAT 540  
 10 TGCCTTTATT GTGTAAGGAC ATGAAATTCC AGTTTTGCAT AGCTAGTGAT GAATACCTGA 600  
 AGGGAATTGC AGACATATTT TATTTTATTT TTAATTGACA GATGGAATTG TATATATTTA 660  
 TCATGTACAT AATCATGCTT TAAAATATGT ACATTATGGA ATGGCTAAAT CAACTAACC 720  
 15 TAGGCATTAT CTCATATAAT TGTCAATTTT GTGGCGAGAA GACTAAAAAT CTACCCTTTC 780  
 AGCATTTTAA AAGAATACAA TGTGTTTAT TAACAACAGT CACCATTTGG TACACTAGAT 840  
 20 CTCTTGAAC TCTTCTCTT ATCTAACTGA GATCTTGTA CTTTGATAA CAGCTCCCAA 900  
 GCCCTTCCCC AACCCTGCT CCACCCGTGG TAACCACCAT TCTATCTCA ACTTCCTGGT 960  
 25 AATCACCATT CTAGACACAG GGAAGACTCT CTACCCTCTG A 1001

30 (2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

40 ATAAACTGAA ATAGGTCATG CAAATATAAA ATATTATTTT TAAATTATTT GTCATAAGAA 60  
 ACGATGGTGG CCATATTTTG CTTAATAAT GGAAAAATG TGGTTAGCAT TCTKTGGAAG 120  
 GTGGTCATCA GATAGTAGAC ATTTTCTAGG ATTTATTTCT ACCTGCATAT GTGGAAATGT 180  
 45 GTACTACTTT AGATTATWT AATGGCAGCT AACTCAGAGG CATCAAAATG TGCTAATGGT 240  
 GTAATATGGC CTTTGTCTTG CTGTCTGTT TTGTARGCCT TCAATCAAGC ARGGGCAGGG 300  
 CCGTACAGTG AACTTGTCTT TTGSCAGACG CCAGCGTCTG CCCCTGACCC CGTCTCCACT 360  
 50 CTCTGTGTCC TGGAGGAGGA GCCCCTGAT GCTTACCTG ATTACCTTC TCGTGCCTT 420  
 GTACTGAAC TGGGAAGGCC GTGCAATAAC GGATCTGAAA TCCTTGCTTA CACCATTGAT 480  
 55 CTAGGAGACA CTAGCATTAC CGTGGGCAAC ACCACCATGC ATGTTATGAA AGATCTCCTT 540  
 CCAGAAACCA CCTACCGGTG AGTGCAAGGG AGTAGAAATC TGCATCAGCA CATCAGCACT 600  
 60 TGGGGATCTA AGTAAACCTC TCGGGGAAAA TGACCAAGTG GATGTCATCT CCCAGCTGTT 660

TCTAAGAGCC CAGATGTCCA GAGTATGTGC TCACCTTGAT CCTCAGGCC AGAAGACCTG 720  
 TGAAAAAGCC ACACTGGTTC AGGGACTCAC TGGACGGTTT TGTGTCCACT TTAACATGCA 780  
 5 CCGTCTCTAC CCCAGAGTGG ACTCARATCC TCAAGTCATC CTCTGAACAT TGGTGTGAGA 840  
 AATTATAAAA GGGCTTTGGC AATATGTTAG CCCAAGPATT TGGCTTCTTC CAGAAATTGT 900  
 GCCGACNTTA ACAGTGGCTT AAATGATGGT AAAACTTTTA AGATTCTTAA AAGGTGGCA 960  
 10 TTGGAGATAC GTTGACTTTT ATTAAACMAC CTATAGTTGT TTAATGATT CTAAAAAAT 1020  
 ATCTGGAGCT CAGGGGTTC ACTGAGGGAA CACATGTTGA GRATCATTT TTAATAATTA 1080  
 15 AATGCCAGGT AAGCCGTGA AATTATCAAA AACATCTTC ACGTACCAGA AAGGCCTCA 1140  
 GAGGATAGTT CTGTTATGGA GAAGATGAAA TGGTTAGTA GTGTAGGAC TATGGAAAGG 1200  
 TGAGCTTAGA TTTGATAGT AAAACCTCAA GACCTATTT AAAAGTATT TTAATGATGC 1260  
 20 AGCATAAATA ATTTAATTCA GTGTTAANAT GCCAAGGCTA GTATATTGAG CTGAATGTGA 1320  
 AAAGAACTC ACATTGGGAG AATGCCACCT TTCTCTTATA AGATAGCTTT GAATATCCA 1380  
 25 TTTTAGACAG ATGGAAATG AATAGCTTTA GAAAAGGCAA ATGTTTGATC TTGGGGAAAA 1440  
 AAA 1443

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(2) INFORMATION FOR SEQ ID NO: 197:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1282 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GAAAAAAGAA AGTATGACCC AGTAGCTAGG CACCTGTGGC CCGCCCAAT TCAACATAA 60  
 AATTAACTGT CACAGTATCA TCTTAGAAGT GAAAGAGCC CTTTATCTT GCAATGCCCC 120  
 45 TCTACCACCA CTTACTGACA AAGAACATGG TGCTATCTGG CATGGGAGAA ATGTTCAAGT 180  
 TGCTATGGCT TGTATGTGTC CCTCAAATT CAAGTGTGC CAATGTGACA GCATCAAGAG 240  
 50 GTGGGTCTT TAAGAGATCA CTAGGCCATG AGGGATTCTC TTAGGACTGG GATGAAGGCC 300  
 CATAATAAAA GAGGTTTCAG GGAGCATCCT GCTAGCTTGC CTTCTGTATG TGAGAACACA 360  
 GCAAGAAAGC CTTAGTCAAC AAGTGCCAGC TCTTGAATCT TAGACTTCCC ATCTCCAGA 420  
 55 ACTGTGAGAA ATACATTCT GTTCTTACA AATTACCCAG TCTCTGTAT TCTTTATAG 480  
 CAGCACAAAA TGAAGATACC ATACCTGAAC ACCTGAACAT TCTTCACAG GTAGTAAATG 540  
 60 CACTGCTTTA TTCTGGTCTC AGTATTGTGT CCTTATAAG GAAATGAGAA AGGTGGATC 600

5 AGGGCATAGG ATGAACAAGT TACTGCTAGA CCTCTCACA TGCCACTAAT GGAAGAGATT 660  
 GTATTTTCAT CATTNCTTGT CTCTTCGGAA GCTAACACCA TGCTATAATA GGCATTAAT 720  
 AGATGTCTAA AAACACCTTA AGTATTTGTC TAGAAATCTG GTGCATTGTC CAGAAAGAAC 780  
 CAAAATTCMA AATAATTTCA AAGGGCCTAA AGCACTATTT AATCGAATT CATTAGTTTT 840  
 10 TAATGGTACT ACCACTCTCA AATTAAATAT GTCATCTTAC GTTCCTCTTC CTGCGATTGG 900  
 ATTTATTGCT AAAACCTGGT AACACTTTA ATCCYTTTCA ATTCCATTAC CACTGCTCTT 960  
 GTCCAGAATT ACTCGCAGAC TAATAGTCAC CTGACTTCTC CCGCTGCTC CGGATTGCT 1020  
 15 GTCTAATTCT GGTACAAAT AAGTAACTGC CAACTAATC TTCTAATAA GCAAGACTGA 1080  
 TCTCGTCACT CTTTGCTCA ACAATGTAAA AGCTCCCATT GTCTCCCAA TAAACCAGC 1140  
 20 TTCCACTGT GTATACAATA CATCATGAT CTGTATCCAG CATCATTTTG TATTGCTCA 1200  
 CTTTATACAC CACCCCCCAT GCCACATCAA ATTAAATTAT CCTGATAAT GCAATGCAA 1260  
 25 AAAAAAAAAA AAAAAAATC GA 1282

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

40 ATTTCCGAAC GAGGACTGAA GTGGGAGCGG CGGCAGGGTA GAAGACAGAA GGGGATCTA 60  
 TGTGGTAACT AAAGAATGTT TCTGTTTGT TAATTATTGT GTGTGTGGG TTTTATTGTT 120  
 TGCTTAAGAG AATCAAAAAC TGAAAAAAT GAGAATACAG GAATGGCTC TTGTTTATTT 180  
 45 TTTTGCTGTG TTTACAGCTT GTTAATGCTC TACTGTCTTT GTTCAAGAG AATTTGTTT 240  
 ACTGCCCAGC TCGTTTGTG TCCTGAGCCC TATGCCCAGC CCACCTTATA AATCATGCCT 300  
 GTTTAGATGT TTGATTTTGT TCTGTTTGT ATTGTTATCT TAAAGGTGTA TAACTCTGAC 360  
 50 ATGCCAGACA TCAAATTAAG CTCAAATTAA GCTCTCGTTT AATGTTTAA ACACCTAAT 420  
 TATATTCTAA TTGATCCAG CCACTGATGC ATGTACTTTA GCTACTTTG CTAAATAAGC 480  
 55 ATATTAATTT TCCACATCAG GCCATCAGAT CTTGAGAACC AACAGTTATC TAGAATTCOG 540  
 TGCTACTAA TGTTTCACCT GCATGCAGCC TTCATTAAAT TTGTAGCAA ATATAAAGTG 600  
 60 ATCATTATGT AGTTTCTGGA TTAATAAAT TTGTGTGTA AGTTGCTTTG TAAAGTGCAT 660



GTGGAATTAA TGGGACAGTG TGCCCTTTGT GTTAGATGTT AGAGCAAAAG AAAGGGCTTA 720  
TAGTGTTAGT ATTGGAGCAC TTTGAAGATA GATATTTTCA GAAAAGATGT AGGATTTAAA 780  
5 AGTTAAATTT TAAATTTTAG AAAAAGATAT GATGGCAATT GGAAATAGTC ACAATGAAGT 840  
TCTTCATCCA GTAGGTGTTT AACAGTGTTA TTTTGCCACT GGTAATGTGT AAACGTGAG 900  
TGATTTACAA TAAATGATTA TGAATTCAAA AAAAAAAAAA AAAAAACTCG A 951  
10

## (2) INFORMATION FOR SEQ ID NO: 199:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1740 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: 'SEQ ID NO: 199:'

TTATTATAAT AATGATGATG ATTCCAAGGA AAAAACCTAC AGCGAATGTT CCATTCTAC 60  
25 CCCCACGCA GACACTCTCC CTAACACTGA TAACCTGAGC CCCCAGCACT GGACGGAAGA 120  
ATGCTGGCGT CTCCTGTGT ACTGGTTCAG GGTCTTGGCC CCAGCCTTGT CAGGACCCCC 180  
30 TGGTGTCAG AGCCCCCACC CCTCCCGCAA CAAGCAGCTG ATGCCCCAGT GATTCTCTAT 240  
ACATTTTCA CCTCGGCCAA TATGTCCAGG AAAACTGCTT ACTTCTCTTT TCTTGCTGG 300  
AGCCTTCATT GTTCACCTT ACGTTGCAAT ATAGGAATTA ATGCTACAAA ATAAAAGTAA 360  
35 AGCTTACCTG AAAAGTGCAT AGTTTGGGC AATGGTATCT ACATCTCCA CTGTGGGAAA 420  
ACCAGCAAAG CATCAAACT CTCAATTCTC CTGTTACCRA ATGCAGATCT GAATTATAAG 480  
40 ATGTTTATGT TTGACCATG TTTCAACAAT GGGATTTTGT TACGAATTAT CCCTTTAACT 540  
GAAACCCTCA GTTTTACTGT TTACATTATT AGGAAAACAG GGATATCTTT TGAATCTAAA 600  
AATTTGATGT ACAGCATGTG ATTTTGAAG TTTACATGTA AAGTCACAGT ATAGGTGAAA 660  
45 TAACGTTTGT CATATTTTGA GACGTATCCT GCAGCCATGT TTTTACGTGA GTGTTTGTAGT 720  
CAAAGTACAT GGTAGACAGT CTTTCACAAT AAAAGGAAAA GGATTTTTTT TCCTCCAAAT 780  
50 GTACATTTAT CAACCTAATG ATTGATTTTT TAAAAAGAG ATTTGCCCC AGTCTGGTTT 840  
ATGAAAGTTC ATTGCCCTAA ACTGTGCTGA TTGTTTTTAA TCAAGTTATA AATTCCAAC 900  
CTAGATCATG TATCTACCAA CTCTCTGCA TTTTCCAAAA GGCATTGAGC TTAATATTA 960  
55 GTCTTGCTTA GAGTAGGTTA TCCACTTACA TGCTGCGCTA AAGCCATGCC TTTGAAACTC 1020  
CTTGTTTAAA ACATGATATG ATTTTGTGG GCAGTTTCAG AAAAGAAAAC AAACAAACRA 1080  
60 AAATCGACCC TTAAATTATT ACTTGCAACT CAACAGATCT CCTGCGGTA CTGCCTTTTT 1140

CAGGAAC TTT ACTTCAGGGC TGTCCAGATT GCAGTTGTGC CCCGTGTATG TGGATCTAGT 1200  
 TCACAGAGTC TTTGGAAGCC AGCAGTCGTG CCCTCCGTAT ACTGTCCACT CATTTTATGT 1260  
 5 AGATTGGTA TCCTCAGCAG CCAGTGTTAA CACCACTGTC ACGTAGTTAN CAGATTCATC 1320  
 TTTTATGTAT TTAAAGTAAT CCATACTATG ATTTGGTTTT TCCCTGCACC ATTAATTCTG 1380  
 10 GCATCAGATC AGTTTTTGTG TTGTGAAGTT CTACTGTGGT TTGACCCAAG ACCACAACCA 1440  
 TGAGACCC TG AAGTAAAGAT AAGGTACACA TACATTATTT GAGTAACTGT TTCCTTGGGG 1500  
 GCCAATCTGT GTATGCTTTT AGAAGTTTAC AGAATGCTTT TATTTTTGTC TATAACAAAC 1560  
 15 AGTCTGTCAT TTATTTCTGT TGATAAACCA TTTGGACAGA GTGAGGACGT TTGCCCTGTT 1620  
 ATCTCCTAGT GCTAACAAATA CACTCCAGTC ATGAGCCGGG CTTTACAAAT AAAGCACTTT 1680  
 20 TGATGACTCA MAAAAAAAAA AAAAAAAMC YCGGGGGGGG GCCGGTAACC CATTTNNCCC 1740

25 (2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1707 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

35 GCTTATAGAA GGGAGAGGAG CGAACATGGC AGCGCGTTGG CGGTTTTGGT GTGTCTCTGT 60  
 GACCATGGTG GTGGCGCTGC TCATCGTTTG CGACGTTCCC TCAGCCTCTG CCCAAAGAAA 120  
 GAAGGAGATG GTGTTATCTG AAAAGGTTAG TCAGCTGATG GAATGGACTA ACAAAGACC 180  
 40 TGTAAATAAGA ATGAATGGAG ACAAGTTCCG TCGCCTGTG AAAGCCCCAC CGAGAAATTA 240  
 CTCCGTTATC GTCATGTTCA CTGCTCTCCA ACTGCATAGA CAGTGTGTCG TTTGCAAGCA 300  
 45 AGCTGATGAA GAATTCCAGA TCCTGGCAAA CTCCTGGCGA TACTCCAGTG CATTCAACCA 360  
 CAGGATAITTT TTTGCCATGG TGGATTTTGA TGAAGGCTCT GATGTATTTT AGATGCTAAA 420  
 CATGAATTCA GCTCCAACTT TCATCAACTT TCCTGCAAAA GGGAAACCCA AACGGGGTGA 480  
 50 TACATATGAG TTACAGGTGC GGGGTTTTTC AGCTGAGCAG ATTGCCCGGT GGATCGCCGA 540  
 CAGAACTGAT GTCAATATTA GAGTGATTAG ACCCCCAAAT TATGCTGGTC CCCTTATGTT 600  
 55 GGGATTGCTT TTGGCTGTTA TTGGTGGACT TGTGTATCTT CGAAGAGTAA TATGGAATTT 660  
 CTCTTTAATA AAAGTGGATG GGCTTTTGCA GCTTTGTGTT TTGTGCTTGC TATGACATCT 720  
 GGTCAAATGT GGAACCATAT AAGAGGACCA CCATATGCCC ATAAGAATCC CCACACGGGA 780  
 60

CATGTGAATT ATATCCATGG AAGCAGTCAA GCCCAGTTTG TAGCTGAAAC ACACATGTGT 840  
 CTTCTGTTTA ATGGTGGAGT TACCTTAGGA ATGGTGCTTT TATGTGAAGC TGCTACCTCT 900  
 5 GACATGGATA TTGGAAGCG AAAGATAATG TGTGTGGCTG GTATTGGACT TGTGTATTA 960  
 TTCTTCAGTT GGATGCTCTC TATTTT TAGA TCTAAATATC ATGGCTACCC ATACAGCTTT 1020  
 CTGATGAGTT AAAAAGGTCC CAGAGATATA TAGACACTGG AGTACTGGAA ATTGAAAAAC 1080  
 10 GAAAATCGTG TGTGTTTGAA AAGAAGAATG CAACTGTAT ATTTTGTATT ACCTCTTTT 1140  
 TTCAAGTGAT TTAAATAGTT AATCATTTAA CCAAAGAAGA TGTGTAGTGC CTTAACAAGC 1200  
 15 AATCCTCTGT CAAAATCTGA GGTATTTGAA AATAATTATC CTCTTAACCT TCTCTTCCCA 1260  
 GTGAACTTTA TGGAACATTT AATTAGTAC AATTAAGTAT ATTATAAAAA TTGTAAACT 1320  
 ACTACTTGT TTTAGTTAGA ACAAAGCTCA AACTACTTT AGTTAACTTG GTCATCTGAT 1380  
 20 TTTATATTGC CTTATCCAAA GATGGGAAA GTAAGTCCTG ACCAGGTGT CCCACATATG 1440  
 CCTGTTACAG ATAACACAT TAGGAATTCA TTCTTAGCTT CTTTCATCTT GTGTGGATGT 1500  
 25 GTATACTTTA CGCATCTTTC CTTTGTAGTA GAGAAATTAT GTGTGTCATG TGGTCTTCTG 1560  
 AAAATGGAAC ACCATTCTTC AGAGCACACG TCTAGCCCTC AGCAAGACAG TTGTTTCTCC 1620  
 TCCTCCTTGC ATATTTCTTA CTGAAATACA GTGCTGTCTA TGATTGTTTT TGTTTTGTG 1680  
 30 TTTTITYGAG ATCACGYTAC TGGGCTC 1707

35

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 779 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

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CTGTCCCCAG TGTTCCAGG TAATGACTTG GCACTCCAGA GAAAGTTTCA TRCTGTTGCG 60  
 TGTTGGTGGCT CCAAGCCAAG CACCTGGCAT GCAGGTCAGC CCTTCCCAGC GGGCGTGGCG 120  
 50 TCGTCTCTT CACAGATGCC ACGTTGCAGC CCAAGGCCT CACCATTTTG CGTTTTTTAG 180  
 AAACCAATT TCTTGGTCAT TTATAAAGCT GCTTTATAGA TATCTTTGAT CCTGGCATGC 240  
 CTTGGTTTCC TCTCCCTTCC CTCTTTCCAA TCCTGGTTTC CTAACCTCCT CTGTAGTAA 300  
 55 TTCTCAACTC AACTCAAAGT CCAAGAATT TGGAATGGTA GGATGCTGTG CGGGGAGCTC 360  
 GAGGCTGAGG CATAATCACT GCTTCGGTTC TGCTCATCAG GGGACACGCT CCCTTACTCA 420  
 60 TGGCAGCCAT GTTTGATTGT CACAGAGCCC CCCGAATACT CTGTCTATAG TGACACACTG 480

5 TAGGTGTCAT AAATTTTAAG AAACCTGCTT TTAAGTACTA TTTATAGGTT TTTCTGTTAT 540  
ACTTGCAACC TAGTTTTAAA ATACATGAGG ATTTTATGAA AGCTTTATAC AGACATTTAT 600  
AGGAAACTCA TTCTTTGATT TTAGGTGCCA TTAAATTGA TAACACTTAC TTTATAAAAA 660  
GATGCTTTTT GTCTGGATAG AGCCTTATAG TTTAAAATAT CTTTATATAT TGCCATTGTA 720  
10 TCAAATAAAT TTCTTACTTA GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAACTCGA 779

15 (2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1617 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

25 GGCACAGCTT TCTGTCTCTT CCTCGCTCCC TCTCTTCTC TCCTCCCTCT GCCTTCCCAG 60  
TGCATAAAGT CTCTGTCGCT CCCGGAAGTT GTTGCCAATG CCTATTTTIT GGCTTTCCCC 120  
CGCGTICTCT AACTAATACT TTAAAGGTC TGCGGTCGCA AATGGTTTGA CTAAACGTAG 180  
30 GATGGGACTT AAGTTGAACG GCAGATATAT TTCCTGATC CTCGCGGTGC AAATAGCGTA 240  
TCTGGTGCAG GCCGTGAGAG CAGCGGGCAA GTGCGATGCG GTCTTCAAGG GCTTTTCGGA 300  
35 CTGTTTGCTC AAGCTGGGCG ACACATGGCC AACTACCCGC AGCCTGGGAC GACAAGACGA 360  
ACATCAAGAC CGTGTGCACA TACTGGGAGG ATTTCCACAG CTGCACGGTC ACAGCCCTTA 420  
CGGATTGCCA GGAAGGGGCG AAAGATATGT GGGATAAACT GAGAAAAGAA TCCAAAACCC 480  
40 TCAACATCCA AGGCAGCTTA TTCGAAGCTT GCGGCAGCGG CAACGGGGCG GCGGGTCCC 540  
TGCTCCCGGC GTTCCCGGTG CTCCTGGTGT CTCTCTCGGC AGCTTTAGCG ACCTGGCTTT 600  
45 CCTTCTGAGC GTGGGGCCAG CTCCCCCGC GCGCCACCC AACTCACTC CATGCTCCCG 660  
GAAATCGAGA GGAAGATCCA TTAGTCTTTT GGGACGTTG TGATTCTCTG TGATGCTGAA 720  
AACACTCATA TAGGATTGTG GGAAATCCTG ATTCTCTTTT TTATTTCGTT TGATTCTTG 780  
50 TGTTTTATTT GCCAAATGTT ACCAATCAGT GAGCAAGCAA GCACAGCCAA AATCGGACCT 840  
CAGCTTTAGT CCGTCTTCAC ACACAAATAA GAAACGGCA AACCCACCCC ATTTTTTAAT 900  
55 TTTATTATTA TTAATTTTTT TGTGTGGCAA AAGAATCTCA GGAACGGCCC TGGGCACCTA 960  
CTATATTAAT CATGCTAGTA ACATGAAAAA TGATGGGCTC CTCCTAATAG GAAGGCGAGG 1020  
AGAGGAGAAG GCCAGGGGAA TGAATTCAAG AGAGATGTCC ACGGACGAAA CATACGGTGA 1080  
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ATAATTCACG CTCACGTCGT TCTTCCACAG TATCTTGTTT TGATCATTTC CACTGCACAT 1140  
 TTCTCCTCAA GAAAAGCGAA AGGACAGACT GTTGGCTTTG TGTTTGGAGG ATAGGAGGGA 1200  
 5 GAGAGGGAAG GGGCTGAGGA AATCTCTGGG GTAAGAGTAA AGGCTTCCAG AAGACATGCT 1260  
 GCTATGGTCA CTGAGGGGTT AGCTTTATCT GCTGTGTGTTG ATGCATCCGT CCAAGTTCAC 1320  
 TGCCTTTATT TTCCCTCCTC CCTCTTGTTT TAGCTGTTAC ACACACAGTA ATACCTGAAT 1380  
 10 ATCCAACGGT ATAGATCACA AGGGGGGGAT GTTAAATGTT AATCTAAAAT ATAGCTAAAA 1440  
 AAAGATTTTG ACATAAAAGA GCCTTGATTT TAAAAAAGAG AGAGAGAGAG ATGTAATTTA 1500  
 15 AAAAGTTTAT TATAAATTAA ATTACGACAA AAAAGATTTG CTACAAAGTA TAGAGAAGTA 1560  
 TAAATAAAA GTTATTGTTT GAAAAAAGAA AAAAAAAGAAW CTCGACCGCA AGGGAAT 1617

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(2) INFORMATION FOR SEQ ID NO: 203:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1974 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

GAATTCGGCA CGAGGCTGAG GGAGCTGCAG CGCAGCAGAG TATCTGACGG CGCCAGGTTG 60  
 CGTAGGTGCG GCACGAGGAG TTTTCCCGGC AGCGAGGAGG TCCTGAGCAG CATGGCCCGG 120  
 35 AGGAGCGCCT TCCCTGCCGC CGCGCTCTGG CTCTGGAGCA TCCTCCTGTG CCTGCTGGCA 180  
 CTGCGGGCGG AGGCCGGGCC GCCGCAGGAG GAGAGCCTGT ACCTATGGAT CGATGCTCAC 240  
 40 CAGGCAAGAG TACTCATAGG ATTTGAAGAA GATATCCTGA TTGTTTCAGA GGGGAAAATG 300  
 GCACCTTTTA CACATGATTT CAGAAAAGCG CAACAGAGAA TGCCAGCTAT TCCTGTCAAT 360  
 ATCCATTCCA TGAATTTTAC CTGGCAAGCT GCAGGCAGG CAGAATACTT CTATGAATTC 420  
 45 CTGTCCTTGC GCTCCCTGGA TAAAGGCATC ATGGCAGATC CAACCGTCAA TGTCCCTCTG 480  
 CTGGGAACAG TGCCTCACAA GGCATCAGTT GTTCAAGTTG GTTTCCTATG TCTTGAAAA 540  
 50 CAGGATGGGG TGGCAGCATT TGAAGTGGAT GTGATTGTTA TGAATTCTGA AGGCAACACC 600  
 ATTCTCCAAA CACCTCAAAA TGCTATCTTC TTTAAACAT GTCAACAAGC TGAGTGCCCA 660  
 GGCGGGTGCC GAAATGGAGG CTTTGTGAAT GAAAGACGCA TCTGCGAGTG TCCTGATGGG 720  
 55 TTCCACGGAC CTCATGTGA GAAAGCCCTT TGTACCCAC GATGTATGAA TGGTGGACTT 780  
 TGTGTGACTC CTGGTTCTG CATCTGCCCA CCTGGATTCT ATGGAGTGAA CTGTGACAAA 840  
 60 GCAAACGCT CAACCACCTG CTTTAATGGA GGGACCTGTT TCTACCCTGG AAAATGTATT 900

5 TSCCCTCCAG GACTAGAGGG AGAGCAGTGT GAAATCAGCA AATGCCACACA ACCCTGTCGA 960  
AATGGAGGTA AATGCATTGG TAAAAGCAAA TGTAAGTKTT CCAAAGGTTA CCAGGGAGAC 1020  
CTCTGTTCAA AGCCTGTCTG CGAGCCTGGC TGTGGTGAC ATGGAACCTG CCATGAACCC 1080  
AACAAATGCC AATGTCAAGA AGGTGGCAT GGAAGACACT GCAATAAAG GTACGAAGCC 1140  
10 AGCCTCATAC ATGCCCTGAG GCCAGCAGGC GCCAGCTCA GGCAGCACAC GCCTTCACTT 1200  
AAAAAGGCCG AGGAGCGGCG GGATCCACCT GAATCCAATT ACATCTGGTG AACTCCGACA 1260  
TCTGAAACGT TTTAAGTTAC ACCAAGTTCA TAGCCTTTGT TAACCTTTCA TGTGTTGAAT 1320  
15 GTTCAAATAA TGTTCAATTAC ACTTAAGAAT ACTGGCCTGA ATTTTATTAG CTTCATTATA 1380  
AATCACTGAG CTGATATTTA CTCTTCCTTT TAAGTTTCT AAGTACGTCT GTAGCATGAT 1440  
20 GGTATAGATT TTCTGTGTTT AGTGCTTTGG GACAGATTTT ATATTATGTC AATTGATCAG 1500  
GTTAAATTT TCAGTGTGTA GTTGGCAGAT ATTTTCAAAA TTACAATGCA TTTATGGTGT 1560  
CTGGGGCAG GGGAACATCA GAAAGGTTAA ATTGGGCAAA AATGCGTAAG TCACAAGAAT 1620  
25 TTGGATGGTG CAGTTAATGT TGAAGTTACA GCATTTTCTGA TTTTATTGTC AGATATTTAG 1680  
ATGTTTGTTA CATTTTAA AATTGCTCTT AATTTTAA CTCTCAATAC AATATATTTT 1740  
30 GACCTTACCA TTATTCCAGA GATTCAGTAT TAAAAA AAAATTACAC TGTGGTAGTG 1800  
GCATTTAAAC AATATAATAT ATTCTAAACA CAATGAAATA GGAATATAA TGTATGAACT 1860  
TTTTGCATTG GCTTGAAGCA ATATAATATA TTGTAAACAA AACACAGCTC TTACCTAATA 1920  
35 AACATTTTAT ACTGTTTGTA TGTATAAAT AAAGGTGCTG CTTTAGTTTT CTGA 1974

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(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

50

CGGCCTTCCG GGGCAACCGT TCGTCCCAAC NCGGAAAGG GTCCTGGAGN CGGGAAGTAG 60  
GAGCCTCGGA AGTCCAAGGG CGGAGCGCCC TTTGCTAATA AGCCAATCAG AACGTGAGAC 120  
55 GCTCCGGTGG GNCGGTGCCG TCGAGCGCGG GGTGGAGTCT GGGTGACTTG GCTGGCGGGA 180  
TCAAGTCAG CTGCTTCAGG CTGAGGTGGC AGATAGTGAG CGCTGGTGCC GGAGTTAAAG 240  
60 TYAAAGCAGG AGAGTAATWA TGAATAGCGC AGCGGGATTC TCACACCTAG ACCGTCGCGA 300

CGGGTTCTC AAGTTAGGG AGAGTTTCGA GAAGCAGCCG CGCTGCGCTT CCACACTGTG 360  
CGCTATGACT TCAAACCTGC TTCTATTGAC ACTTCTTCTG AAGGATACCT TGAGKTTGGC 420  
5 GAAGKTGAAC AGKTGACCAT WACTCTGCCM AATATAGAAA GTTGAAGGAA GCAGTAAAT 480  
TCAGTATCGT AAAGAACAAC AGCAACAACA ATGTGGAATT CASCAGGAC TCCCAATCTT 540  
GTAAACATT CTCCATCTGA AGATAAGATG TCCCCAGCAT CTCCAATAGA TGATATCGAA 600  
10 AGAGAACTGA AGGCAGAAGC TAGTCTAATG GACCAGATGA GTAGTTGTGA TAGTTCATCA 660  
GATTCCAAAA GTTCATCATC TTCAAGTAGT GAGGATAGTT CTAGTGACTC AGAAGATGAA 720  
15 GATTGCAAAT CCTCTACTTC TGATACAGGG NAATTGTGTC TCAGGACATC CTACCATGAC 780  
ACAGTACAGG ATTCTTGATA TAGATGCCAG TCATAATAGA TTTGAGACA ACAGTGGCCT 840  
TCTGATGAAT ACTTTAAGAA ATGATTGCA GCTGAGTGAA TCAGGAAGTG ACAGTGATGA 900  
20 CTGAAGAAAT ATTTAGCTAT AAATAAAAT TTATACAGCA TGTATAATTT ATTTGTATT 960  
AACAATAAAA ATTCCTAAGA CTGAGGGAAA TATGTCTTAA CTTTGTATGA TAAAGAAAT 1020  
25 TAAATTGAT TCAGAAAAA AAAAAAAAAA AACTCGA 1057

30 (2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 721 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

40 GAATTCGGCA CGAGTCATCC CTCTCCCTCT TCACTCCCT TACTCTTACT CTGTTTTTTG 60  
TGCTCCAGAC AGACAGACCC TACCTCTTTT GCTTCTTTT TGTGTGTTG TTTGAGATG 120  
GAGTGTGCT CTGTGTCCT AGGCTGGAGT GCAGTGGCGC AATCTCGGCT CACCACAACC 180  
45 TCTGCCTCCC GGGTTCAAGC AATTCTCCTG CCTCAGCCTC CCGAGAAGCT GGGGATTACA 240  
GGCATCGCC ACCACACCCA GCTNAATTTT ATATTTT TAGAGATGGT GTTCTCCAT 300  
50 GTTGGTCAGG CTGGCCTCAA ACTCCAACC TCAGGTGATN CCGCCTGCTT TGGCCTCCCC 360  
AAAGTGCTGG GATTACAGGC GTGAGCCACT GCGCCAGCC TCTTTGCTC CTTTATACTC 420  
ATTAACCTAC GCCTGTAATC CCGTTTGG GAGGCCAAAG TGAGAAGGTT GCTTGAGGCC 480  
55 AAGAGTTGA GACTAGCCTG GGCAACACAG CAAGATGCCA TCTTTATAAT AAAAAATAAA 540  
ATAAAAATCA ATTAGCTGGG CATGGTGGAA CGCACCTGTA GTCCCAGCCA ATGAGAGGC 600  
60 TGAAGTGGGA GGATCATTGA GCCCAGGAGT TGAGGTGCA GTGAGCCATG ATCATGTCAC 660

TACACTCAGC CTGGGCAATA GAGGGACATG TTGTCTCTAA AAAAAAAAAA AAAAAACTCG

720

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721

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(2) INFORMATION FOR SEQ ID NO: 206:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

20

CCACCATTTA TCCAAC TGAA GAGGAGTTAC AGGCAGTTCA GAAAATGTGT TCTATTACTG

60

AACGTGCTTT AAAACTCGTT TCAGACAGTT TGTCTGAACA TGAGAAGAAC AAGAACAAAG

120

AGGGAGATGA TAAGAAAGAG GGAGGTAAAG ACAGAGCTTT GAAAGGAGTT TTGCGAGTGG

180

25

GAGTATTGGC AAAAGGATTA CTTCTCCGAG GAGATAGAAA TGTCAACCTT GTTTTGCTGT

240

GCTCAGAGAA ACCTTCAAAG ACATTATTAA GCCGTATTGC AGAAAACCTA CCCAACAGC

300

30

TTGCTGTTAT AAGCCCTGAG AAGTATGACA TAAATGTGC TGTATCTGAA GCGGCAATAA

360

TTTTGAATTC ATGTGTGGAA CCCAAATGC AAGTCACTAT CACACTGACA TCTCCAATTA

420

TTTGAGAAGA GAACATGAGG GAAGGAGATG TAACCTCGGG TATGGTGAAA GACCCACCGG

480

35

ACGTCTTGGA CAGGCAAAAA TGCCTTGACG CTCTGGCTGC TCTACGCCAC GCTAAGTGGT

540

TCCAGGCTAG AGCTAATGGT CTGCAGTCTT GTGTGATTAT CATACGCATT CTTGAGAGCC

600

40

TCTGTCAGCG AGTTCCAAC TGGTCTGATT TTCCAAGCTG GGCTATGGAG TTACTAGTAG

660

AGAAAGCAAT CAGCAGTGCT TCTAGCCCTC AGAGCCCTGG GGATGCACTG AGAAGAGTTT

720

TTGAATGCAT TTCTTCAGGG ATTATTCTTA AAGGTAGTCC TGGACTTCTG GATCCTTGTG

780

45

AAAAGGATCC CTTTGATACC TTGGCAACAA TGA CTGACCA GCAGCGTGAA GACATCACAT

840

CCAGTGACCA GTTTGCATTG AGACTCCTTG CATTCCGCCA GATACACAAA GTTCTAGGCA

900

50

TGGATCCATT ACCGCAAATG AGCCAACGTT TTAACATCCA CAACAACAGG AAACGAAGAA

960

GAGATAGTGA TGGAGTTGAT GGATTGAAG CTGAGGGGAA AAAAGACAAA AAAGATTATG

1020

ATAACTTTTA AAAAGTGTCT GTAAATCTTC AGTGTAAAA AAACAGATGC CCATTGTGTG

1080

55

GCTGTTTTTC ATTCATAATA ATGTCTACAT TGAAAAATTT ATCAAGAATT TAAAGGATTT

1140

CATGGAAGAA CCAAGTTTTT CTATGATATT AAAAAATGTA CAGTGTTAGG TATTATTTGA

1200

60

ATGGAAAGAC ACCCAAAAAA AAAAATGTGC TCCGACTAGG GGGAAAACAG TAGTTCCGAT

1260



TTTTCCCAT TATTTTATT TTATTTCTG GTTGCCCTAG CTTCCCCCCC TATTTTGTG 1320  
 TCTTTTATTA ACTAGTGCAT TGTCTTATTA AATCTTCACT GTATTTAATG CAGGATGTGT 1380  
 5 GCTTCAGTTG CTCTGTGTAT TTGATATTT TAATTTAGAG GTTTGTGTG CTTTGTGACA 1440  
 CTAGTGTAA GTTACTTTGT TATAGATGGT ATCCTTTACC CCTTCTTAAT ATTTTACAGC 1500  
 AGTACGTTTT TTTGTAACGT GAGACTGCAG AGTTTGT TCTATATGTG AAGGATTACA 1560  
 10 ACACAAAAG TTATCCTGCC ATTCGAGTGC TCAGAACTGA ATGTTTCTGC AGATCTGTG 1620  
 GCATTTGTCT CTAGTGTGAT ATATAAAGGT GTAATTAAGA CAGAGTTCTG TTAATCTAAT 1680  
 15 CAAGTTTGCT GTTAGTTGTG CATTAGCAGT ATAAAAGCTA ATATATACTA TATGGTCTTG 1740  
 CAACAGTTTT AAAGCCTCTG CATAATTGAT AATAAAAATG CATGACATTC TTGTTTTTAA 1800  
 TAGACTTTTA AAATCATAAT TTTAGGTTTA ACACGTAGAT CTTGTACAG TTGACTTTTT 1860  
 20 GACATAGCAA GGCCAAAAT AACTTTCTGA ATATTTTTTT CTGTGTATA AGTGAAAGG 1920  
 GCATTTTTCA CATATAAGTG GGCTAACCA TATTTTCAA AGAATTCAT CATGTACAA 1980  
 25 CTAACAACAG TAACTAGCCC TTAATTATGG TGACAGTTCC TTATTGGTGT GTGTGAGATT 2040  
 ACTCTAGCAA CTATTACAGT ATAACACAGA TGATCTTCTC CACACACCCC ATCACCCAGA 2100  
 TAATTTACAG TTCTGTTAAC AGTGAGGTG ATAAAGTATT ACTGATAAAA AATTATCTAA 2160  
 30 GGAAAAAAC AGAAAATTAT TTGGTGTGGC CATCTTACCT GCTTATGTCT CCTACACAA 2220  
 GCTAAATATT CTAGCAGTGA TGTAATGAAA AATTACATCT TACTGTGAT ATATGTATGC 2280  
 35 TCTGGTACAC AGATGTCATT TTGTGTGAC AGCACTACAG TGAAATACAC AAAAAATGAA 2340  
 ATTCATATAA TGACTTAAAT GTATTATATG TTAGAATTGA CAACATAAAC TACTTTTGCT 2400  
 40 TTGAAATGAT GTATGCTTCA GTAAAATCAT ATTCAAATTT AAAAAAAAAA AAAAAAAAAA 2460  
 CTCGA 2465

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(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

55

GAATTCGGCA CGAGCTCAAG CTGGCAGGTG GTCGGGGGAG CGGCCGGAGA GGAGCTGCCG 60  
 GGAGTTCGTG CCCTGCAGGA CATGACACCA GTGGCATATC ACGGCCATGG GGTCTCAGCA 120  
 60 TTCCGCTGCT GCTGCCCCCT CCTCTGCAG GCGAAAGCAA GAAGATGACA GGGACGGTTT 180

5 GCTGGCTGAA CGAGAGCAGG AAGAAGCCAT TGCTCAGTTC CCATATGTGG AATTCACCGG 240  
GAGAGATAGC ATCACCTGTC TCACGTGCCA GGGGACAGGC TACATTCCAA CAGAGCAAGT 300  
AAATGAGTTG GTGGCTTTGA TCCCACACAG TGATCAGAGA TTGCGCCCTC AGCGAACTAA 360  
GCAATATGTC CTCCTGTCCA TCCTGCTTTG TCTCCTGGCA TCTGGTTTGG TGGTTTCTT 420  
10 CCTGTTTCCG CATTCAGTCC TTGTGGATGA TGACGGCATC AAAGTGGTGA AAGTCACATT 480  
TAATAAGCAA GACTCCCTTG TAATTCTCAC CATCATGGCC ACCCTGAAAA TCAGGAACTC 540  
CAACTTCTAC ACGGTGGCAG TGACCAGCCT GTCCAGCCAG ATTCAGTACA TGAACACAGT 600  
15 GGTGAATTTT ACCGGGAAGG CCGAGATGGG AGGACCGTTT TCCTATGTGT ACTTCTTCTG 660  
CACGGTACCT GAGATCCTGG TGCACAACAT AGTGATCTTC ATGCGAACTT CAGTGAAGAT 720  
20 TTCATACATT GGCCTCATGA CCCAGAGCTC CTGGAGACA CATCACTATG TGGATTGTGG 780  
AGGAAATTC ACAGCTATTT AACAACTGCT ATTGGTTCTT CCACACAGCG CCTGTAGAAG 840  
AGAGCACAGC ATATGTTCCC AAGGCCTGAG TTCTGGACCT ACCCCCACGT GGTGTAAGCA 900  
25 GAGGAGGAAT TGGTTCACTT AACTCCCAGC AAACATCCTC CTGCCACTTA GGAGGAAACA 960  
CCTCCCTATG GTACCATTTA TGTTTCTCAG AACCAGCAGA ATCAGTGCCT AGCCTGTGCC 1020  
30 CAGCAAATAG TTGGCACTCA ATAAAGATTT GCAGAATTTA ATACAGATCT TTTCACTGT 1080  
TCTTAGGGCA TTATAAATGG AAATCATAAC GTGGTTCTAG GTTATCAAAC CATGGAGTGA 1140  
TGTGGAGCTA GGATTGTGAG TGACCTGCAG GCCATTATCA GTGCCTCATC TGTGCAGAAG 1200  
35 TCGCAGCAGA GAGGGACCAT CCAAATACCT AAGAGAAAAC AGACCTAGTC AGGATATGAA 1260  
TTTGTTCAG CTGTTCCCAA AGGCCTGGGA GCTTTTGTAA AAGAAAGAAA AAAGTGTGTT 1320  
40 GGCTTTTTTT TTTTITAGAA AGTTAGAATT GTTTTACCA AGAGTCTATG TGGGGCTTGA 1380  
TTCACCTTC ATCCATTGGC TGAACATGG ATTGGGGATT TGATAGAAAA ATAAACCCTG 1440  
CTTTTGATTC AAAAAAAAAA AAAAAWAAA AAAAATCGA 1480  
45

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CAGTATTTCC CTCAGTACTG TAAGCAAAAG TGGTATGTTT TTCTTTCTTT ATGTCTACTC 60  
60

	TGTCCTCTGT GGCCTTCTGG TGTACCCCTC TCTTCTAGC CATTCACTCT CTCTAGTCAC	120
	CTCCCTAGTA GCTAGTGCTC TCTAAGTTT TATTTAATTA GAACAACTCC ATTTCCATTT	180
5	CAAGGTAGGT CAATGGGGG AAAAGCCTCA TGATTTAAAC TGAAGTTAAC AACACAGCTT	240
	TTAAATGAA AACTCATACT CCAACTTCTA AAGTATATTT GAGCTGATTT GTTTCCAAAA	300
	CAAAGATATG CTGTACCTAA AACTGCTAAA ACAAATAT AAAGACAAGG ACTAGGTGAT	360
10	TAAGGGGAGA GAAAAATCAT YTCTTTTCCA GGAAACCTTT GCTAAAATAA GCAAAACTTG	420
	ANTCTATGCT TCATGGAAAC TGACACAAAG AAAAGAACT GATGGATTGC ACAGGCCTTG	480
15	TTATAGAAAT AGATCTATAA AAAGATCTGT CCACAGGAAA TATACACCTT CTCCTGGTTC	540
	TGAACCTCAA TGGGGATTG TCACCTAGGT CTCCATCTAT AGGAATACCT TCACATACCT	600
	ATCTATTCAT GCACATATTC TGAAACAGG TACATACAAA ATTACAACAA AGGAAAAAAA	660
20	TTCTATTGAA CACTTAAAA TAGAAACAGG CCAGGCACGG TGGCTCATGC TGTAATCCCA	720
	ACAATTTGGG AGGCTGAGGC TGGTGGATCA CCTGAGGTCA GGAGTGTGAG ACCAGCTTGG	780
25	CCAACATGGT GAAACCCCGT CACTACTAAA AATACAAAA AAATTAGCCT GTGTGGTGGC	840
	ACACTCNTAC AATCCNGGCT GACTCGGGAA AN	872

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(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1779 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

	AATTGCCAAG ACTGCACAAA ATTACAGTGC TAATGTATAT GGTTCAGTT CACATAAAGA	60
	CAAAAGCATC TGTATGAAA TGAGTAGTAA TATTGGGTGG TTGATTGTT CTTAGCAGAC	120
45	TTGGCTTCAT WTTGGTCTTG AGATAAAATG GCCAGCATAA ATGCTGTTTA TATTCACGTT	180
	TTCTAGGTG TGTGTGTGCA GGCCACAGCA GCATGCCCTT GGTGTAGTCA GTGCCGAAAS	240
50	GGGTCTGTTT CTCTTGAGC CTGCCTGCAG GGATGGTCTC CTTTAAAGC AGGTGTGTG	300
	CAGCATTCAG TACACTGAAG GTAAGCTAAA CCATCAACAT CTCTGGTGT TTAAGATGTT	360
	ATTTTATTGG ACAAAGTAC AAATGAGGGA TGTTAGCTTT GTGGCAGAAT TCCCTGCATG	420
55	TGTGATAACT GATCTTGTTT TATTTTGGT CATGCAACT GTGGCATAGT TACAATTTCT	480
	GTTTGKTCAT CACATTTAAA ATTGGRAGAG AACGCGCTG AKGGATAGAG CGCCTTCAGK	540
60	GTACTGTTTC TTATTAACCT TACTTTTTTT AAATCAACTT GCTATAGACT TTATATACAT	600

	TTTGTTAAAT ATAGTTCCTA GTGACATAGA AACGATGCGT AGTITTCATT TACTAATTAC	660
	AAATGTTGAG GCCTAATTCT GAAAGTCCTC ATATTTAAAG GCTAGACAAC GTAATGAAAT	720
5	TTTTAACTAT TTGTATGTCA TTTTGAAAGT GTACTGCTTT ATGGTAAAAG TGTTTTTCAT	780
	TTGTTCATTG TTTTCATTAT TTGTGATCAT GTTGTCTTTC AATACAGGCA TAAACCTTCC	840
10	ACTCTGAAC AAAGCAGCTG CTTTTTAAAA GCGGTAATTG CTTCTTTACC TTTTATTCT	900
	TTTGTAATG AAGCTTTTCT TTAAGAATGT GACTTTAAAG TGTTGTCTAT TGCATAAAAC	960
	AGTTGACACT CACTTATTGT AAAGTGAAGA TTGTTCTACT GCATGTGAAG TGGACCATGC	1020
15	AGATTCTGT ATGTTCTCAG TATGCATCAC TAGATAATAA AGTCTTTTGT GAACAAGGCA	1080
	TTTGTAGCCA TTTTAAAAG TTTTGTCTT CAGTGCTGGT AAGTCAGGTA AACCATAAAT	1140
20	AGTTAAAAGC AACCTTTTGT TTTTTTCCTG AAAGTTTTTA ATTGAAAGTA TTATTAGTTA	1200
	AAGATGTAAA CCTAGCCAAA ATTACCAGTT TATTAATAAT TAGGATCCTA ATTATTTCAA	1260
	AAAATCCTAC AAATATTGTC AGCTTTCAGT GTAGTGAGAT TATTCCTGTA GGTATGGGG	1320
25	TATAATTCAG GATTAACTA ATGTTCTGC TATTTCTCA CTTTTCCTTT TGATGGTGCG	1380
	GAAAGAGAAA AAGGAAAACG GGGCACAGGC CATTCGACGC CTTCTCCAAG GGTCTGATT	1440
30	TGCTGAGACA CCAGCTTCAC CTTCTTAACA AGGCACCTAA TTACAACAAG CATGCACATT	1500
	TTGGTGCAAT CAAGAAATGA AAATCAGAAT AGCAGCATTG ATTCTTCTGG TGCAGCTCAG	1560
	TGGAAGATGA TGACAACCAG AAGACATGAG CTAAGGGTAA GGGACTGTTT TGAAGAACCT	1620
35	TTCCATTAG TGATCAAGAT ATGGAAGCTG ATTTCTGAAA ATGCTCAGTG TGTACTCTAA	1680
	TTATTTATGG TACCATTGA ATTGTAACCT GCATTTTAGC AGTGCATGTT TCTAATTGAC	1740
40	TTACTGGGAA ACTGAATAAA ATATGCCTCT TATTATCAA	1779

45 (2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 2110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

55	GCGGCCGCTG CAGCCCGGAG CTGAGCTAGC CGTCCGAGCC GAGCCGTCCG AGCCGGGGAA	60
	GCCGGCGCGT GCTGCCGCTC GTGGCGGCCA GAGGAGAGGA GAGGCAGCAG CATGGCGAGT	120
	GTCTGTCCC GACGCCTTGG AAAGCGGTCC CTCCTGGGAG CCCGGGTGTT GGGACCCAGT	180

	GCCTCGGAGG GGCCTCGGCT GCCCCACCCT CGGAGCCACT GCTAGAAGGG GCCGCTCCCC	240
	AGCCTTTCAC CACCTCTGAT GACACCCCTT GCCAGGAGCA GCCCAAGGAA GTCCTTAAGG	300
5	CTCCCAGCAC CTCGGGCCCTT CAGCAGGTGG CCTTTMAGCC TGGGCAGAAG GTTTATGTGT	360
	GGTACGGGGG TCAAGAGTGC ACAGGACTGG TGGWGCAGCA CAGCTGGATG GAGGGTCAGG	420
	TGACCGTCTG GCTGCTGGAG CAGAAGCTGC AGGTCTGCTG CAGGGTGGAG GAGGTGTGGC	480
10	TGGCAGAGCT GCAGGGCCCC TGTCCCCAGG CACCACCCCT GGAGCCCGGA GCCCAGGCCC	540
	TGGCCTACAG GCCCGTCTCC AGGAACATCG ATGTCCCAA GAGGAAGTCG GACGCATGGA	600
15	AATGGATGAG ATGATGGCGG CCATGGTGCT GACGTCCCTG TCCTGCAGCC CTGTTGTACA	660
	GAGTCCTCCC GGGACCGAGG CCAACTTCTC TGCTTCCCGT GCGGCCTGCG ACCCATGGAA	720
	GGAGAGTGGT GACATCTCGG ACAGCGGCAN CAGCACTACC AGCGGTCACT GGAGTGGGAG	780
20	CAGTGGTGTG TCCACCCCTT CGCCCCCCA CCCCAGGCC AGCCCCAAGT ATTTGGGGGA	840
	TGCTTTTGGT TCTCCCCAAA CTGATCATGG CTTTGAGACC GATCCTGACC CTTTCCTGCT	900
25	GGACGAACCA GCTCCACGAA AAAGAAAGAA CTCTGTGAAG GTGATGTACA AGTGCCTGTG	960
	GCCAACTGT GGCAAAGTTC TGCCTCCAT TGTGGGCATC AAACGACACG TCAAAGCCCT	1020
	CCATCTGGGG GACACAGTGG ACTCTGATCA GTTCAAGCGG GAGGAGGATT TCTACTACAC	1080
30	AGAGGTGCAG CTGAAGGAGG AATCTGCTGC TGCTGCTGCT GCTGCTGCCG CAGACCCCCA	1140
	GTCCCTGGGA CTCCACCTC CGAGCCAGCT CCCACCCCA GCATGACTGG CCTGCCTCTG	1200
35	TCTGCTCTTC CACCACCTCT GCACAAAGCC CAGTCTCCG GCCCAGAACA TCCTGGCCCG	1260
	GAGTCTCCC TGCCCTCAGG GGCTCTCAGC AAGTCAGCTC CTGGGTCTT CTGGCACATT	1320
	CAGGCAGATC ATGCATACCA GGCTCTGCCA TCCTTCCAGA TCCCAGTCTC ACCACACATC	1380
40	TACACCAGTG TCAGCTGGGC TGCTGCCCC TCCGCCGCCT GCTCTCTTTC TCCGGTCCGG	1440
	AGCCGGTCGC TAAGCTTCAG CGAAGCCCCA GCAGCCAGCA CCTGCGATGA AATCTCATCT	1500
45	GATCGTCACT TCTCCACCCC GGGCCAGAG TGGTGCCAGG AAAGCCCGAG GGGAGGCTAA	1560
	GAAGTGCCGC AAGTGTATGG CATCGAGCAC CGGGACCACT GGTGCACGGC CTGCCGGTGG	1620
	AAGAAGGCCT GCCAGCGCTT TCTGGACTGA GCTGTGCTGC AGGTCTACT CTGTTCTTGG	1680
50	CCCTGCCGGC AGCCACTGAC AAGAGGCCAG TGTGTACCA GCCCTCAGCA GAAACCGAAA	1740
	GAGAAAGAAC GGAAACACGG AGTTTGGGCT CTGTTGGCTA AGGTGTAACA CTTAAAGCAA	1800
55	TTTCTCCCA TTGTGCGAAC ATTTTATTTT TTAACAAAAA GAAACAAAAA TATTTTCCC	1860
	CCTAAATAG GAGAGAGCCA AACTGACCA AGGCTATTCA GCAGTGAACC AGTGACCAA	1920
60	GAATTAATTA CCCTCCGTTT CCCACATCCC CACTCTCTAG GGGATTAGCT TGTGCGTGTG	1980

AAAAGAAGGA ACAGCTCGTT CTGCTTCCTG CTGAGTCGGT GAATTCCTTG CTTTCTAAAC 2040  
TCTTCCAGAA AGGACTGTGA GCAAGATGAA TTTACTTTTC TTAAAAAAA AAAAAAAAAA 2100  
5 AAAAACTCGA 2110

10 (2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 938 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

20 GGCACAGGAA AAAAAAGAAA AAAGAAAAA GAAAAAGTT TTGTACCCA CAGATTAGCA 60  
TTTTCTTGAT GTTTGAAAAA AGTTTAAGCT ATGTCCTAAT TTAAAAATGA GCACAAACTA 120  
CTTAACAGAT GTCTGTTCCC TCTTCTCTTA CTAAATTAT CTTTATTTTC ACCATCACCT 180  
25 CCCAGTGCCG AACACCTGAN CTCTGTGTTT TGTGGTTGGA TCCTGGGTG CCAAGTTCCT 240  
ATTTGGTCAG TCCCTGGCCT GTGGGGCGGT CTCAGGAAGT GGCATGCTCT TCAMGRAGGA 300  
30 TCGTTCATYT CCAGTATAAC CAWTTTGTTA ATAATAGTTG ATAATTCCCA GCTTTTACCA 360  
GATGARTTTT GACTTATTTT TCCTCCTTTG ACCTGTTCAA AGCTAACATA TCTCGGTCAG 420  
TTCCGAGAGG GTGGGGGATT TGAGAATGTG AGGAGGAGTG GGGTTAGAAT GGGTTTGCCT 480  
35 ATCTGGGCAA GGAAGAGTT CCTAGTCGAT TGGGCACAAT GACAAAATGA TTCCATGGAT 540  
AGAATCGTCC CATGTTGCTG GAACACCTCA CGTGTGTGA ACGCCTTAA TTCTGCCAT 600  
40 CCCTTCTCTG ATTCCCCACC TCCCTGTAGT TTCCACAGGA TTTATCTCTC TGTACCCCCG 660  
TCCTCCAAC CTACTCTGTC AGCCTCTCCT CCATCCCTTA CTCCCTTCT AAATTCCAGG 720  
AGATGACCTC ACTTTGCAA GCAAATGGA GCCACCAAAT TGTAGCTCTC CTCGGTGGAA 780  
45 ACTGCATCTG TGCTCATCCC TGCACCTTCT TGCAGAAAGC CGCCCCCTCA GGCCAAGATG 840  
AGTGCCTGGC CCCCATGGGA GACTCAGACA CTTTGACCCC TTGTGACTTC AGCATCTCCC 900  
50 TCTTTAAAGA TTCTCTCCCA ACATTCAGTC GTGCTCGA 938

55 (2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1551 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

5	AGGCTGGACT AAGCATAGAG AACCAGGAGA GAAAGAAAGA TTTAAGAGAC TGAGTAATAT	50
	TTTTTGACAG ATCATTTAAG AAAGTGAGTA ATTTTTTTTT TCTCCAAAAG GGCATGGGTT	120
	TTTTTTTTGT TTGTTTTTTT CTCTATTGG CACTTCTAG GGATGGTCT ATAAATTTT	130
10	TGAAAGATCA TAGGATAAAT TTCTTTGTAG CAACTTCCTA TTTTAGTGTT TATGTTAGGG	240
	GARCCCCARG TGTCCCTGCT GATACGCCAT TAGGGCCACT TCTCAGCCTC TGGCTACATC	300
15	ATAATGCTTT TTTTCTATC TTGCCAAAGT TTCCMGAAAA TTKAKGTTTT CTAATTTTAA	350
	AAAAATGGT TGTGGAGATG GGATGGGACC TCTTTATAAG CCCTGAAAAT AAGTGATTN	420
	TTTTAAGTGC TATTCTGCTA TAAACCTGAT TCTCACTTTT TTCTGTAGAC AACAGTTTTT	430
20	TATAATATAT CTATTTTGTG TGGACATTAT TTCCTTTTAA CCAATACTGA AATTCATAG	540
	TGTAWACTTT CTCCACATTT TCTTTGATTA ATACTTYCTT AAAATAGACA CTTGGATTGG	630
25	CACCAGCTGT CACCAATAAA GCTGCCCTGA ACATTGTCAA TCAATCCTGT TAACCAATTT	650
	GAGAATTTTT CTGGAATGCT TAGTTAGGGA TGAAATGCT GGGTTATAGG TATGAGTATG	720
	CTTGATATAC TTTTCTCCAG AATGTCTACA CCTGTGTGTA CACCACATCT CCAGAGATAG	730
30	GGGAATCTTA TGTCCCTGCT AACTGCTCTC GTTATTTAAT TTCTGACAT TTGCCGCCGC	840
	CGCCGCCCCC TGCCCCAAC ACACACATGG TATAAAGTGG TAGTTTCTTG TTTTAAATTG	930
35	AACTTTTGAA TGATTTGAAT TTGGGCATTT CTTGTATCC TGAGTTATTT TGGTTTCCCG	950
	TTATGTGAAT ATCCTTTTCC TATGCTTTAA CTACTTTTCT AATTTGTCCC TTTTTNGGT	1020
	TATCAAATTC CAGGCCATTG TCTATCCAT CGTCACTTTT GGGTATTGGA AACATCTTTC	1030
40	CATTCTGTAG CCTGTCTGTT GAACATAAAT CTTGATTTTT ATGTAATCAG ATTTTCTCC	1140
	TTACGGTTAT GTTCTTGAA TTTTATTTAA GAAATCTTTT TCTATCCTGA GACCACAAAA	1200
45	ATGTCCCCAC CATTTTCTTC TGTTTCATAG TTTTGCCTTG TATGTTTAAAT CCTTTAAGGC	1250
	ATGTGTAGTT CATTTTATAT GGTGTGAAAT AGTCTTATT CATTTATTCA ACACATATTG	1320
	GTGGAGTGCC TGCTGATGGT AGTACTCTTC AGAGTACTTT GTATATATTT GTGAACACAT	1330
50	ATTCCTGCCC TGGAAGCTTA TGTGTCTTT CAAGGTAGAT CCNACTCGG TTTCCACCTG	1440
	TTTTCTTCAG CCCTCAGGAT GAATTCCACA ATTTTACACA TAGCACCAGT TAAGGAATAG	1500
55	GCTTTATTGG AGAAAAGGAA GGCTTATTAG ACCAGCATCA GCAAAAAAAA A	1551

60 (2) INFORMATION FOR SEQ ID NO: 213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 997 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

10 AGAGAGTCCT CAACAGAACC TAATCATGCT GGCACCCCTAA TCTCATACTT CTAGCCCTCA 50  
 GAACTGAGAG AACATAAACT CCAGTTGTTT AAGCTACCCA GCTCATGGTA TTTGTTATTA 120  
 TAGCCCAAGC TAAGTCAGGT GGAAAGGCAG AAATATTTTG AAGAGATCA TTTCTACAAA 180  
 15 AACAGAGTTG TTCTAAATGA AATGGCCAGA TATTTCATCT TCTTCATCT AGTATTATG 240  
 AAAGTTTCAT TAAACACCAC TTGGCCAGCA CCCAGGCCCTG CTACCTCTAG AACGGCAAC 300  
 20 AAAAGCAAAT GATTTGAGGA ACAAAGAGT GGACACAGAG CTTCTCAGAA GATGGCTCCA 360  
 TCTTCTGAGA TGATCTTCTG AGATCATCAA TTTTCTGCAC CTGATGCTCT ACTCCAATG 420  
 TAGTAGATAA GAGCAAAGAC ACTTCCTGAT CCTGTGGAAA ATGCTGGAGC CCTGCTGATG 480  
 25 GAGAGGCTGA CACTGGGACC AACAGAAGGC CGGACATTTA TTTGCTGCAG CCTTCTGCA 540  
 CCTGGGCCCT CTTCAGGCCT TGTACCTTGC ACTCCCCATG CCACTGTAGC ACCTGGTAG 600  
 30 CTGAAGTTAG GTATTTGAAG AGATAATTTG CCCCCAACCA AGAATTACTT AAAAGAAAA 660  
 GGAAACCACT AAATTCCTCT TGACAAACCA GTTTGTTTCA TTTTCACTTT TGCAAAATTTG 720  
 AAACTTTCTC TTTGGCACCA TATGATTCTG TTACATTAGG GGTCTCTCAT GCTAAGATAC 780  
 35 ACAGCTAGGT CTACCAGCTG CCAGTGGTCA AGAATGAAG AACCTCTCAG AGAGAGATCA 840  
 GTTTCTAATA ACCTAACAGT TTTCTTGGG TATTACAAA AAAAAAAAAA TTAGAATAAA 900  
 40 ATGTCAGTGC CATGCAGGCA AGTACAGATA TGGAAATGAA AGCTCTGTCT ACAAATGCAA 960  
 GATTGTGTTT TTAATAAAAT TGATTGGGAT CACTCGA 997

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## (2) INFORMATION FOR SEQ ID NO: 214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1496 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

50 GAATTCGGCA CGAGTGACCA CAGATATCTT TGGCTTTTCA CCTACCCACA ATGCTGTCCA 60  
 CTATGTTTTT TTAATCGAT TGACATCTCA TGAATCCACA AATTTAGCCG CTTTTCCTTC 120  
 60



TTTTCCATCT TTGTCATAGC TTCATCACGC ACGATGGAGG TCACTTCAGC ACTATCCGGA 180  
 GCGGCCTCAC GGACAGATCR GTGAATTTC TTTTCCTTTT TCTTGATGTA CCGGATTGTC 240  
 5 GACTCGTTAA CATTGAGCTC ATGGCCAACA GCACTGTAAC TCATGCCTGA TTGGAGCTTA 300  
 TCCAACACGC GGAMTTTCTC CGTAAGGSAM ATCAMGGTCT TCTTTGCTT AGGAACACTG 360  
 10 GGCARARCTT AARCACTACG CTGGGGGCC ATTTTAGAAA GCAAAACCAC CCACAAAAG 420  
 CAGAAAAAA AGTGTCAGTA AACAGACTGN NGANAGGACT CTTTGTTTAC AGCACAGGAG 480  
 CTGCGACTAG AAGCGGGCGC TTCTCCCAG TTCAAACCTC AGCTGGGAAC CTTACCTCCG 540  
 15 CCAACTCCAA ATTTTCACCC TCTGCGCATG CCCGGGAAAS AAACCCCGAG AACAGTACCG 600  
 TGATGATTGA TTTTAGGGT ACAATAACAT TTTAGCAAGT AAGTGAATT GGCATTACGA 660  
 ATTAATGATT AATGAAGGTC ACCTGTATTT CCATAGATAT GTAATTTTAT TTAAGCAGGT 720  
 20 TTATTATATT AAGGCGGSGA GGCAGCGCGC AAGACTACAA GTTCCAGCAT GCACCGCGTC 780  
 CGGGCGGGTT CGGGCTCCCA GCGAGGGCTT CAGGGACGCC AGCCCGGAGG CATCGGCCGG 840  
 25 AAGTGTGTA GGGCAACCAC GTAGTACTCT CTGCGCATGT GCAAAGCGCT GTCGGGGGCC 900  
 GCCCTAGCTG CCGTCGCCGC CGCCGGGGCT CTATGGTCTC TCCCTAGAGC TTTGCCGTTG 960  
 GAGGCGGCTG CTGCGGTCTT GTGAGTTGA CCAGCGTGA GCGGCAGCAA CATGGAGGAA 1020  
 30 TTCGACTCCG AAGACTTCTC TACGTCGGAG GAGGACGAGG ACTACGTGCC GTCGGGTGAG 1080  
 CGATTCCGCC TGAGGCGAGA AGCGAATTGC CCCGCCCCAC GCCTCACGTG AGGCGCGCTC 1140  
 35 TGCCCCCGCG GCGTCTGCC CTGTGCCCCA GGTGGTCCAG GGGGGCTCCT GTTCTCGAGC 1200  
 GTCCGCTCCC TCAGGCCCTT CATCTCGGC CGCTCCGGCC CGAGGCGTGT GCGGTGGCG 1260  
 GTTCTGTGCT CCCCTCCCGT TGGGCAGCTC CGGCCGCCGC CCCCTCTTGC AGCGCGGGAA 1320  
 40 CGGCACATGG ACACGGCCCC TTGTCGCTAG GGACGCTCGT CGGTCAGCCC CGAACGACAA 1380  
 CGCTGCTTCA GAAGTCGGGG CGGCAGTTCG AGCCTTGAA GTTTTTCG GCGCTGGCCC 1440  
 45 GAGAGAGCTG CTGGCCAACA ACCCGTCCAA GATAGAGCTG TCCGNTCTCC GNCCTGG 1496

50 (2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

60 TTGGCANCNG GGAGAGGGAA AGAGGAGGAA ATGGGGTTTG AGGACCATGG CTTACCTTTC 60

CTGCCTTTGA CCCATCACAC CCCATTTCCT CCTCTTTCCC TCTCCCCGCT GCCAAAAAAA 120  
 AAAAAAAGG AAACGTTTAT CATGAATCAA CAGGGTTTCA GTCCTTATCA AAGAGAGATG 180  
 5 TGGAAAGAGC TAAAGAAACC ACCCTTTGTT CCCAACTCCA CTTTACCCAT ATTTTATGCA 240  
 ACACAAACAC TGTCTTTTGG GGTCCCTTTC TTACAGATGG ACCTCTTGAG AAGAATTATC 300  
 10 GTATTCACG TTTTATAGCC TCAGGTTACC AAGATAAATA TATGTATATA TAACCTTTAT 360  
 TATTGCTATA TCTTTGTGGA TAATACATTC AGGTGGTGCT GGGTGATTTA TTATAATCTG 420  
 AACCTAGGTA TATCCTTTGG TCTCCACAG TCATGTTGAG GTGGGCTCCC TGGTATGGTA 480  
 15 AAAAGCCAGG TATAATGTAA CTTCAACCCA GCCTTTGTAC TAAGCTCTTG ATAGTGGATA 540  
 TACTCTTTTA AGTTTAGCCC CAATATAGGG TAATGGAAAT TTCCTGCCCT CTGGGTTCCT 600  
 20 CATTTTACT ATTAAGAAGA CCAGTGATAA TTAAATAATG CCACCAACTC TGGCTTAGTT 660  
 AAGTGAGAGT GTGAAGTGTG TGGCAAGAGA GCCTCACACC TCACTAGGTG CAGAGAGCCC 720  
 AGGCCTTATG TTAAATCAT GCACTTGAAA AGCAAACCTT AATCTGCAA GACAGCAGCA 780  
 25 AGCATTATAC GGTCACTCTG AATGATCCCT TTGAAATTTT TTTTTGTTT GTTTGTTTAA 840  
 ATCAAGCCTG AGGCTGGTGA ACAGTAGCTA CACACCCATA TTGTGTGTTT TGTGAATGCT 900  
 30 AGCTCTCTG AATTTGGATA TTGGTTATTT TTTATAGAGT GTAAACCAAG TTTTATATTC 960  
 TGCAATGCGA ACAGGTACCT ATCTGTTTCT AAATAAACT GTTTACATTC ATTATGGGGT 1020  
 ATGTATGACC TTCATTTTCC AAGAAATAGA ACTCTAGCTT AGAATTATGG ATGCTCTAAA 1080  
 35 ATGTCAGAAT GGGAACTCTC CTCGAAGTTC TCCCAAATC AGAGACAGCA CTGCCTTCTC 1140  
 CTAAATGATT ATTCTTTTCT CCCTGTTTTC TGGTATTTTC TAGGCATCCT TCTCACCACA 1200  
 40 GCCATAACCC TTTTTTACTT CCATTAGGCC GTATAACTGG NGGGACNGCT GGTCCGTATA 1260  
 TAATACTGGT WCCAACAMAG GGGTCTGGA TGTACACMAG GTTATCTT 1308

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(2) INFORMATION FOR SEQ ID NO: 216:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1705 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

TGGCCATGGA AGCGCTAGAA GGTTAGATT TTGAAACAGC AAAGAAGGAT TTCCTTGGAT 60  
 CTGGAGACCC CAAAGAAACA AAGATGCTAA TCACCAAACA GGCTGACTGG GCCAGAAATA 120  
 60

	TCAAGGAGCC CAAAGCCGCC GTGGAGATGT ACATCTCAGC AGGAGAGCAC GTCAAGGCCA	180
	TGCAGATCTG TGGTGACCAT GGCTGGGTTG ACATGTTGAT CGACATCGCC CGCAAACCTGG	240
5	ACAAGGCTGA GCGCGAGCCC CTGCTGCTGT GCGCTACCTA CCTCAAGAAG CTGGACAGCC	300
	CTGGCTATGC TGCTGAGACC TACCTGAAGA TGGGTGACCT CAAGTCCCTG GTGCAGCTGC	360
	AGTGGAGACC CAGCGCTGGG ATGAGGCCTT TGCTTTGGGT GAGAAGCATC CTGAGTTTAA	420
10	GGATGACATC TACATGCCGT ATGCTCAGTG GCTAGCAGAG AACGATCGCT TTGAGGAAGC	480
	CCAGAAAGCG TTCCACAAGG CTGGGCGACA GAGAGAAGCG GTCCAGGTGC TGGAGCAGCT	540
15	CACAAACAAT GCCGTGGCGG AGAGCAGGTT TAATGATGCT GCCTATTATT ACTGGATGCT	600
	GTCCATGCAG TGCCTCGATA TAGCTCAAGA TCCTGCCAG AAGGACACAA TGCTTGCCAA	660
	GTTCTACCAC TTCCAGCGTT TGGCAGAGCT GTACCATGGT TACCATGCCA TCCATCGCCA	720
20	CACGGAAGAT CCGTTCAGTG TCCATCGTCC TGAAACTCTT TTCAACATCT CCAGGTTCTT	780
	GCTGCACAGC CTGCCCCAAG ACACCCCCTC GGGCATCTCT AAAGTGAAAA TACTCTTCAC	840
25	CTTGCCCAAG CAGAGCAAGG CCCTCGGTGC CTACAGGCTG GCCCGGCACG CCTATGACAA	900
	GCTGCGTGGC CTGTACATCC CTGCCAGATT CCAAAAGTCC ATTGAGCTGG GTACCCTGAC	960
	CATCCGCGCC AAGCCCTTCC ACGACAGTGA GGAGTTGGTG CCCTTGTGCT ACCGCTGCTC	1020
30	CACCAACAAC CCGCTGCTCA ACAACCTGGG CAACGTCTGC ATCAACTGCC GCCAGCCCTT	1080
	CATCTTCTCC GCCTCTTCCT ACGACGTGCT ACACCTGGTT GAGTTCTACC TGGAGGAAGG	1140
35	GATCACTGAT GAAGAAGCCA TCTCCCTCAT CGACCTGGAG GTGCTGAGAC CCAAGCGGGA	1200
	TGACAGACAG CTAGAGATTT GCAAACAACA GCTCCAGAT TCTTGCGGCT AGTGGGAGAC	1260
	CAAGGGACTC CATCGGAGAT NAGGACCCGT TCACAGCTAA GCTRAGCTTT GAGCAAGGTG	1320
40	GCTCARAGTT CGTGCCAGTG GTGGTGAGCC GGCTGGTGCT GCGCTCCATG AGCCGCCGGG	1380
	ATGTCCTCAT CAAGCGATGG CCCCCACCC TGAGGTGGCA ATACTTCCGC TCACTGCTGC	1440
45	CTGACGCCTC CATTACCATG TGCCCTCCT GCTTCCAGAT GTTCCATTCT GAGGACTATG	1500
	AGTTGCTGGT GCTTCAGCAT GGCTGCTGCC CTTACTGCCG CAGGTGCAAG GATGACCCTG	1560
	GCCCATGACC AGCATCTCTG GGACGGCCTG CACCCTCTGC CCGCCTTGGG GTCTGCTGGG	1620
50	CTGTGAAGGA GAATAAAGAG TTAACTGTC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1680
	AAAAAAAAAA AAAAAAAAAA AAANA	1705

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(2) INFORMATION FOR SEQ ID NO: 217:

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(1) SEQUENCE CHARACTERISTICS:

470

- (A) LENGTH: 999 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

AGCAAATCAC CTTAACGATC TGAATGAAA CTGTGACCAG TGCCGCCCTG GGTGGTCTG 60  
10 GAGAGACTGC CGTCTTCTTG TTTGGCCATA GGTGCTGGGG CCCCGGCTTC AGTCACTGTC 120  
TCAGACAGKA GTCCCGATAA GCAGATCACC AGTCCTCCAC TGTCTTCCT GTCCGCCTTG 180  
CTGCATGAGA AGATAGCTGC TTCCTCCCTC TTTTCTTACA CTGTAAATTA TTGTTTACA 240  
15 ATTGAGTGYC TTAATAATAG TYTACAAATA CTATGTATTT ATGCAAAACT GTTAAAGTTC 300  
TCATCTGTTA TGATTGGATA CTGGTCTTG TCAGTAGTGG TCAGCATTGG GTTGTGAGCT 360  
20 TGTCTACTC CATACGTGTT TATCCTGCTA TGCATTTTAC ATTGTGTGTT CACATCTATT 420  
CCAAGGAGCC TTGCTAGAAA CAACACTGGC GGTTCCTGCA GGCCAGGCAG GCATTGGCCC 480  
ATGCTGTGTC CCATAGGAGC CAATGGAAAG AACGTAGCTT GGTCTGCTAG CCAGCCGTGG 540  
25 GGTGGCGCAG GCCAGGCAGC CTCTGCACCA GAGTCCAGCA CCTGCCCATT CCCAGTCAC 600  
ACAATCATAC TCTTCTTTCA TAGAGATTTT ATTACCACCT AGACCACCCT AGTTTTCCTC 660  
30 TCTGTTAGTG TCCTGAGCTC TTTTGCAACA AAATGTAGGT ACAGACCAAT CCCTGTCCCT 720  
TCCCAATCA GGAGCTCCAC ACCATGAGTT GTTTGGTTT CCAGAAGCTG CCAGTGGGTT 780  
CCCGTGAATT GCGTTAAGAT ATCGATGATK TTTTATTATG TTTTCTTCT TGTMTTTTA 840  
35 AATAATATAT TTAAAGGCAG TATCTTTTGT ACTGTGAATT TGCAGTAGAA GATGCAGAAT 900  
GCACTTTTTT TTTACTTCTG TTGGTGTGTA TTGTATATAG TGTGTGTGCT TCTTGTGATG 960  
40 AAAATAAACT TTTTCTTTAT AAAAAAAAAA AAAAAAAC 999

45 (2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 941 base pairs  
(B) TYPE: nucleic acid  
50 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

55 GGCACGAGTA GCATTTTCATT TAATCTGCAG GTATATCTC CCAACAGTTT ATTGTCATGT 60  
GATGTCCTCA GCCAAGATTG TRAGGCAGAG AGGAGCTGTC CCAACCTACT ATACCACCGA 120  
60 GGCTGGAGAG ATCATATTTT TGGTATTAAA CTGGAGTCTC TCCATCCTTC ACATTGTTGA 180

TGTCCTCTGT AGCAAACCGG AAAAGTCAGT GACAGAAGAT GCCGCTAGCG GTTTGAGCCA 240  
GAGAATGACA GCTCTGGTTT GGAGAAAAGG GCCGGATGGT GGCTCTAGAA AGCCCATCCT 300  
5 TCTGCTCTTC TTTTCTCTCC CCCTTATATT GTGCTTTCAT TCATTCATTG ATTCATCAAA 360  
CATTTGTTGA GCACCTATTA TGTGTCAAGC TCTGTGCTAG CCTCTGGAAA ACCTGCCCTC 420  
ATGTAGCTCA CTGTGGAGTA GGAGAAACAA TGACTACACT ATGATAAGCA CGGGTTGTCA 480  
10 GGGTCTCACA GAGCAGTGGC CCCTCATCCA GACCGATGAG GTCAAAGAAG GCATCCAGGC 540  
GAGGATGGTG TCAGAGCTAA CTGAAGAATG AGAGGGAGCT GCACCASCAG GGGTTGGAAC 600  
15 TGAAGGTGGC AGTGCCTGGA GTCTTGATTG CAGCAGAGGG AGAGCAGTCT GTGAAAAGGC 660  
ACCAAGGGTG GGAGAGGGCA GAGCACATGG AGGAACCTCA GGTAGTCTG GATGGCCTG 720  
GGGCAAAGCT AGAGAGGTAA GAAGAATCTA CAAATGTTCC TCGAGTTACA TGAACCTCCA 780  
20 TCCCAATAAA CCCATTGGAA ACGAAAAATT TAAGTCAGAA GTGCATTAA GGCTGGTCCG 840  
AGTAGAATGA TTTTACAAC GAATTGATCA CAACCAGTTA CAGATGTCTT TGTTCCTTCT 900  
25 CCACTCCAC TGCTTCACCT GACTAGCCTT TAAAAA A 941

30 (2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 575 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

40 TAAGTGAAT CCCCGGGGT TGCAGGAAT TCGGCAGAG GCATTCTGAG AAGCTTAAGA 60  
CATACTTTGA AGACAACCT AGGGACCTCC AGCTGCTGCG GCATGACCTA CCTTGCACC 120  
CCGCAGTGGT GAAGCCCCAC CTGGGCCATG TTCCTGACTA CCTGGTTCCT CTGCTCTCC 180  
45 GTGGCCTGGT RCGCCCTCAC AAGAAGCGGA AGAAGCTGTC TTCCTCTTGT AGGAAGGCCA 240  
AGAGAGCAAA GTCCCAGAAC CCACTGCGCA GCTTCAAGCA CAAAGGAAAG AAATTCAGAC 300  
50 CCACAGCCAA GCCCTCTGA GGTGTGTTGG CCTCTCTGGA GCTGAGCACA TTGTGGAGCA 360  
CAGGCTTACA CCCTTCGTGG ACAGGCGAGG CTCTGGTGCT TACTGCACAG CCTGAACAGA 420  
CAGTTCTGGG GCCGGCAGTG CTGGGCCCTT TAGCTCCTTG GCACTTCCAA GCTGGCATCT 480  
55 TGCCCTTGA CAACAGAATA AAAATTTTAG CTGCCCCAAA AAAAAAAAAA AAAAAAAAAA 540  
CTCGAGGGGG GGCCCGTACC CAATTGCCCC TATAA 575

60

## (2) INFORMATION FOR SEQ ID NO: 220:

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## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3018 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

	GCCAGCCTTA CAGGTTTTAC GTGAAATGAA AGCCATTGGA ATAGAACCCT CGCTTGCAAC	60
15	ATATCACCAT ATTATTCGCC TGTTCGATCA ACCTGGAGAC CCTTTAAAGA GATCATCCTT	120
	CATCATTTAT GATATAATGA ATGAATTAAT GGGAAAGAGA TTTCTCCAA AGGACCCGGA	180
20	TGATGATAAG TTTTTCAGT CAGCCATGAG CATATGCTCA TCTCTCAGAG ATCTAGAACT	240
	TGCCTACCAA GTACATGGCC TTTTAAAAAC CGGAGACAAC TGGAAATTCA TTGGACCTGA	300
	TCAACATCGT AATTCTATT ATTCCAAGTT CTTGATTG ATTTGTCTAA TGAACAAAT	360
25	TGATGTTACC TTGAAGTGGT ATGAGGACCT GATACCTTCA GCCTACTTTC CCCACTCCCA	420
	AACAATGATA CATCTTCTCC AAGCATTGGA TGTGGCCAAT CGGCTAGAAG TGATTCCTAA	480
	AATTGGGAA AGATAGTAAA GAATATGGTC ATACTTTCCG CAGTGACCTG AGAGAAGAGA	540
30	TCCTGATGCT CATGGCAAGG GACAAGCACC CACCAGAGCT TCAGGTGGCA TTTGCTGACT	600
	GTGCTGCTGA TATCAAATCT GCGTATGAAA GCCAACCCAT CAGACAGACT GCTCAGGATT	660
35	GGCCAGCCAC CTCTCTCAAC TGTATAGCTA TCCTCTTTT AAGGCTGGG AGAACTCAGG	720
	AAGCCTGGAA AATGTTGGG CTTTTCAGGA AGCATAATAA GATTCCTAGA AGTGAGTTGC	780
	TGAATGAGCT TATGGACAGT GCAAAGTGT CTAACAGCCC TTCCCAGGCC ATTGAAGTAG	840
40	TAGAGCTGGC AAGTGCCTTC AGCTTACCTA TTTGTGAGG CCTCACCCAG AGAGTAATGA	900
	GTGATTTTGC AATCAACCAG GAACAAAAGG AAGCCCTAAG TAATCTAACT GCATTGACCA	960
45	GTGACAGTGA TACTGACAGC AGCAGTGACA GCGACAGTGA CACCAGTGAA GGCAAATGAA	1020
	AGTGGAGATT CAGGAGCAGC AATGGTCTCA CCATAGCTGC TGGAAATCACA CCTGAGAACT	1080
	GAGATATACC AATATTTAAC ATTGTTACAA AGAAGAAAAG ATACAGATTT GGTGAATTG	1140
50	TTACTGTGAG GTACAGTCAG TACACAGCTG ACTTATGTAG ATTTAAGCTG CTAATATGCT	1200
	ACTTAACCAT CTATTAATGC ACCATTAAAG GCTTAGCATT TAAGTAGCAA CATGCGGTT	1260
55	TTGACACACA TGGTGAGGTC CATGGCTCTT GTCATCAGGA TAAGCCTGCA CACCTAGAGT	1320
	GTCGGTGAGC TGACCTCAG ATGCTGTCTT CGTGCGATTG CCCTCTCCTG CTGCTGGACT	1380
60	TCTGCCTTTG TTGGCCTGAT GTGCTGCTGT GATGCTGGTC CTTTCATCTTA GGTGTTTCATG	1440

	CAGTTCTAAC ACAGTTGGGG TTGGGTCAAT AGTTTCCCAA TTTCAGGATA TTTCGATGTC	1500
	AGAAATAACG CATCTTAGGA ATGACTAAAC AAGATAATGG CAGTTTAGGC TGCACAACG	1560
5	GTAAAATGAC TGTAGATAAA TGTGTAAATT AGTGACACG TTTGTATTTT TGTTAATATA	1620
	GCCGCTGCCA TAGTTTCTA ACTTGAACAG CCATGAATGT TTCATGTCTC CCTTTTTTTT	1680
10	TTGTCTATAG CTGTTACCTA TTTTAGTGGT TGAAATGAGA GCTAGTGATG ACAGAAGGAT	1740
	GTGGAATGTC TTCTTGACAT CATTGTGTAT TGCTGGTAAT CAAGTTGGTA ACGACTACTT	1800
	CTAGCAGCTC TTACCACTAT GACTTAAGTG GTCCTGGAAG GCAGTAAGTG GAGGTTTGCA	1860
15	GCATTCCTGC CTTCATGAGG GCTTCTACCA CTGACCACTT TGCACGTACC TGGCTCCCAG	1920
	ATTTACTTAG GTACCCACG AGTCGTCCAC ATAAGCAGCT TCATCTTTAC CTGCCAGAG	1980
20	TTGACAATTA TGGGATACTC TAGTCTACTT ATACTTGTGT TCCCATCTGT CTGCCATCCT	2040
	CTGAAGGCCA GGACCCAGTC ATACATCCTT AGAAACCAA GTATGGTTT TGTTTTCTCT	2100
	TGGAATGTCA GGTCTTAAGG CATTTAATTG AGGGACAAA AAAAAAAAAA GCCGATATAG	2160
25	TAGCTAGCTA CTTAAGCATC CATGGGTATT GCTCCATATC AAAGCAGATT TGCAGGACAG	2220
	AAAGAGTAA TTAGCCTTCA GTCTTGGTTT ACAGCTTCCA AGGAGAGCCT TGGSCACCTG	2280
30	AAATGTTAAC TCGGTCCCTT CCTGTCTCTA GTTCATCAGC ACCTGCAGAT GCCTGACTCT	2340
	TGTTAGCCTT ACTATTCAAT ACAGTCCTTA GATTACGGT ATGCCTCTTC CTATCCAGGC	2400
	ACCTATCTCTG AATCACCATG TTGCTCTGCA GCTAGAGTTG ATAGGAGAAA ATCCATTTGG	2460
35	GTAGATGGCC TATGAATTTG TAGTAGACTT TCAAATGAG TGATTGTGTA GCTTGGTACT	2520
	TTTAAGTTTG TGGTACAGAT CCTQCAAACC CATACTCTGA GCAATTAAC GCCTTGAACA	2580
40	TAGAGAAAAA TTAAGGCCTC ACAGGATGAG TCTCCATTCT CTGTAAATGC TTATTTTATC	2640
	ATAGTCTTTA GCCTCTAACT ATGAGTAAAA TGTCTCTTC GGCCGGGTGT GGTGACTCAC	2700
	ACCTGTAACC TCAGCACTTT GGGAGGCAGA GGTGGGAGGA TCACCTAGGT CCAGGAGTTC	2760
45	GAGACTAGCC TGGGCAACAT AGTGAGACAC CGGATCTACA AAAAAATAA AAGCCAGACT	2820
	GGTGGTATGT ATCTGTGTCC CAGCTAATTG GGAGGGTGAG ATGGGAGGAT TGTTTGAGCC	2880
50	TAGGAGAGGG AGGTTGCAGT GAGCCGTGAT CGCACCCTG CACTCCAGCC TGGGCAACAG	2940
	AGCAAGACCC TGTCTTGAG AAACCAGAAT TTTGGAAGAG CAAATGGGGC TGAGTGCAGT	3000
	GGCTCATGCC TGTAAATCC	3018
55		

(2) INFORMATION FOR SEQ ID NO: 221:

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 968 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

GGCACGAGGG CCGCGGGACA TCCACGGGGC GCGAGTGACA CGCGGGAGGG AGAGCAGTGT 60  
10 TCTGCTGGAG CCGATGCCAA AAACCATGCA TTTCTTATTC AGATTCAATG TTTTCTTTTA 120  
TCTGTGGGGC CTTTFTACTG CTCAGAGACA AAAGAAAGAG GAGAGCACCG AAGAAGTGAA 180  
AATAGAAGTT TTGCATCGTC CAGAAAAC TG CTCTAAGACA AGCAAGAAGG GAGACCTACT 240  
15 NAAATGCCCA TTATGACGGC TACCTGGCTA AAGACGGCTC GAAATTCTAC TGCAGCCGGA 300  
CACAAAATGA AGGCCACCCC AAATGGTTTG TTCTTGGTGT TGGGCAAGTC ATAAAAGGCC 360  
20 TAGACATTGC TATGACAGAT ATGTGCCCTG GAGAAAAGCG AAAAGTAGTT ATACCCCTT 420  
CATTTGCATA CGGAAAGGAA GGCTATGCAG AAGGCAAGAT TCCACCGGAT GCTACATTGA 480  
TTTTTGAGAT TGAAC TTTAT GCTGTGACCA AAGGACCACG GAGCATTGAG ACATTTAAAC 540  
25 AAATAGACAT GGACAATGAC AGGCAGCTCT CTAAAGCCGA GATAAACCTC TACTTGCAAA 600  
GGGAATTTGA AAAAGATGAG AAGCCACGTG ACAAGTCATA TCAGGATGCA GTTTTAGAAG 660  
30 ATATTTTAA GAAGAATGAC CATGATGGTG ATGGCTTCAT TTCTCCAAG GAATACAATG 720  
TATACCAACA CGATGAAC TA GCATATTT GTATTTCTAC TTTT TTTT TAGCTATTTA 780  
CTGTACTTTA TGTATWAAAC AAAGTCMCTT TTCTCCMAGT TGKATTTGCT ATTTT TCCCC 840  
35 TATGAGAAGA TATTTTGATC TCCCAATAC ATTGATTTTG GTATAATAAA TGTGAGGCTG 900  
TTTTGCAAAC TTA AAAAAA ATTTAAAAA ACTGGAGGGG GGCCCGTACC CAANTCGCCG 960  
40 NATATGAT 968

45 (2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

55 CGTTTCCGG CCGTGCGTTT GTGGCGTCC GGCTCCCTG ACATGCAGCC CTCTGGACCC 60  
CGAGGTTGGA CCTACTGTG ACACACCTAC CATGCGGACA CTCTTCAACC TCCTCTGGCT 120  
TGCCCTGGCC TGCAGCCCTG TTCACACTAC CCTGTCAAAG TCAGATGCCA AAAAAGCCGC 180  
60



	CTCAAAGACG CTGCTGGAGA AGAGTCAGTT TTCAGATAAG CCGGTGCAAG ACCGGGGTTT	240
	GGTGGTGACG GACCTCAAAG CTGAGAGTGT GGTCTTGAG CATCGCAGCT ACTGCTCGGC	300
5	AAAGGCCCGG GACAGACACT TTGCTGGGGA TGTACTGGGC TATGTCACCTC CATGGAACAG	360
	CCATGGCTAC GATGTCACCA AGGTCTTTGG GAGCAAGTTC ACACAGATCT CACCCGTCTG	420
10	GCTGCAGCTG AAGAGACGTG GCCGTGAGAT GTTTGAGGTC ACGGGCCTCC ACGACGTGGA	480
	CCAAGGGTGG ATGCGAGCTG TCAGGAAGCA TGCCAAGGGC CTGCACATAG TGCCTCGGCT	540
	CCTGTTTGAG GACTGGACTT ACGATGATTT CCGGAACGTC TTAGACAGTG AGGATGAGAT	600
15	AGAGGAGCTG AGCAAGACCG TGGTCCAGGT GGCAAAGAAC CAGCATTTCTG ATGGCTTCGT	660
	GGTGGAGGTC TGAACACAGC TGCTAAGCCA GAAGCGCGTG GGCCTCATCC ACATGCTCAC	720
20	CCACTTGCC GAGGCTCTGC ACCAGGCCCG GCTGCTGGCC CTCCTGGTCA TCCCGCTGTC	780
	CATCACCCCC GGGACCGACC AGCTGGGCAT GTTCACGCAC AAGGAGTTTG AGCAGCTGGC	840
	CCCCGTGCTG GATGGTTTCA GCCTCATGAC CTACGACTAC TCTACAGCGC ATCAGCCTGG	900
25	CCCTAATGCA CCCCTGTCCT GGGTTCGAGC CTGCGTCCAG GTCCTGGACC CGAAGTCCAA	960
	GTGGCGAAGC AAAATCCTCC TGGGGCTCAA CTTCATGGT ATGGACTACG CGACCTCCAA	1020
30	GGATGCCCGT GAGCCTGTTG TCGGGGCCAG GTACATCCAG AACTGAAGG ACCACAGGCC	1080
	CCGGATGGTG TGGACAGCC AGGYCTCAGA GCACTTCTTC GAGTACAAGA AGAGCCGCAG	1140
	TGGGAGGCAC GTCGTCTTCT ACCCAACCCT GAAGTCCCTG CAGGTGCGGC TGGAGCTGGC	1200
35	CCGGGAGCTG GCGTGTGGG TCTCTATCTG GGAGCTGGCC AGGGCCTGGA CTACTTCTAC	1260
	GACCTGCTCT AGGTGGGCAT TGCGCCCTCC GCGGTGGACG TGTCTTTTC TAAGCCATGG	1320
40	AGTGAGTGAG CAGGTGTGAA ATACAGGCCT NCACTCCGTT TGCTGTGAAA AAAAAAAAAA	1380
	AAAAAAAAAA AAAAAAAAAA AAAA	1404

45

(2) INFORMATION FOR SEQ ID NO: 223:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

60

NGCGCGCTG CAGTCGACAC TAGTGGATCC AAAGAATTCG GCACGAGGGC AGGTCCAGGG	60
CTCAGAAATC AGCTCTATTG ACGAATTCTG CCGCAAGTTC CGCCTGGAAT GCCCGCTGGC	120
CATGGAGCGG ATCAAGGAGG ACCGGCCCAT CACCATCAAG GACGACAAGG GCAACCTCAA	180

5 CCGCTGCATC GCAGACGTGG TCTGCTCTTT CATCACGGTC ATGGACAGGC TGGGCTTGA 240  
 GATCCGCGCC ATGGATGAGA TCCAGCCCGA COTGCGAGAG CTGATGAGA CCAAGCACCG 300  
 CATGAGCCAC CTCCACCCG ACTTTGAGGG CCGCCAGACG GTCAGCCAT GGTGACAGAC 360  
 CCTGAGCGGC ATGTGCGCGT CAGTGAAGT GGCAGACTCA CAGGTGCTC AGATGCTGTT 420  
 10 CGACCTGGAG TCAGCCTACA ACGCCTTCA CCGCTTCTG CATGCTGAG CCGGGGGCAC 480  
 TAGCCCTTGC ACAGAAGGGC AGAGTCTGAG GCGATGGCTC CTGTTCCCTT GTCCGCCACA 540  
 CAGGCCGTGG TCATCCACAC AACTCACTGT CTGCAGTGC CTGTCTGGT TCTGCTTTG 600  
 15 GTGTGAGAAC TTTTGGGCCG GGGCCCTCC CACAATAAAG ATGCTCTCG ACCTCAAAA 660  
 AAAAAAAAAA AAAAAGTCRG GGGGGGCCG GTCCCATCC CCCCCTT 707

## (2) INFORMATION FOR SEQ ID NO: 224:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GGGGAAGTGC AGTGACAGCA GGAGTAAGAG TGGAGGAGC GACAGAGTG GGACACAGGT 60  
 35 ATGGAGAGGG GGTTCAGCGA GCCTAGAGAG GGCAGACTAT CAGGTGCTG CCGGTGAGAA 120  
 TCCAGGGAGA GGAGCGGAAA CAGAGAGGG GCAGAGAGC GGGGCTTTG TGGGTTCAG 180  
 AGCCCTCAG CCATGTGGG AGCCAAGCCA CATTGGCTAC CAGGTCTCTT ACAGAGTCCC 240  
 40 GGGCTGCCCT TGGTCTGCTT GCTTCTGGCC CTGGGGGCCG GGTGGGGTCA GGAGGGGTCA 300  
 GAGCCCGTCC TGCTGGAGGG GGAGTGCCTG GTGTCTGTG AGCCTGCTCG AGCTGCTGCA 360  
 45 GGGGGGGCCG GGGGAGCAGC CTTGGGAGAG GCACCCCTG GCGAGTGGC ATTGCTGCG 420  
 GTCCGAAGCC AACACCATGA GCCAGCAGGG GAAACCGCA ATGGCATTA TGGGGCCATC 480  
 TACTTCGACC AGGTCTCGGT GAACGAGGGC GGTGGCTTTG ACCGGGCTC TGGCTCCTTC 540  
 50 GTAGCCCTG TCCGGGTGT CTACAGCTTC CGGTTCATG TGGTGAAGT GTACAACCGC 600  
 CAAACTGTCC AGGTGAGCCT GATGCTGAAC ACGTGGCCTG TCATCTCAGC CTTTGCCAAT 660  
 55 GATCCTGACG TGACCCGGGA GGCAGCCACC AGCTCTGTC TACTGCTTT GGACCTGGG 720  
 GACCGAGTGT CTCTGCGCT GCGTCGGGG AATCTACTGG GTGGTGGAA AATCTCAAGT 780  
 60 TTCTCTGGCT TCCTCATCTT CCTCTCTGA GGACCCAAGT YTTTCAGCA CAGAATCCA 840

	GCCCCTGACA ACTTTCTTCT GCCCTCTCTT GCCCCAGAAA CAGCAGAGGC AGGAGAGAGA	900
	CTCCCTCTGG YTCCTATCCC ACYTCTTTGC ATGGGAMCCT GTGCCAAACA CCCAAGTTTA	960
5	AGARAARARY ARARCTGWGG CAGGTATACA GAGCTGGAAG TGGACCATGG AAAACATSGA	1020
	TAACCATGCA TCYTCTTGCT TGGCCACCTC CTGAAACTGT CCACCTTTGA AGTTTGAACT	1080
10	TTAGTCCCTC CAMACTCTGA CTGCTGCCTC CTTCTCTCCA GCTCTCTCAC TGAGTTATYT	1140
	TCACTGTACC TGTTCAGCA TATCCCACT ATCTCTCTTT CTCCTGATCT GTGCTGTCTT	1200
	ATTCTCTCC TTAGGCTTCC TATTACCTGG GATTCCATGA TTCATTCTT CAGACCCTCT	1260
15	CCTGCCAGTA TGCTAAACCC TCCCTCTCTC TTTCTTATCC CGCTGTCCA TTGGCCCAGC	1320
	CTGGATGAAT CTATCAATAA AACAACTAGA GAATGGTGGT CAAAAAAAAA AAAAAAAAAAC	1380
20	TCGA	1384

25 (2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 760 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

35	GGGTGACCC ACGCGTCGC TGACCAGTCC GTTATAGATA CTTCTTCTTA TACCAAAACT	60
	GTTTAAACAG GTGCCACCAC AAGGGATGTC GTCCTTACTC TCTGCGGGTC TTCAAGCATC	120
	CCTTTGTGGG AAARGTCTCT GGGCAAGCAC GTGGTATTG GTCTGCTGCT TGCTTCCCTT	180
40	TTCCACCAG GGATGTTGTG ATCATAAGTC AAAACAACAG TATATTCCAA ATCTCAAAG	240
	CTATTGTGGC CTGAGCACAA TTGAAATCTA GCAGAGTTTT TCCTATGTAG CTTTAGAGTA	300
45	ACTCTTCTGC TTCTCTGTCA CTTACAATTC AGGTTCTGCC TTGCGCTAAG AGCATGAGCA	360
	GAAGAGTCCT CATGTGACGC TTAGTTCTAT TGCAGTCCTG GGTGAAACTA TTTAAGCWAT	420
	GGGGCTGCTK CTCCCANWT CCTCCCTAAC AATTCGTTGT GTGGACTTCT CATCTAAAAG	480
50	GTTAGTGGCT TTTGCTTGGG ATCAGTGCTC TCTATTGATG TTCTTGCTGG TCTCCAGACA	540
	CATTCCTGTT GCATTAAGAC TTGAAAGACT TGTAGATGTG TGATGTTTCT GCACAGGATG	600
55	CTGAAAGCTA TGTTACTATT CTTAGTTTGT AAATTGTCCT TTTGATACCA TCATCTTGTT	660
	TTCTTTTGT AGGTATAAAT AAAAACAACG TTGACAATAA AAAAAAAAAA AAAAAAAAAA	720
60	AAAAAAAAA AAAAAAAAAA NAAAAAAAAA AAAAAAAAAA	760

## (2) INFORMATION FOR SEQ ID NO: 226:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2057 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

CCGAGCCGGC	TGCGCCGGGG	GAATCCGTGC	GGGCGCCTTC	CGTCCCRGTC	CCATCCTCGC	60
CGCGCTCCAG	CACCTCTGAA	GTTTTGCAGC	GCCCAGAAAG	GAGGCGAGGA	AGGAGGGAGT	120
GTGTGAGAGG	AGGGAGCAAA	AAGCTCACCC	TAAAACATTT	ATTTCAAGGA	GAAAAGAAAA	180
AGGGGGGGCG	CAAAAATGGC	TGGGGCAATT	ATAGAAAACA	TGAGCACCAA	GAAGCTGTGC	240
ATTGTTGGTG	GGATTCTGCT	CGTGTTCCAA	ATCATCGCCT	TTCTGGTGGG	AGGCTTGATT	300
GCTCCAGGGC	CCACAACGGC	AGTGTCTTAC	ATGTGGTGA	AATGTGTGGA	TGCCCCTAAG	360
AACCATCACA	AGACAAAATG	GTTCTGTCCT	TGGGGACCCA	ATCATTGTGA	CAAGATCCGA	420
GACATTGAAG	AGGCAATTCC	AAGGGAAATT	GAAGCCAATG	ACATCGTGTT	TTCTGTTTAC	480
ATTCCCTTCC	CCCACATGGA	GATGAGTCCT	TGGTTCCAAT	TCATGMTGTT	TATCCTGCAG	540
CTGGACATTG	CCTTCAAGCT	AAACAACCAA	ATCAGRGAAA	ATGCAGAAGT	CTCCATGGAC	600
GTTTCCCTGG	CTTACCGTGA	TGACGCGTTT	GCTGAGTGA	CTGAAATGGC	CCATGAAAGA	660
GTACCACGGA	AACTCAAATG	CACCTTCACA	TCTCCAAGA	CTCCAGAGCA	TGGAGGGCCG	720
GTTACTATGA	ATGTGATGTC	CTTCTTTTCA	TGGAAATTGG	GTCTGTGGCC	CATGAAGTTT	780
TACCTTTTAA	ACATCCGGCT	GCCTGTGAAT	GAGAAGAAGA	AAATCAATGT	GGGAATTGGG	840
GAGATAAAGG	ATATCCGGTT	GGTGGGGATC	CACCAAAATG	GAGGCTTCAC	CAAGGTGTGG	900
TTTGCCATGA	AGACCTTCCT	TACGCCAGC	ATCTTCATCA	TTATGGTGTG	GTATTGGAGG	960
AGGATCACCA	TGATGTCCCG	ACCCCCAGTG	CTTCTGGAAA	AAGTCATCTT	TGCCCTTGGG	1020
ATTTCATGA	CCTTTATCAA	TATCCAGTG	GAATGGTTT	CCATCGGGTT	TGACTGGACC	1080
TGGATGCTGC	TGTTTGGTGA	CATCCGACAG	GCATCTTCTA	TGCRATGCTT	CTKTCCTTCT	1140
GGATCATCTT	CTGTGGCGAG	CACATGATGG	ATCAGCACGA	GCGGAACCAC	ATCGCAGGGT	1200
ATTGGAAGCA	AGTCGGACCC	ATTGCCGTTG	GTCTTCTGTC	CTCTTCATAT	TTGACATGTG	1260
TGAGAGAGGG	GTACAACTCA	CGAATCCCTT	CTACAGTATC	TGGACTACAG	ACATTGGGAA	1320
CAGAGCTGGC	CATGGCTTTC	ATCATCGTGG	CTGGAATCTG	CCTCTGCCTC	TAACCTCCTG	1380
TTTCTATGCT	TCATGGTATT	TCAGGTGTTT	CGGAACATCA	GTGGGAAGCA	GTCCAGCCTG	1440

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CCAGCTATGA GCAAAATCCG GCGGCTACAC TATGAGGGGC TAATTTTTAG GTTCAAGTTC 1500  
 CTCATGCTTA TCACCTTGGC CTGCGGTGGC ATGACTGTCA TCTTCTTCAT CGTTAGTCAG 1560  
 5 GTAAAGGAAG GCGATTGGGA AATGGGGCGG CGTCACATC CCAAGTGAAC AGTGCCTTTT 1620  
 TCACAGGCAT CTAAGGGATG TGGAAATCTG ATGCTTTTGC TCTGATGTC TTGTATGCAC 1680  
 CATCCCATTA AACTATGGA GAGACCACT CCAATGGAAT GCAACTCCCA TGTAAATCGA 1740  
 10 GGGAGGATG TGTCTGTCTT GTTTCGGGAC TTATCAAGA ATTGTTTCAGC GCTTCGAAAT 1800  
 ATTCTTCAT CAATGACAC GAGCTTCTG GTATTGAGT CAACAAGGCA ACACATGTTT 1860  
 15 ATCAGCTTTC CATTTGCACT TCTCAGATC ACATTGATTG TACTTGATA CGCACACAAA 1920  
 TACACTCAT TACCTTTAT CTCAAAATG TAATATTAAG GAAAAAGCG TCAACAATAA 1980  
 ATATTCTTTC AGTATTGTCT TACTTCTCTT AAAAAAAA AAAAAAATC GTGCCGAATT 2040  
 20 CGGCACGAGC GGCACGA 2057

25

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2084 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(ii) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

35

GGCAGAGGGC CATTCCTGTC AAAGAGCCAA ACCCCGATTC CTCTGTGCCC CTCCTCTCCC 60  
 ACCAAGTGCT TTATAAAAT AGCTCTTGT ACCCGAATA ACTGTTCAAT TTCTACTCCT 120  
 40 CCTCTTAGG TCACACTTTT CAGAAAAA ATCTGCATCC TGGAAACCAG AAGAAAAATA 180  
 TGAGACGGGG AATCATCTG TATGTGTGT SCTGCCCTTG GCTGAGTGTG TGGAGTCCTG 240  
 CTCAGGTGTT AGGTACAGTG TGTGTGATCG TGGTGGCTTG AGGGGAACCG CTTGTTTACA 300  
 45 GCTGTGACTG CCGCTGCACT GCAGAGAAAC TGCCCTTGGC TGCTCGTAGC GCCGGGCCTT 360  
 CTCTCTCTGT CATCATCCAG AAGAGCCACT GTCCGGGAGG CAGAAGGTAC CGGGGCAGCT 420  
 50 ACTGGAGGAC TGTGCGGGCC TCCCTGGGCT GCGCCCTCCG CCGTGGGGCC CTGTTGCTGC 480  
 TGTCCATCTA TTTCTACTAC TCCCTCCCAA ATGCGGTCCG CCGGCCCTTC ACTTGATGC 540  
 TTGCCCTCCT GGGCCTTCTC GCAGGCACTG AACATCCTCC TGGGCCTCAA GGGCCTGGCC 600  
 55 CCAGCTGAGA TCTCTGCACT GTGTGAATAA GGAATTTC ACGTGGCCCA TGGGCTGGCA 660  
 TGGTCATATT ACATCGAATA TGTGCGGCTG ATCTTGCCAG AGCTCCAGGC CCGGATTCTA 720  
 60 ACTTACAATC AGCATTACAA CAACCTGCTA CGGGGTGCAG TGAGCCAGCG GTGTNATATT 780

CTCCTCCCAT TGGACTGTGG GGTGCCTGAT AACCTGAGTA TGGCTGACCC CAACATTGCG 840  
TTCCTGGATA AACTGCCCCA GCAGACCGGT GACCGTGCTG GCATCAAGGA TCGGGTTTAC 900  
5 AGCAACAGCA TCTATGAGCT TCTGGAGAAC GGGCAGCGGG CGGGCACCTG TGTCTTGAG 960  
TACGCCACCC CCTTGCAGAC TTTGTTTGCC ATGTCACAAT ACAGTCAAGC TGGCTTTAGC 1020  
10 GGGGAGGATA GGCTTGAGCA GGCCAAATC TTCTGCCGA CACTTGAGGA CATCCTGGCA 1080  
GATGCCCCTG AGTCTCAGAA CAACTGCCGC CTCATTGCCCT ACCAGGAACC TGCAGATGAC 1140  
AGCAGCTTCT CGCTGTCCCA GGAGGTTCTC CGGCACCTGC GGCAGGAGGA AAAGGAAGAG 1200  
15 GTTACTGTGG GCAGCTTGAA GACCTCAGCG GTGCCAGTA CCTCCACGAT GTCCCAAGAG 1260  
CCTGAGCTCC TCATCAGTGG AATGGAAGA CCCCTCCCTC TCCGCACGGA TTTCTCTTGA 1320  
20 GACCCAGGGT CACCAGGCCA GAGCCTCCAG TGGTCTCCA GCCTCTGGAC TGGGGGCTCT 1380  
CTTCAGTGGC TGAATGTCCA GCAGAGCTAT TTCCTTCCAC AGGGGGCCTT GCAGGAAGG 1440  
GTCCAGGACT TGACATCTTA AGATGCGTCT TGTCCCCTTG GGCCAGTCAT TTCCCCTCTC 1500  
25 TGAGCCTCGG TGTCTTCAAC CTGTGAAATG GGATCATAAT CACTGCCTTA CCTCCCTCAC 1560  
GGTTGTGTG AGGACTGAGT GTGTGGAAGT TTTTCATAAA CTTTGATGC TAGTGACTT 1620  
30 AGGGGTGTG CCAGGTGTCT TTCATGGGGC CTTCAGACC CACTCCCCAC CTTCTCCCC 1680  
TTCCTTTGCC CGGGGACGCC GAACTCTCTC AATGGTATCA ACAGGCTCCT TCGCCCTCTG 1740  
GCTCCTGGTC ATGTTCCATT ATTGGGGAGC CCCAGCAGAA GAATGGAGAG GAGGAGGAG 1800  
35 CTGAGTTTGG GGTATTGAAT CCCCCGGCTC CCACCCTGCA GCATCAAGGT TGCTATGGAC 1860  
TCTCCTGCCG GGCAACTCTT GCGTAATCAT GACTATCTCT AGGATCTTGG CACCACTTCC 1920  
40 TTCCCTGGCC CCTTAAGCCT AGCTGTGTAT CGGCACCCCC ACCCCACTAG AGTACTCCCT 1980  
CTCACTTGGC GTTTCCTTAT ACTCCACCCC TTCTCAACG GTCCTTTTTT AAAGCACATC 2040  
45 TCAGATTAAA AAAAAAAAAA AAAAAAAAAA AGGGGGGCN GCNT 2084

50 (2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2143 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

60 TCGACCCACG CGTCCGGTTG AATTCCTTGA CTGCAAACA CATATTTATT AGCCTGACTC 60

	AAACAATGAA GCTATTAAAA CTTCGGAGGA ACATTGTAAA ACTCTCTTTG TATCGGCATT	120
	TCACCAACAC GCTTATTTTG GCAGTGGCAG CATCCATTGT GTTTATCATC TGGACAACCA	180
5	TGAAGTTCAG AATAGTGACA TGTCAGTCGG ACTGGCGGGA GCTGTGGGTA GACGATGCCA	240
	TCTGGCGCTT GCTGTTCTCC ATGATCCTCT TTGTCATCAT GGTTCCTCTG CGACCATCTG	300
10	CAAACAACCA GAGGTTTGCC TTTTCACCAT TGTCTGAGGA AGAGGAGGAG GATGAACAAA	360
	AGGAGCCTAT GCTGAAAGAA AGCTTTGAAG GAATGAAAAT GAGAAGTACC AAACAAGAAC	420
	CCAATGGAAA TAGTAAAGTT AACAAAGCAC AGGAAGATGA TTTGAAGTGG GTAGAAGAGA	480
15	ATGTTCTTTC TTCTGTGACA GATGTAGCAC TTCCAGCCCT TCTGGATTCA GATGAGGAAC	540
	GAATGATCAC ACACTTTGAA AGGTCCAAAA TGGAGTAAGG AATGGGAAGA TTTGCAGTTA	600
20	AAGATGGCTA CCATCAGGGA AGAGATCAGC ATCTGTGTCA GTCTTCTGTA CGGCTCCATG	660
	GGATTAAAGG AAGCAATGAC ATCCTGATCT GTTCCTTGAT CTTTGGGCAT TGGAGTTGGC	720
	GAGAGGTGTC AGAACAAAGA GAACATCTTA CTGAAAACAA GTTCATAAGA TGAGAAAAAT	780
25	CTACGAGCTT CTTATTTACA ACACTGCTGC CCCCTTTCCT CCCAGACTCT GACATGGATG	840
	TTCATGCAAC TTAAGTGTGT TGTTCCTGAA CTTTCTGTAA TGTTTCATTT TTTAAATCTG	900
30	ACAAACTAAA AAGTTTAAAG TCTTCTAAAA GATTGTCAATC AACACCATAA TATGTAATCT	960
	CCAGGAGCAA CTGCCTGTAA TTTTATTTTA TTTAGGGAGT TACATAGGTG ATGGGGGAAA	1020
	TTGTTAACTA CCTTTCATTT TCCTGGGAAG TCAAGGTTAC ATCTTGCAGA GGTGTGTTTG	1080
35	AGAAAAAAGG GCCCTTCTGA GTTAAGGAGC CATAGTTCTA TCAATGATCA AAAGAAAAAA	1140
	AAAAAAAAGA GAAACTGTTA CAGTATGATT CAGATCATT TAAAAAGCAA AATCAAGTGC	1200
40	AATTTTGT TT ACAATGGTG TATATTAAAG ATTTTCTAT TTCAGATGTA CTTTAAAGAG	1260
	AAATATTAGC TTAACCTTTT TGACATCTGC TATTGTGACA CATCCCATTG CTGGCAATGT	1320
	GGTGACACT CCGAAACTTT TAACTACTGT TTTGTAAGCC TCCAAGGGTG GCATTGCAGG	1380
45	GTCCCTTAGGC AATGTTTTGT TTGCCCTTAT GCAGAGAGGT GCTCCAAGTG CTGTGATTGA	1440
	GCACCGTGCT AGAGGAACTG TAATGCTTCA GAAGTTGTAG CTTATACAAA GGAAACAGGT	1500
50	CCTGCTGGCT TAATTTAAAC AGTTATTGCA TGAAGTAGCG TGGAGGCCCT GGACTGCTGC	1560
	TCGTCTTTTA GGATGGACTG TTCTGGTATC TGGTATTGGT TTAGAGACTG TTAATAAGGG	1620
	ACATCACAAG GTGATGGGAT TCATTTGAAG CACTCTATTT CTGTTTTAAT GGTTTTATCC	1680
55	AATTTTGCCT TCCCAAGATT TTGTTCTAC ATAAAAAGTT CATGCCACTT TTTAATATAA	1740
	AAAAATTTAA CAAAATTAAT GTATTTTCT CATTTTTC TAAAGACTCT	1800
60	TTCTGTCAAA CTCATGAAAA ATTCTTTCT ATGGCTTTTA TTCTAGATTG TCTTATTTTC	1860

TGTAAAACC AATGACCACA TGACCACAAT CTTCACTAAC TCATACTGCA GTGAAAGTGT 1920  
 TAACCCTTAG GTAGTTTCTC TACAACCTCT TGCTATGGTG ATTTTAAAA AAGTTTCCTA 1980  
 5 GGGAAAGTATC TCTGAGGGAA CAGGCAATCT GAAGGAACTG ACTATATTCT CCATGGCTAA 2040  
 GTCCATTAGG CCAAAAGNCT GGGTGGGTAT TGGTTGTCAN GCTGTCTATT GGCATATTAA 2100  
 AAACGTAGGC CGGANGGAAT AATTAGGTTG TNATGCCGGC GGG 2143  
 10

(2) INFORMATION FOR SEQ ID NO: 229:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1025 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

20

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

CCTGGCCAC ATTGCTTCAT TGGCCTGGCC ATGCGCCTGT ACTATGGCAG CCGCTAGTCC 60  
 25 CTGACAACTT CCACCCTGAT TCCGGACCCT GTAGATTGGG CGCCACCACC AGATCCCCCT 120  
 CCCAGGCTT CCTCCCTCTC CCATCAGCAG CCCTGTAACA AGTGCCTTGT GAGAAAAGCT 180  
 30 GGAGAAGTGA GGGCAGCCAG GTTATTCTCT GGAGGTTGGT GGATGAAGGG GTACCCTAGG 240  
 AGATGTGAAG TGTGGGTTTG GTTAAGGAAA TGCTTACCAT CCCCCACCC CAACCAAGTT 300  
 CTTCCAGACT AAAGAATTAA GGTAACATCA ATACCTAGGC CTGAGAAATA ACCCCATCCT 360  
 35 TGTGCGCAG CTCCCTGCTT TGTCCTGCAT GAACAGAGTT GATGAAAGTG GGGTGTGGGC 420  
 AACAAGTGGC TTTCTTGCC TACTTTAGTC ACCCAGCAGA GCCACTGGAG CTGGCTAGTC 480  
 40 CAGCCAGCC ATGGTGCATG ACTCTTCCAT AAGGGATCCT CACCCTTCCA CTTTCATGCA 540  
 AGAAGGCCCA GTTGCCACAG ATTATACAAC CATTACCCAA ACCACTCTGA CAGTCTCCTC 600  
 CAGTCCAGC AATGCCTAGA GACATGCTCC CTGCCCTCTC CACAGTCTG CTCCCCACAC 660  
 45 CTAGCCTTTG TTCTGGAAAC CCCAGAGAGG GCTGGGCTG ACTCATCTCA GGAATGTAG 720  
 CCCCTGGGCC CTGGCTTAAG CCGACACTCC TGACCTCTCT GTTCACCCTG AGGGCTGTCT 780  
 50 TGAAGCCCGC TACCCACTCT GAGGCTCCTA GGAGGTACCA TGCTTCCAC TCTGGGCGCT 840  
 GCCCTGCGCT AGCAGTCTCC CAGCTCCCAA CAGCCTGGGG AAGCTCTGCA CAGAGTGACC 900  
 TGAGACCAGG TACAGGAAAC CTGTAGCTCA ATCAGTGTCT CTTAACTGC ATAAGCAATA 960  
 55 AGATCTTAAT AAAGTCTTCT AGGCTGTAGG GTGGTTCTTA CAACCACAGC CAAAAAATA 1020  
 AAAAA 1025

60



## (2) INFORMATION FOR SEQ ID NO: 230:

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## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1250 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

5 G C C C A C G C G T C C G C C C A C G C G T C C G G C G G T G C G G A G T A T G G G C G C T G A T G G C C A T G G A G 60

15 G G C T A C T G G C G C T T C C T G G C G C Y G C T G G G G T C G G C A C T G C T C G T C G G C T T C C T G T C G G T G 120

A T S T T C G C C C T C G T C T G G G T C C T C C A C T A C C G A G A G G G C T T G G C T G G G A T G G G A G C G C A 180

C T A G A G T T T A A C T G G C A C C C A G T G C T S A T G G T C A C C G G C T T C G T C T T C A T C C A G G G C A T C 240

20 G C A T C A T C G T C T A C A G A C T G C C G T G G A C C T G G A A A T G C A G C A A G C T C C T G A T G A A A T C C A 300

T C C A T G C A G G G T T A A A T G C A G T T G C T G C C A T T C T T G C A A T T A T C T C T G T G T G G G C G T G T 360

25 T T G A G A C C A C A A T G T T A A C A A T A T A G C C A A T A T G T A C A G T C T G C A C A G C T G G G T T G G A C 420

T G A T A G C T G T C A T A T G C T A T T G T T A C A G C T T C T T T C A G G T T T T T C A G T C T T C T G C T T C 480

C A T G G G C T C C G C T T T C T C T C G A G C A T T T C T C A T G C C C A T A C A T G T T T A T T C T G G A A T T G 540

30 T C A T C T T T G G A A C A G T G A T T G C A A C A G C A C T T A T G G G G A T T G A C A G A G A A A C T G A T T T T T T 600

C C C T G A G A G A T C C T G C A T A C A G T A C A T T C C C G C C A G A A G G T G T T T T C G T A A A T A C G C T T G 660

35 G C C T T C T G A T C C T G G T G T T C G G G C C C T C A T T T T T G G A T A G T C A C C A G A C C G C A A T G G A 720

A A C G T C C T A A G G A G C C A A A T T C T A C C A T T C T T C A T C C A A A T G G A G G C A C T G A A C A G G G A G 780

C A A G A G G T T C A T G C C A G C C T A C T C T G G C A A C A A C A T G G A C A A T C A G A T T C A G A G T T A A 840

40 A C A R T G A A G T A G C A G C A A G G A A A A G A A A C T A G C T C T G G A T G A G G C T G G G C A G A G A T C T A 900

C C A T G T A A A A T G T T G T A G A G A T A G A G C C A T A T A A C G T C A C G T T C A A A A C A G C T C T A C A 960

45 G T T T G C T T C T C T A T T A G C C A T A T G A T A A T T G G C T A T G T A G T A T C A A T A T T A C T T T A 1020

A T C A C A A A G G A T G G T T T C T T G A A A T A A T T T G A T T G A T T G A G G C C T A T G A A C T G A C C T G A 1080

50 A T T G G A A A G G A T G T G A T T A A T A T A A A T A A T A G C A G A T A T A A A T T G T G G T T A T G T T A C C T T 1140

T A T C T T G T T G A G G A C C A C A A C A T T A G C A C G G T G C C T T G T G C A K A A T A G A T A C T C A A T A T G 1200

T G A A T A T G T G T C T A C T A G T A G T A A T T G G A T A A A C T G G C A G C A T C C C T G A 1250

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## (2) INFORMATION FOR SEQ ID NO: 231:

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## (i) SEQUENCE CHARACTERISTICS:

484

(A) LENGTH: 1811 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

	CNGNCAGTAC CGGTCNGATT CCCGGGTCGA CCCACGCGTC CGCTGCATTC CAGGGCCTTT	60
10	CAGTGGCTTT CATCTGAAG TTCCTGGATA ACATGTTCCA TGTCTTGATG GCCCAGGTTA	120
	CCASTGTCAT TATCACAACA GTGTCTGTCC TGGTCTTTGA CTTCAGGCCC TCCCTGGAAT	180
	TTTTCTTGA AGCCSCATCA GTCSTYCTCT CTATATTTAT TTATAATGCC AGCAAGCCTC	240
15	AAGTCCGGA ATACGCACCT AGGCAAGAAA GGATCCGAGA TCTAAGTGGC AATCTTTGGG	300
	AGCGTCCAG TGGGGATGGA GAAGAACTAG AAAGACTTAC CAAACCCAAG AGTGATGAGT	360
20	CAGATGAAGA TACTTTCTAA CTGGTACCCA CATAGTTTGC AGCTCTCTTG AACCTTATTT	420
	TCACATTTTC AGTGTTTGTA ATATTTATCT TTTCACTTTG ATAAACCAGA AATGTTTCTA	480
	AATCCTAATA TTCTTTGCAT ATATCTAGCT ACTCCCTAAA TGGTTCCATC CAAGGCTTAG	540
25	AGTACCCAAA GGCTAAGAAA TTCTAAAGAA CTGATACAGG AGTAACAATA TGAAGAATTC	600
	ATTAATATCT CAGTACTTGA TAAATCAGAA AGTTATATGT GCAGATTATT TTCCTTGGCC	660
30	TTCAAGCTTC CAAAAAAGTT GTAATAATCA TGTTAGCTAT AGCTTGTATA TACACATAGA	720
	GATCAATTTG CCAAATATTC ACAATCATGT AGTTCTAGTT TACATGCCAA AGTCTTCCCT	780
	TTTTAACATT ATAAAAGCTA GGTGTCTCT TGAATTTTGA GGCCCTAGAG ATAGTCATTT	840
35	TGCAAGTAAA GAGCAACGGG ACCCTTTCTA AAAACGTTGG TTGAAGGACC TAAATACCTG	900
	GCCATACCAT AGATTTGGGA TGATGTAGTC TGTGCTAAAT ATTTTGCTGA AGAAGCAGTT	960
40	TCTCAGACAC AACATCTCAG AATTTTAATT TTTAGAAATT CATGGGAAAT TGGATTTTTC	1020
	TAATAATCTT TTGATGTTTT AAACATTGGT TCCCTAGTCA CCATAGTTAC CACTTGTATT	1080
	TTAAGTCATT TAAACAAGCC ACGGTGGGGC TTTTCTCTCC TCAGTTTGAG GAGAAAAATC	1140
45	TTGATGTCAT TACTCCTGAA TTATTACATT TTGGAGAATA AGAGGGCATT TTATTTTATT	1200
	AGTTACTAAT TCAAGCTGTG ACTATTGTAT ATCTTTCCAA GAGTTGAAAT GCTGGCTTCA	1260
50	GAATCATACC AGATTGTCAG TGAAGCTGAT GCCTAGGAAC TTTTAAAGGG ATCCTTTCAA	1320
	AAGGATCACT TAGCAAACAC ATGTTGACTT TTAAGTGATG TATGAATATT AATACTCTAA	1380
	AAATAGAAAG ACCAGTAATA TATAAGTCAC TTTACAGTGC TACTTCACAC TTAAGTGC	1440
55	ATGGTATTTT TCATGGTATT TTGCATGCAG CCAGTTAACT CTCGTAGATA GAGAAGTCAG	1500
	GTGATAGATG ATATTAAAAA TTAGCAAACA AAAGTGACTT GCTCAGGCTC ATGCAGCTGG	1560
60	GTGATGATAG AAGAGTGGGC TTTAACTGGC AGGCCTGTAT GTTTACAGAC TACCATACTG	1620

5 TAAATATGAG CTTTATGGTG TCATTCTCAG AAACPTATAC ATTTCTGCTC TCCTTTCTCC 1680  
TAAGTTTCAT GCAGATGAAT ATAAGGTAAT ATACTATTAT ATAATTCATT TGTGATATCC 1740  
ACAATAATAT GACTGGCAAG AATTGGTGA AATTTGTAAT TAAATAATT ATTAAACCTA 1800  
AAAAAAAAAN N 1811

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## (2) INFORMATION FOR SEQ ID NO: 232:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CTGACCTCAT GCGTAGAGC CTAGCAACAG CGCAGGCTCC CAGCCGAGTC CGTTATGGCC 60  
25 GCTGCCGTCC CGAAGAGGAT GAGGGGGCCA GCACAAGCGA AACTGCTGCC CGGGTCGGCC 120  
ATCCAAGCCC TTGTGGGGTT GCGCGGGCCG CTGGTCTTGG CGCTCCTGCT TGTGTCCGCC 180  
GCTCTATCCA GTGTTGTATC ACGGACTGAT TCACCGAGCC CAACCGTACT CAACTCACAT 240  
30 ATTTCTACCC CAAATGTGAA TGCTTTAACA CATGAAAACC AAACCAAACC TTCTATTTCC 300  
CAAATCAGCA CCACCTCTCC TCCCACGACG AGTACCAAGA AAAGTGGAGG AGCATCTGTG 360  
35 GTCCCTCATC CCTCGCTAC TCCTCTGTCT CAAGAGGAAG CTGATAACAA TGAAGATCCT 420  
AGTATAGAGG AGGAGGATCT TCTGATGCTG AACAGTTCTC CATCCACAGC CAAAGACACT 480  
CTAGACAATG GCGATTATGG AGAACCAGAC TATGACTGGA CCACGGGGCC CAGGGACGAC 540  
40 GACGAGTCTG ATNGACACCT TGGAAGAAAA CAGGGGTAC ATGGAAATTG AACAGTCAGT 600  
GAAATCTTTT AAGATGCCAT CCTCAAATAT AGAAGAGGAA GACAGCCATT TCTTTTTC 660  
45 TCTTATTATT TTTGCTTTTT GCATTGCTGT TGTTTACATT ACATATCACA ACAAAGGAA 720  
GATTTTTCTT CTGGTTCAAA GCAGGAAATG GCGTGATGGC CTTTGTTCCA AAACAGTGA 780  
ATACCATCGC CTAGATCAGA ATGTTAATGA GGCAATGCCT TCTTTGAAGA TTACCAATGA 840  
50 TTATATTTTT TAAAGCACTG TGATTGAAT TTGCTTATGT AATTTTATTT GCTTGACTTT 900  
TTATATGATA TTGTGCAAT GTTTGCCATA GGCAATTGGT ACTTAAATGA GAGGTGAGTC 960  
55 TCTCTTTTGC CTGGTGCTT TGGAAATTAA ATGTCACAAA CGAGTATATA ATTTTTTATC 1020  
TGTACTTTTA GAGCTGAGTT TAATCAGGTG TCCAAATGT GAGTTAAACA TTACCTTATA 1080  
TTTACACTGT TAGTTTTTAT TGTTTTAGAT TTATTATGCT TCTTCTGGAA GTATTAGTGA 1140  
60

TGCTACTTTT AAAAGATCCC AAACITGTAA CTAAATTCTG ACATATCTGT TACTGCTGAC 1200  
 TCACATTCAT TCTCCGCCAT TCAAACTACTA TTTTITATCC ACATTTTTTT TTGTTCCCAA 1260  
 5 ACTGTAATGT ACAAGGATAT GTGTGATAAT GCTTTGGATT TGAGTAATAT TTTTTTTTCT 1320  
 TCCAAGAAAA CTGCTTTGGA TATTTTTAGA TAATTTAAAC ATAATTTAGG ATAATGATAT 1380  
 10 TGCTCAATCT GACCACAATT TTAGGTAAAA CATTAAATGT GTCAAGAAAT CTGGCAACA 1440  
 GAGACTCTGC AGCTTGCACT GGACATAGAT AAAATGTTAC AGAGATACTA TTTTTTTGGT 1500  
 TGGAATTACT ATATTAAAT TAGAAGCAGA AACTGGTAAA ATGTTAAATA CATGTACAAT 1560  
 15 TGCTTTTAGT TAGCAATTGA TTGTAGCATG GGTTCCTCCA AGGTTTCAAG CAATGGGCAG 1620  
 AGTTTAAAT TATATCAGAT TCGTTTACTT CGTTTATTAT TTTACAGTAA ATTGAATAA 1680  
 ATCTTAGGGG TCATTATCAC TTAAATAATA CTGTACCTAG GTCTTTCAAA TTAAATTAT 1740  
 20 ACCTGAATGA AGTTGTTTGT ATACATAAAG GATATTGTG TACAATTACC TTTTTTCCCC 1800  
 CACACTGTT TTCTTTGTTT TTGTTTTTTA TGGCAACTGG AAAGTATTTA CTATGGGATT 1860  
 25 CATTTATGTC TGCTTTCTA TCATAAGAA TTGATCAATA TGTAAATATG TGATTTGAAC 1920  
 CATGGTTGAC TTACAAGTGT CACTACAGCT TTTTAGAAAA CATAGCCCTA ATATATGTTA 1980  
 AGCAGGACCC GGGTGAGCCA GTGGGCTTGC GCTTTATGTA GAGCTGGAAG AAGGCCGTCC 2040  
 30 ATCTGTCTC TTGGGCGGAC AGTGTACTTT CTAATAGGG AAGGGAAGCA CAATGGAAT 2100  
 ACCCTGAAC CGTTTTATTG CAGTAATTTT TTTCATATCT GAACTATTA TTTAATATTT 2160  
 35 TGAATAAGAT TTTAAAAAAT AAATGGCAA GATATAAATC TAAAAAANA AAAAAAANA 2220  
 AAAAAAANA AAAAAAANA AAAAAAANA AAAAAAANA AAAAAAANA N 2271

40

(2) INFORMATION FOR SEQ ID NO: 233:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

CTTCGGGTTT TCCGGGCAGC TGCCACTGCT GTAGCTTCTG CCACCTGCCA CGACCGGGCC 60  
 TCTCCCTGGC GTTGGTTCAC CTCTGCTTCA TTCTCCACCG CGCCTATGGT CCCTCTTGGA 120  
 55 GCCAGCGTGG CGNGCCTGGC GGCTCCCGGG TGGTGAGAGA GCGGTCCGGG AACGATGAAG 180  
 GCCTCGCACT GCTGCTGCTG TCTCAGCCAC CTCTGGGCTT CCGTCCTCCT CCTGCTGTTG 240  
 60 CTGCCTGAAC TAAGCGGGYC CCTGGMAGTC CTGCTGCAGG CAGCCGAGGC CGCGCCAGGT 300

YTTGGGCTC CTGACCCTAG ACCAGGACAT TACCGCCGCT GCCACCGGGC CWTWACCCCT 360  
 GCCCAGCAGC CGGGCCGTGG TCTGGCTGAA GCTGCGGGGG CCGCGGGGCT CCGAGGGAGG 420  
 5 CAATGGCAGC AACCTGTGG CCGGGCTTGA GACGGACGAT CACGGAGGGA AGGCCCGGGA 480  
 ARGCTCGGTG GGTGGCGGCC TTGCTGTGAG CCCAACCCCT GCGGACAAGC CCATGACCCA 540  
 10 GCGGGCCCTG ACCGTGTTGA TGGTGGTGAG CGGCGCGGTG CTGCTGTACT TCGTGGTCAG 600  
 GACGGTCAGG ATGAGAAGAA GAAACCGAAA GACTAGGAGA TATGGAGTTT TGGACACTAA 660  
 CATAGAAAAT ATGGAATTGA CACCTTTAGA ACAGGATGAT GAGGATGATG ACAACACGTT 720  
 15 GTTTGATGCC AATCATCCTC GAAGATAAGA ATGTGCCTTT TGATGAAAGA ACTTTATCTT 780  
 TCTACAATGA AGAGTGGAAAT TTCTATGTTT AAGGAATAAG AAGCCACTAT ATCAATGTTG 840  
 20 GGGGGGTATT TAAGTTACAT ATATTTNAAC AACCTTTAAT TTGCTGTTGC AATAAATACC 900  
 GTATCCTTTT ATTATATCTT TATATGTATA GAAGTACTCT GTTAATGGGC TCAGAGATGT 960  
 TGGGGATAAA GTATACTGTA ATAATTATC TGTTTGAAAA TTACTATAAA ACGGTGTTTT 1020  
 25 CTGRTCGGTT TTTGTTTCCT GCTTACCATA TGATTGTAAA TTGTTTTATG TATTAATCAG 1080  
 TTAATGCTAA TTATTTTTCG TGATGTCATA TGTTAAAGAG CTATAAATTC CAACAACCAA 1140  
 30 CTGGTGTGTA AAAATAATTT AAAATYTCCT TTAAGTAAAG GTATTTCCCA TTTTGTGGG 1200  
 GAAAAGAAGC CAAATTTATT ACTTTGTGTT GGGGTTTTTA AAATATTAAG AAATGTCTAA 1260  
 35 GTTATGTTT GCAAAACAAT AAATATGATT TTAAATCTC TTAATAAAAA AAAAAAAC 1320  
 CCGGGGGGGG GGCCCGGN 1338

40

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

50

Met Leu Ser Thr Gly Ile Glu Val Ala Arg Pro Pro Ala Thr Leu Leu  
 1 5 10 15

Gly Leu Met Phe Val Leu Thr Gly Met Pro Arg Gly Leu Arg Xaa  
 20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

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488

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

5 Met Asn Val Val Ile Val Ile Ile Leu Phe Ser Phe Asp Ser Val Gly  
 1 5 10 15

Thr Met Phe Ser Cys Asn Arg Ile Pro Lys Ile Thr Val Leu Asn Lys  
 20 25 30

10 Leu Lys Phe Xaa Cys Glu Val Leu Leu Arg Ile Gln Thr Ile Gln Gly  
 35 40 45

Phe Tyr Arg Cys Thr Arg Ile Ser Arg Tyr Lys Gly Ile Phe Pro Asp  
 15 50 55 60

Phe Cys Gln Ser Gln Cys Met Gly Cys Asn Pro Glu Ser Xaa Met Ala  
 65 70 75 80

20 Val Pro Ala Leu Val Thr Pro Ile Leu Ala His Arg Lys Lys Glu Lys  
 85 90 95

Gly Met Cys Leu Phe Thr Leu Ile Ile Ala Pro Thr Arg Cys Thr His  
 100 105 110

25 Tyr Phe Cys Xaa  
 115

30

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

40 Met Ser Ser Ala Lys Ile Val Arg Gln Arg Gly Ala Val Pro Thr Tyr  
 1 5 10 15

Tyr Thr Thr Glu Ala Gly Glu Ile Ile Phe Leu Val Leu Asn Trp Ser  
 20 25 30

45 Leu Ser Ile Leu His Ile Val Asp Val Leu Cys Ser Lys Pro Glu Lys  
 35 40 45

Ser Val Thr Glu Asp Ala Ala Ser Gly Leu Ser Gln Arg Met Thr Ala  
 50 55 60

50 Leu Val Trp Arg Lys Gly Pro Asp Gly Gly Ser Arg Lys Pro Ile Leu  
 65 70 75 80

Leu Leu Phe Phe Phe Leu Pro Leu Ile Leu Cys Phe His Ser Phe Ile  
 85 90 95

55 His Ser Ser Asn Ile Cys Xaa  
 100

60

## (2) INFORMATION FOR SEQ ID NO: 237:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

5 Met Ile Leu Phe Pro Gln Xaa Ala Leu Arg Leu Gly Xaa Trp Pro Arg  
 1 5 10 15  
 Thr Trp Ser Ile Leu Xaa Lys Tyr Ser Val Asn Phe Phe Ser Ala Tyr  
 20 25 30  
 15 Ser Pro Met Gly Ala Val Gly Thr Glu Phe  
 35 40

## (2) INFORMATION FOR SEQ ID NO: 238:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

20 Met Ile Ile Leu Leu Leu Phe Met Leu Leu Asn Asn Val Val Leu Val  
 1 5 10 15  
 Gln Glu Asp Asn Cys Gln Arg Lys Asn Thr Val Gln Glu Arg Arg Xaa  
 20 25 30  
 35 Trp Ser Gln Trp Xaa  
 35

## (2) INFORMATION FOR SEQ ID NO: 239:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

40 Met Ala Ala Xaa Pro Pro Gly Cys Thr Pro Pro Xaa Leu Leu Asp Ile  
 1 5 10 15  
 50 Ser Trp Leu Thr Glu Ser Leu Gly Ala Gly Gln Pro Val Pro Val Glu  
 20 25 30  
 55 Cys Arg His Arg Leu Glu Val Ala Gly Pro Arg Lys Gly Pro Leu Ser  
 35 40 45  
 Pro Ala Trp Met Pro Ala Tyr Ala Cys Gln Arg Pro Thr Pro Leu Thr  
 50 55 60  
 60 His His Asn Thr Gly Leu Ser Glu Leu Leu Glu His Gly Val Cys Glu

490

	65		70		75		80
	Glu Val Glu Arg Val Arg Arg Ser Glu Arg Tyr Gln Thr Met Lys Val						
			85		90		95
5	Arg Arg Ala Gly Leu Gly Pro Thr Pro Gly Met Ser Cys Pro Gly Asn						
		100		105		110	
10	Asp Asn Thr Val His Thr Met His Gly Glu Ala Asn Arg Gly Ser Xaa						
		115		120		125	

15

(2) INFORMATION FOR SEQ ID NO: 240:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

25 Met Ser Ile Leu Cys Cys Pro Xaa Leu Cys Leu Phe Phe Ser Phe Cys
    1                      5                      10                      15

Ile Ser Ser Gly Ser Cys Pro Phe Ser His Val Ser Gln Leu Ser Phe
    20                      25                      30

30 Ile Ala Thr Phe Ser Gln Ser Ser Pro Val Leu Leu Val Pro Ala Tyr
    35                      40                      45

Asn Thr Tyr Leu Ser Phe Leu Ala Phe Leu Asp Cys Ala Ser Leu Thr
35 50                      55                      60

Ser Thr Xaa
    65

```

40

(2) INFORMATION FOR SEQ ID NO: 241:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

50 Met Ser Thr Phe Gln Leu Leu Leu Leu Ile Leu Ala Gln Ser Thr Tyr  
1 5 10 15

Lys Ile Lys Ser Lys Pro Leu His Met Thr Asn His Thr Leu Leu Asn  
20 25 30

55 Ser Pro Gly Leu Asn Pro Ser Ser Pro Thr Leu Asn Phe Lys Thr Gln  
35 40 45

Gln His Glu Ser Val Ser Tyr Ala Cys Cys His Met Arg Ser Leu His  
50 55 60



His Ala Phe Ala Xaa  
65

5

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

15 Met Val Ser Val Val Leu Ile Phe Ser Phe Leu Ser Leu Thr Ile Ser  
1 5 10 15

Thr Thr Ala Ser Ala Tyr Asn Gly Asn Asp Thr Gln Gly Trp Asn Asp  
20 25 30

20

Lys Phe His Xaa Xaa Ser Val Lys Thr Gln Thr Xaa  
35 40

25

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

35 Met Ile Ser Asp Ala Gly Ala Gly Phe Gly Val Phe Leu Leu Val Pro  
1 5 10 15

Arg Ala Gly His Cys Trp Gly Ala Gly Lys Pro Leu Pro Ser Cys Pro  
20 25 30

40 Ser Val Ala Ser Ile Pro Ser Trp Val Leu Pro Ser Phe Leu Glu Arg  
35 40 45

Gly Arg Xaa  
50

45

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

55

Met Val Gln Thr Ile Gln Asp Phe Leu Ser Leu Phe Ser Thr Pro Ile  
1 5 10 15

60

Phe Leu Leu Leu Leu Met Phe Glu Thr Leu Ser Leu Ala Pro Ala Trp  
20 25 30

Leu Lys Pro Leu Arg Val Thr Ser His Ser Xaa  
35 40

5

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

15 Met Ile Leu Met Pro Gly Leu Gly Thr Ser Arg Gln Arg Ser Val Pro  
1 5 10 15

Phe Val Pro Thr Leu Asn Ala Ser Thr Pro Gly Ala Met Thr Gly Pro  
20 25 30

20

Thr Ala Thr Leu Thr Ser Cys Gln Trp Thr Thr Ala Cys Arg Val Ser  
35 40 45

25

Trp Ala Asn Gly Trp Thr Ser Leu Arg Thr Phe Arg Xaa  
50 55 60

(2) INFORMATION FOR SEQ ID NO: 246:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Met Ser His His Ala Gln Pro Arg Phe Leu Leu Ile Thr Met Leu Leu  
1 5 10 15

40

Gln Glu Ala Lys Pro Val Ser Asn Ile Pro His Leu Leu Glu Ser Trp  
20 25 30

Tyr Phe Gly Xaa  
35

45

(2) INFORMATION FOR SEQ ID NO: 247:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Met Asn Ser Leu Phe Trp Met Ile Leu Leu Pro Val Ser Gln Asp Gln  
1 5 10 15

60

Val Val Glu Gly Leu Gln Gly Gly Phe Ser Gln Ile His Met Arg Ile  
20 25 30

Leu Arg Lys His Leu Xaa  
35

5

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

15 Met Ser Arg Ser Xaa Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala  
1 5 10 15  
Ala Ser Ile Tyr Leu His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala  
20 25 30  
Leu His Gln Gly Asp Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile  
35 40 45  
Leu Leu Lys Leu Asp Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg  
25 50 55 60  
Met Gln Asp Leu Asp Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala  
65 70 75 80  
30 Trp Val Ser Leu Ala Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr  
85 90 95  
Ile Phe Gln Glu Met Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu  
100 105 110  
35 Asn Gly Gln Ala Ala Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala  
115 120 125  
Glu Gly Leu Leu Gln Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu  
40 130 135 140  
Thr Leu Val Asn Leu Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro  
145 150 155 160  
45 Glu Val Thr Asn Arg Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser  
165 170 175  
His Pro Phe Ile Lys Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg  
180 185 190  
50 Leu Val Leu Gln Tyr Ala Pro Ser Ala Glu Ala Gly Pro Glu Leu Ser  
195 200 205  
Gly Pro Xaa  
55 210

60

(2) INFORMATION FOR SEQ ID NO: 249:

494

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Met Glu Asp Ser Glu Ala Leu Gly Phe Glu His Met Gly Leu Asp Pro  
 1 5 10 15  
 10 Arg Leu Leu Gln Ala Val Thr Asp Leu Gly Trp Ser Arg Pro Thr Leu  
 20 25 30  
 Ile Gln Glu Lys Ala Ile Pro Leu Ala Leu Glu Gly Lys Asp Leu Leu  
 35 40 45  
 15 Ala Arg Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Tyr Ala Ile Pro  
 50 55 60  
 20 Met Leu Gln Leu Leu Leu His Arg Lys Ala Thr Gly Pro Val Val Glu  
 65 70 75 80  
 Gln Ala Val Arg Gly Leu Val Leu Val Pro Thr Lys Glu Leu Ala Arg  
 85 90 95  
 25 Gln Ala Gln Ser Met Ile Gln Gln Leu Ala Thr Tyr Cys Ala Arg Asp  
 100 105 110  
 Val Arg Val Ala Asn Val Ser Ala Ala Glu Asp Ser Val Ser Gln Arg  
 115 120 125  
 30 Ala Val Leu Met Glu Lys Pro Asp Val Val Val Gly Thr Pro Ser Arg  
 130 135 140  
 Ile Leu Ser His Leu Gln Gln Asp Ser Leu Lys Leu Arg Asp Ser Leu  
 145 150 155 160  
 35 Glu Leu Leu Val Val Asp Glu Ala Asp Leu Leu Phe Ser Phe Gly Phe  
 165 170 175  
 40 Glu Glu Glu Leu Lys Ser Leu Leu Cys His Leu Pro Arg Ile Tyr Gln  
 180 185 190  
 Ala Phe Leu Met Ser Ala Thr Phe Asn Glu Asp Val Gln Ala Leu Lys  
 195 200 205  
 45 Glu Leu Ile Leu His Asn Pro Val Thr Leu Lys Leu Gln Glu Ser Gln  
 210 215 220  
 Leu Pro Gly Pro Asp Gln Leu Gln Gln Phe Gln Val Val Cys Glu Thr  
 225 230 235 240  
 50 Glu Glu Asp Lys Phe Leu Leu Leu Tyr Ala Leu Leu Lys Leu Ser Leu  
 245 250 255  
 55 Ile Arg Gly Lys Ser Leu Leu Phe Val Asn Thr Leu Glu Arg Ser Tyr  
 260 265 270  
 Arg Leu Arg Leu Phe Leu Glu Gln Phe Ser Ile Pro Thr Cys Val Leu  
 275 280 285  
 60

495

Asn Gly Glu Leu Pro Leu Arg Ser Arg Cys His Ile Ile Ser Gln Phe  
 290 295 300  
 5 Asn Gln Gly Phe Tyr Asp Cys Val Ile Ala Thr Asp Ala Glu Val Leu  
 305 310 315 320  
 Gly Ala Pro Val Lys Gly Lys Arg Arg Gly Arg Gly Pro Lys Gly Asp  
 325 330 335  
 10 Lys Ala Ser Asp Pro Glu Ala Gly Val Ala Arg Gly Ile Asp Phe His  
 340 345 350  
 His Val Ser Ala Val Leu Asn Phe Asp Leu Pro Pro Thr Pro Glu Ala  
 355 360 365  
 15 Tyr Ile His Arg Ala Gly Arg Thr Ala Arg Ala Asn Asn Pro Gly Ile  
 370 375 380  
 Val Leu Thr Phe Val Leu Pro Thr Glu Gln Phe His Leu Gly Lys Ile  
 20 385 390 395 400  
 Glu Glu Leu Leu Ser Gly Glu Asn Arg Gly Pro Ile Leu Leu Pro Tyr  
 405 410 415  
 25 Gln Phe Arg Met Glu Glu Ile Glu Gly Phe Arg Tyr Arg Cys Arg Asp  
 420 425 430  
 Ala Met Arg Ser Val Thr Lys Gln Ala Ile Arg Glu Ala Arg Leu Lys  
 435 440 445  
 30 Glu Ile Lys Glu Glu Leu Leu His Ser Glu Lys Leu Lys Thr Tyr Phe  
 450 455 460  
 Glu Asp Asn Pro Arg Asp Leu Gln Leu Leu Arg His Asp Leu Pro Leu  
 35 465 470 475 480  
 His Pro Ala Val Val Lys Pro His Leu Gly His Val Pro Asp Tyr Leu  
 485 490 495  
 40 Val Pro Pro Ala Leu Arg Gly Leu Val Arg Pro His Lys Lys Arg Lys  
 500 505 510  
 Lys Leu Ser Ser Ser Cys Arg Lys Ala Lys Arg Ala Lys Ser Gln Asn  
 515 520 525  
 45 Pro Leu Arg Ser Phe Lys His Lys Gly Lys Lys Phe Arg Pro Thr Ala  
 530 535 540  
 50 Lys Pro Ser Xaa  
 545

(2) INFORMATION FOR SEQ ID NO: 250:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

496

Met Thr Thr Val Pro Pro Ser Pro Arg Pro Met Ser Arg Pro Ser Glu  
 1 5 10 15  
 5 Arg Asn Met Arg Arg Pro Arg Gly Pro Ser Pro Leu Pro Ala Ser Pro  
 20 25 30  
 Arg Asn Ser Thr Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe  
 35 40 45  
 10 Leu Asn Val Phe Met Ser Gly Arg Ser Arg Ser Ser Ala Glu Ser  
 50 55 60  
 Phe Gly Leu Phe Ser Cys Ile Ile Asn Gly Glu Glu Gln Glu Gln Thr  
 15 65 70 75 80  
 His Arg Ala Ile Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu  
 85 90 95  
 20 Leu Glu Val Asp Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr  
 100 105 110  
 Trp Tyr Glu Ala Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro  
 115 120 125  
 25 Ala Tyr Tyr Ala Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala  
 130 135 140  
 Leu Ala Lys Asn Ser Asp Trp Val Asp Gln Phe Arg Val Lys Phe Leu  
 145 150 155 160  
 Gly Ser Val Gln Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala  
 165 170 175  
 35 Ala Met Gln Lys Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn  
 180 185 190  
 Pro Pro Ser Ser Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile  
 195 200 205  
 40 Gly Val Lys Ala Asp Asp Ser Gln Glu Ala Lys Gly Asn Lys Cys Ser  
 210 215 220  
 His Phe Phe Gln Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys  
 225 230 235 240  
 Asn Asn Lys Tyr Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg  
 245 250 255  
 50 Phe Ala Cys His Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala  
 260 265 270  
 Glu Ser Val Gly Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu  
 275 280 285  
 55 Tyr Thr Cys Pro Thr Glu Asp Ile Tyr Leu Glu  
 290 295  
 60

## (2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

5  
 10 Leu Leu Tyr Leu Leu Lys Val Xaa Val Ile Phe Val Phe Ser Ser Ser  
 1 5 10 15  
 Lys Gly Val Thr Leu Val Ser Met Asn Leu Thr Ser Phe Phe Val Ser  
 20 25 30  
 15 Ser Val Leu Ala Cys Phe Ser Xaa  
 35 40

## 20 (2) INFORMATION FOR SEQ ID NO: 252:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 594 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

25  
 30 Met Pro Ala Ser Ser Leu Glu Ser Arg Ser Phe Leu Leu Ala Lys Lys  
 1 5 10 15  
 Ser Gly Glu Asn Val Ala Lys Phe Ile Ile Asn Ser Tyr Pro Lys Tyr  
 20 25 30  
 35 Phe Gln Lys Asp Ile Ala Glu Pro His Ile Pro Cys Leu Met Pro Glu  
 35 40 45  
 Tyr Phe Glu Pro Gln Ile Lys Asp Ile Ser Glu Ala Ala Leu Lys Glu  
 50 55 60  
 40 Arg Ile Glu Leu Arg Lys Val Lys Ala Ser Val Asp Met Phe Asp Gln  
 65 70 75 80  
 Leu Leu Gln Ala Gly Thr Thr Val Ser Leu Glu Thr Thr Asn Ser Leu  
 85 90 95  
 45 Leu Asp Xaa Leu Cys Tyr Tyr Gly Asp Gln Glu Pro Ser Thr Asp Tyr  
 100 105 110  
 50 His Phe Gln Gln Thr Gly Gln Ser Glu Ala Leu Glu Glu Asn Asp  
 115 120 125  
 Glu Thr Ser Arg Arg Lys Ala Gly His Gln Phe Gly Val Thr Trp Arg  
 130 135 140  
 55 Ala Lys Asn Asn Ala Glu Arg Ile Phe Ser Leu Met Pro Glu Lys Asn  
 145 150 155 160  
 Glu His Ser Tyr Cys Thr Met Ile Arg Gly Met Val Lys His Arg Ala  
 165 170 175  
 60

Tyr Glu Gln Ala Leu Asn Leu Tyr Thr Glu Leu Leu Asn Asn Arg Leu  
 180 185 190  
 5 His Ala Asp Val Tyr Thr Phe Asn Ala Leu Ile Glu Ala Thr Val Cys  
 195 200 205  
 Ala Ile Asn Glu Lys Phe Glu Glu Lys Trp Ser Lys Ile Leu Glu Leu  
 210 215 220  
 10 Leu Arg His Met Val Ala Gln Lys Val Lys Pro Asn Leu Gln Thr Phe  
 225 230 235 240  
 Asn Thr Ile Leu Lys Cys Leu Arg Arg Phe His Val Phe Ala Arg Ser  
 245 250 255  
 15 Pro Ala Leu Gln Val Leu Arg Glu Met Lys Ala Ile Gly Ile Glu Pro  
 260 265 270  
 Ser Leu Ala Thr Tyr His His Ile Ile Arg Leu Phe Asp Gln Pro Gly  
 275 280 285  
 20 Asp Pro Leu Lys Arg Ser Ser Phe Ile Ile Tyr Asp Ile Met Asn Glu  
 290 295 300  
 25 Leu Met Gly Lys Arg Phe Ser Pro Lys Asp Pro Asp Asp Asp Lys Phe  
 305 310 315 320  
 Phe Gln Ser Ala Met Ser Ile Cys Ser Ser Leu Arg Asp Leu Glu Leu  
 325 330 335  
 30 Ala Tyr Gln Val His Gly Leu Leu Lys Thr Gly Asp Asn Trp Lys Phe  
 340 345 350  
 Ile Gly Pro Asp Gln His Arg Asn Phe Tyr Tyr Ser Lys Phe Phe Asp  
 355 360 365  
 35 Leu Ile Cys Leu Met Glu Gln Ile Asp Val Thr Leu Lys Trp Tyr Glu  
 370 375 380  
 40 Asp Leu Ile Pro Ser Ala Tyr Phe Pro His Ser Gln Thr Met Ile His  
 385 390 395 400  
 Leu Leu Gln Ala Leu Asp Val Ala Asn Arg Leu Glu Val Ile Pro Lys  
 405 410 415  
 45 Ile Trp Lys Asp Ser Lys Glu Tyr Gly His Thr Phe Arg Ser Asp Leu  
 420 425 430  
 Arg Glu Glu Ile Leu Met Leu Met Ala Arg Asp Lys His Pro Pro Glu  
 435 440 445  
 50 Leu Gln Val Ala Phe Ala Asp Cys Ala Ala Asp Ile Lys Ser Ala Tyr  
 450 455 460  
 55 Glu Ser Gln Pro Ile Arg Gln Thr Ala Gln Asp Trp Pro Ala Thr Ser  
 465 470 475 480  
 Leu Asn Cys Ile Ala Ile Leu Phe Leu Arg Ala Gly Arg Thr Gln Glu  
 485 490 495  
 60



499

Ala Trp Lys Met Leu Gly Leu Phe Arg Lys His Asn Lys Ile Pro Arg  
                   500                  505                  510

5 Ser Glu Leu Leu Asn Glu Leu Met Asp Ser Ala Lys Val Ser Asn Ser  
                   515                  520                  525

Pro Ser Gln Ala Ile Glu Val Val Glu Leu Ala Ser Ala Phe Ser Leu  
                   530                  535                  540

10 Pro Ile Cys Glu Gly Leu Thr Gln Arg Val Met Ser Asp Phe Ala Ile  
       545                  550                  555                  560

Asn Gln Glu Gln Lys Glu Ala Leu Ser Asn Leu Thr Ala Leu Thr Ser  
                   565                  570                  575

15 Asp Ser Asp Thr Asp Ser Ser Ser Asp Ser Asp Ser Asp Thr Ser Glu  
                   580                  585                  590

20 Gly Lys

25 (2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Met Lys Leu Asn Leu Cys Ile Pro Asn Trp Ala Arg Cys Pro Leu Leu  
   1                  5                  10                  15

35 Leu Leu Phe Pro Gln Leu Leu Pro Phe Gln Gly Glu Asp Asp Asp Pro  
                   20                  25                  30

Leu Lys Ala Lys Ala Ala Asn Leu Val Glu Ala Val Pro Trp Gly Ile  
                   35                  40                  45

40 Lys Ala Pro Ser Phe Gln Val Thr Cys Leu Val Arg Val Gln Leu Gln  
                   50                  55                  60

45 Ser Cys Thr Pro Ser Arg Pro Ser Thr Leu Leu Ala Thr Ser Gln Ser  
       65                  70                  75                  80

Pro Gly Arg Ile Ser Cys Tyr Ser Pro Leu Ser His Leu Pro Pro Val  
                   85                  90                  95

50 Thr Thr Ser Ile Gln Pro Ser Pro Val Met Val Pro Phe Gln Tyr Gln  
                   100                  105                  110

Ala Phe Leu Leu Gln Val Lys Glu Pro Ala Ala Gln Thr Leu Leu Gly  
                   115                  120                  125

55 Gln Gln Xaa  
       130

60

500

## (2) INFORMATION FOR SEQ ID NO: 254:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Met Arg Tyr His Ala Gln Leu Ile Phe Cys Ile Phe Cys Xaa Phe Val  
 1 5 10 15  
 Phe Val Xaa Lys Xaa  
 20

15

## (2) INFORMATION FOR SEQ ID NO: 255:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Met Asn Asp Asn Ser Pro Asn His Ser Ser Ser Tyr Leu Pro Leu Pro  
 1 5 10 15  
 Leu Thr Ile Val Ile Leu Gln Thr Gly His Lys Gly Thr Leu Xaa  
 20 25 30

30

## (2) INFORMATION FOR SEQ ID NO: 256:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr Leu Trp Gly Leu  
 1 5 10 15  
 Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr Glu Glu Val Lys  
 20 25 30  
 Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys Thr Ser Lys Lys  
 35 40 45  
 Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu Ala Lys Asp Gly  
 50 55 60  
 Ser Lys Phe Tyr Cys Ser Arg Thr Gln Asn Glu Gly His Pro Lys Trp  
 65 70 75 80  
 Phe Val Leu Gly Val Gly Gln Val Ile Lys Gly Leu Asp Ile Ala Met  
 85 90 95  
 Thr Asp Met Cys Pro Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser  
 100 105 110

60

501

Phe Ala Tyr Gly Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp  
 115 120 125  
 5 Ala Thr Leu Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro  
 130 135 140  
 Arg Ser Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln  
 145 150 155 160  
 10 Leu Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys  
 165 170 175  
 Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu Asp  
 180 185 190  
 15 Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser Pro Lys  
 195 200 205  
 20 Glu Tyr Asn Val Tyr Gln His Asp Glu Leu Xaa  
 210 215

25 (2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Met Trp Val Ile Arg Val Phe Gln Lys Thr Phe Leu Phe Phe Val Leu  
 1 5 10 15  
 35 Phe Trp Ser Val His Cys Ile Ser Asp Lys Phe Gly Cys Leu Trp His  
 20 25 30  
 40 Val Cys Met Lys Arg Glu Gly Asp Xaa Asn Cys Leu Ser Phe Ser Xaa  
 35 40 45  
 Leu Xaa  
 50

45

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 122 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

55 Met Pro Ser Gln Thr Glu Xaa Phe Ala Ala Cys Gly Gly His Ser Leu  
 1 5 10 15  
 Leu Leu Val Xaa Leu Pro Leu Gly Leu Pro Phe Cys Pro Arg Ala Ala.  
 20 25 30  
 60

502

Leu Cys Asp Leu Pro Phe Ser Leu Pro Ser Phe Pro Gly Gln Ala Arg  
 35 40 45  
 Arg Gly Gly Ala Glu Lys Gln Gly Ala Glu Gly Arg Gly Leu Gln Val  
 5 50 55 60  
 Lys Pro Arg Gly Gln Arg Thr Phe Gln Val Ser Arg Thr Ala Pro Ala  
 65 70 75 80  
 Ala Pro Arg Ser Arg Gln Pro Arg Pro Pro Ala Ala Leu Pro Ala Leu  
 10 85 90 95  
 Gly Phe Gly Gly Arg Gly Val Ala Lys Gly Arg Phe Leu Cys Phe Trp  
 100 105 110  
 Cys Leu Tyr Met Leu Arg Ile Asp Gln Xaa  
 115 120

20

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 88 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Met Thr Ala Phe Cys Ser Leu Leu Leu Gln Ala Gln Ser Leu Leu Pro  
 1 5 10 15  
 Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro Gly Glu Glu Asp  
 20 25 30  
 Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Ser Met Ala Lys Gly Ala  
 35 40 45  
 Arg Pro Gly Ala Xaa Arg Gly Arg Ala Arg Trp Gly Leu Ala Tyr Thr  
 50 55 60  
 Leu Leu His Asn Pro Thr Leu Gln Val Phe Arg Lys Thr Ala Leu Leu  
 65 70 75 80  
 Gly Ala Asn Gly Ala Gln Pro Xaa  
 85

50

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Met Ile Gln Val Ser Val Pro Leu Leu Thr Ile Met Ile Phe Leu Leu  
 1 5 10 15  
 Tyr Leu Gln Ile Gly Pro Gly Lys Leu Xaa

20

25

## 5 (2) INFORMATION FOR SEQ ID NO: 261:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Met Leu Leu Asp Pro Phe Ile Leu Leu Phe Cys Leu Phe Ser Thr Ala  
 1 5 10 15  
 Ala Gln Ser Cys Leu Glu Phe Ile Tyr Ile Gln Phe Xaa  
 20 25

20

## (2) INFORMATION FOR SEQ ID NO: 262:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Met Lys Phe Leu Ser Ile Leu Leu Asp Asp Asn Asn Phe Xaa Leu Met  
 1 5 10 15  
 Leu Met Leu Ala Pro Phe Gly Cys Leu Ala Phe Glu Arg Ser Met Lys  
 20 25 30  
 Met Arg Asn Gly Ala Leu Gly Leu Glu Glu Val Xaa  
 35 40

## 40 (2) INFORMATION FOR SEQ ID NO: 263:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

45 (B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro  
 1 5 10 15  
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys  
 20 25 30  
 Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg  
 35 40 45  
 Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His  
 50 55 60  
 Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp

504

	65		70		75		80									
	Val	Leu	Gly	Tyr	Val	Thr	Pro	Trp	Asn	Ser	His	Gly	Tyr	Asp	Val	Thr
					85					90					95	
5	Lys	Val	Phe	Gly	Ser	Lys	Phe	Thr	Gln	Ile	Ser	Pro	Val	Trp	Leu	Gln
				100					105					110		
10	Leu	Lys	Arg	Arg	Gly	Arg	Glu	Met	Phe	Glu	Val	Thr	Gly	Leu	His	Asp
			115					120					125			
	Val	Asp	Gln	Gly	Trp	Met	Arg	Ala	Val	Arg	Lys	His	Ala	Lys	Gly	Leu
		130					135					140				
15	His	Ile	Val	Pro	Arg	Leu	Leu	Phe	Glu	Asp	Trp	Thr	Tyr	Asp	Asp	Phe
	145					150					155					160
	Arg	Asn	Val	Leu	Asp	Ser	Glu	Asp	Glu	Ile	Glu	Glu	Leu	Ser	Lys	Thr
					165					170					175	
20	Val	Val	Gln	Val	Ala	Lys	Asn	Gln	His	Phe	Asp	Gly	Phe	Val	Val	Glu
			180						185					190		
25	Val	Trp	Asn	Gln	Leu	Leu	Ser	Gln	Lys	Arg	Val	Thr	Asp	Gln	Leu	Gly
		195						200					205			
	Met	Phe	Thr	His	Lys	Glu	Phe	Glu	Gln	Leu	Ala	Pro	Val	Leu	Asp	Gly
		210					215					220				
30	Phe	Ser	Leu	Met	Thr	Tyr	Asp	Tyr	Ser	Thr	Ala	His	Gln	Pro	Gly	Pro
	225					230					235					240
	Asn	Ala	Pro	Leu	Ser	Trp	Val	Arg	Ala	Cys	Val	Gln	Val	Leu	Asp	Pro
				245					250					255		
35	Lys	Ser	Lys	Trp	Arg	Ser	Lys	Ile	Leu	Leu	Gly	Leu	Asn	Phe	Tyr	Gly
			260					265						270		
40	Met	Asp	Tyr	Ala	Thr	Ser	Lys	Asp	Ala	Arg	Glu	Pro	Val	Val	Gly	Ala
		275						280					285			
	Arg	Tyr	Ile	Gln	Thr	Leu	Lys	Asp	His	Arg	Pro	Arg	Met	Val	Trp	Asp
		290					295					300				
45	Ser	Gln	Xaa	Ser	Glu	His	Phe	Phe	Glu	Tyr	Lys	Lys	Ser	Arg	Ser	Gly
	305					310					315					320
	Arg	His	Val	Val	Phe	Tyr	Pro	Thr	Leu	Lys	Ser	Leu	Gln	Val	Arg	Leu
				325					330					335		
50	Glu	Leu	Ala	Arg	Glu	Leu	Gly	Val	Gly	Val	Ser	Ile	Trp	Glu	Leu	Gly
			340					345						350		
55	Gln	Gly	Leu	Asp	Tyr	Phe	Tyr	Asp	Leu	Leu	Xaa					
		355						360								

(2) INFORMATION FOR SEQ ID NO: 264:

60

505

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Leu Pro Thr Lys Ile Leu Val Lys Pro Asp Arg Thr Phe Glu Ile Lys  
 1 5 10 15  
 10 Ile Gly Gln Pro Thr Val Ser Tyr Phe Leu Lys Ala Ala Ala Gly Ile  
 20 25 30  
 Glu Lys Gly Ala Arg Gln Thr Gly Lys Glu Val Ala Gly Leu Val Thr  
 35 40 45  
 15 Leu Lys His Val Tyr Glu Ile Ala Arg Ile Lys Ala Gln Asp Glu Ala  
 50 55 60  
 Phe Ala Leu Gln Asp Val Pro Leu Ser Ser Val Val Arg Ser Ile Ile  
 65 70 75 80  
 Gly Ser Ala Arg Ser Leu Gly Ile Arg Val Val Lys Asp Leu Ser Ser  
 85 90 95  
 25 Glu Glu Leu Ala Ala Phe Gln Lys Glu Arg Ala Ile Phe Leu Ala Ala  
 100 105 110  
 Gln Lys Glu Ala Asp Leu Ala Ala Gln Glu Glu Ala Ala Lys Lys Xaa  
 115 120 125  
 30

35

## (2) INFORMATION FOR SEQ ID NO: 265:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

45 Met Leu Leu Gln Ile His Pro Leu Leu Pro Ser Pro Thr Ile Pro His  
 1 5 10 15  
 Ile Leu Leu Leu Phe Leu Tyr Pro Thr Phe Ser Ile Leu Glu His Ser  
 20 25 30  
 50 Cys Ser Tyr Cys Ile Glu Tyr Leu Trp Val Cys Leu Leu Phe Cys Leu  
 35 40 45  
 Ser Leu Trp Phe Leu Xaa  
 50  
 55

60

## (2) INFORMATION FOR SEQ ID NO: 266:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

5

Met Cys Leu Trp Cys Cys Gly Asp Val Cys Ser Gly Leu Ser Ser Leu  
 1 5 10 15

10

Leu Ser Leu Cys Val Cys Cys Val Val Leu Ala Val Cys  
 20 25

(2) INFORMATION FOR SEQ ID NO: 267:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Glu Gly Leu Arg Leu Leu Leu Ser Leu Pro Ala Ala Leu Pro Arg Ser  
 1 5 10 15

25

Cys Cys His Pro Arg Trp Leu Pro Val Xaa  
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Met Phe His Gly Ile Pro Ala Thr Pro Gly Ile Gly Ala Pro Gly Asn  
 1 5 10 15

40

Lys Pro Glu Leu Tyr Glu Glu Val Lys Leu Tyr Lys Asn Ala Arg Glu  
 20 25 30

45

Arg Glu Lys Tyr Asp Asn Met Ala Glu Leu Phe Ala Val Val Lys Thr  
 35 40 45

Met Gln Ala Leu Glu Lys Ala Tyr Ile Lys Asp Cys Val Ser Pro Ser  
 50 55 60

50

Glu Tyr Thr Ala Ala Cys Ser Arg Leu Leu Val Gln Tyr Lys Ala Ala  
 65 70 75 80

Phe Arg Gln Val Gln Gly Ser Glu Ile Ser Ser Ile Asp Glu Phe Cys  
 85 90 95

55

Arg Lys Phe Arg Leu Asp Cys Pro Leu Ala Met Glu Arg Ile Lys Glu  
 100 105 110

60

Asp Arg Pro Ile Thr Ile Lys Asp Asp Lys Gly Asn Leu Asn Arg Cys  
 115 120 125



507

Ile Ala Asp Val Val Ser Leu Phe Ile Thr Val Met Asp Lys Leu Arg  
 130 135 140

5 Leu Glu Ile Arg Ala Met Asp Glu Ile Gln Pro Asp Leu Arg Glu Leu  
 145 150 155 160

Met Glu Thr Met His Arg Met Ser His Leu Pro Pro Asp Phe Glu Gly  
 165 170 175

10 Arg Gln Thr Val Ser Gln Trp Leu Gln Thr Leu Ser Gly Met Ser Ala  
 180 185 190

15 Ser Asp Glu Leu Asp Asp Ser Gln Val Arg Gln Met Leu Phe Asp Leu  
 195 200 205

Glu Ser Ala Tyr Asn Ala Phe Asn Arg Phe Leu His Ala  
 210 215 220

20

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 3 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

30 Met Lys Xaa  
 1

35 (2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 40 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Met Gln Ala Pro Phe Xaa His Phe Ser Phe Arg Met Phe Ser Asn Leu  
 1 5 10 15

45 Tyr Cys Phe Ser Asp Phe Gln Pro Asn Ile Ser Pro Cys Pro Leu Cys  
 20 25 30

His Cys Ile Leu Pro Xaa His His His Val Phe Leu Leu Ala Val  
 50 35 40 45

Xaa

55

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:  
 60 (A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

5 Met Lys Leu Val Thr Met Phe Asp Lys Leu Ser Arg Asn Arg Val Ile  
 1 5 10 15  
 Gln Pro Met Gly Met Ser Pro Arg Gly His Leu Thr Ser Leu Gln Asp  
 20 25 30  
 10 Ala Met Cys Glu Thr Met Glu Gln Gln Leu Ser Ser Asp Pro Asp Ser  
 35 40 45  
 Asp Pro Asp Xaa  
 15 50

(2) INFORMATION FOR SEQ ID NO: 272:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

Met Ala Val Gly Glu Ala Val Phe Val Pro Leu Gln His Pro Pro Leu  
 1 5 10 15  
 30 Leu His Gly Ser Pro Ile Pro Lys Leu Leu Pro Gly Pro Leu Leu Xaa  
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO: 273:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

Met Asn Gly Cys His Arg Arg Lys Arg Leu His Leu Cys Lys Thr Ile  
 1 5 10 15  
 50 Tyr Leu Leu Trp Phe Val Phe Ser Phe Leu Leu Ser Asn Glu Val Val  
 20 25 30  
 Ser Ser His Trp His Ile Leu Arg Ala Val Gln Ile Ile Cys Thr Leu  
 35 40 45  
 55 Phe His Arg Xaa Ile Ser Ala Phe Xaa  
 50 55

60

(2) INFORMATION FOR SEQ ID NO: 274:

509

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

Met Gly Trp Val Ser Ser Pro His Val Lys Arg Arg Glu Cys Val Leu  
 1 5 10 15  
 Lys Lys Pro Phe Phe Xaa  
 20

## (2) INFORMATION FOR SEQ ID NO: 275:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Met Phe Asn Phe Phe Lys Asn Pro Leu Leu Thr Cys Leu Phe Ile Ser  
 1 5 10 15  
 Cys Tyr Leu Tyr Leu Ser Leu Leu Val Asn Lys Val Leu Phe Ala Glu  
 20 25 30  
 Glu Gly Leu Cys Cys Thr Tyr Cys Thr Thr Ser Asn Thr Gly Glu Gly  
 35 40 45  
 Gly Val Xaa  
 50

## (2) INFORMATION FOR SEQ ID NO: 276:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

Met Xaa  
 1

## (2) INFORMATION FOR SEQ ID NO: 277:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

Met Leu Cys Thr Ile Leu Thr Val Val Ile Ile Ala Ala Gln Thr  
 1 5 10 15

510

Thr Arg Thr Thr Gly Ile Pro Lys Asn Ala Pro Gly Pro Ala Pro Leu  
 20 25 30

5 Cys Ala Pro Arg Ser Pro Arg Leu Phe Leu Gln Xaa Tyr Arg Gly Pro  
 35 40 45

Asn Gly Arg Pro Ala His Pro Phe Leu Gly Pro Ser Asp Leu Asp Thr  
 50 55 60

10 Ser Xaa  
 65

15 (2) INFORMATION FOR SEQ ID NO: 278:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 257 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

20 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser Pro  
 1 5 10 15

Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly Trp Ala  
 20 25 30

30 Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys Leu Val Val  
 35 40 45

Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly Gly Ala Ala Leu  
 50 55 60

35 Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Xaa Ala Val Arg Ser His  
 65 70 75 80

40 His His Glu Pro Ala Gly Glu Thr Gly Asn Gly Thr Ser Gly Ala Ile  
 85 90 95

Tyr Phe Asp Gln Val Leu Val Asn Glu Gly Gly Gly Phe Asp Arg Ala  
 100 105 110

45 Ser Gly Ser Phe Val Ala Pro Val Arg Gly Val Tyr Ser Phe Arg Phe  
 115 120 125

His Val Val Lys Val Tyr Asn Arg Gln Thr Val Gln Val Ser Leu Met  
 130 135 140

50 Leu Asn Thr Trp Pro Val Ile Ser Ala Phe Ala Asn Asp Pro Asp Val  
 145 150 155 160

55 Thr Arg Glu Ala Ala Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly  
 165 170 175

Asp Arg Val Ser Leu Arg Leu Arg Arg Gly Xaa Ser Thr Gly Trp Leu  
 180 185 190

60 Glu Ile Leu Lys Phe Leu Trp Leu Pro His Leu Pro Ser Leu Lys Asp

511

195                      200                      205

Pro Ser Leu Ser Ser Thr Arg Ile Gln Pro Leu Thr Thr Phe Phe Cys  
 210                      215                      220

5                      Pro Leu Leu Pro Xaa Lys Gln Xaa Lys Gln Xaa Xaa Xaa Ser Leu Trp  
 225                      230                      235                      240

10                      Leu Leu Ser His Leu Phe Ala Trp Glu Pro Val Pro Asn Thr Gln Val  
                                  245                      250                      255

Xaa

15

(2) INFORMATION FOR SEQ ID NO: 279:

20                      (i) SEQUENCE CHARACTERISTICS:  
                                  (A) LENGTH: 103 amino acids  
                                  (B) TYPE: amino acid  
                                  (D) TOPOLOGY: linear  
                                  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

25                      Met Ala Pro Arg Ala Leu Pro Gly Ser Ala Val Leu Ala Ala Ala Val  
                                  1                      5                      10                      15

                         Phe Val Gly Gly Ala Val Ser Ser Pro Leu Val Ala Pro Asp Asn Gly  
                                  20                      25                      30

30                      Ser Ser Arg Thr Leu His Ser Arg Thr Glu Thr Thr Pro Ser Pro Ser  
                                  35                      40                      45

35                      Asn Asp Thr Gly Asn Gly His Pro Glu Tyr Ile Ala Tyr Ala Leu Val  
                                  50                      55                      60

                         Pro Val Phe Phe Ile Met Gly Leu Phe Gly Val Leu Ile Xaa Pro Xaa  
                                  65                      70                      75                      80

40                      Xaa Xaa Lys Lys Lys Gly Tyr Arg Cys Thr Thr Glu Ala Glu Gln Asp  
                                  85                      90                      95

                         Ile Glu Glu Glu Lys Gly Xaa  
                                  100

45

(2) INFORMATION FOR SEQ ID NO: 280:

50                      (i) SEQUENCE CHARACTERISTICS:  
                                  (A) LENGTH: 33 amino acids  
                                  (B) TYPE: amino acid  
                                  (D) TOPOLOGY: linear  
                                  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

55                      Met Pro Val Thr Leu Ser Ser Leu Gly Phe Trp Val Leu Leu Ser Leu  
                                  1                      5                      10                      15

60                      Leu Phe Pro Trp Arg Thr Asp Gln Gly Cys Gly Pro Ala Thr Cys Tyr  
                                  20                      25                      30

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 281:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

15

Met	Val	Leu	Gly	Leu	Leu	Leu	Leu	Xaa	Phe	Phe	Ser	Phe	Ser	Ser
1				5				10					15	

Ser	Pro	Ser	Pro	Ser	Ser	Ser	Leu	Leu	Leu	Ser	Ser	Phe	Phe	Phe
			20				25					30		

20

Gln	Ser	Leu	Ala	Leu	Ser	Pro	Arg	Leu	Glu	Xaa
		35					40			

25

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

30

Glu	Trp	Leu	Val	Phe	Thr	Phe	Leu	Leu	Val	Phe	Gly	Ser	Pro	Leu	Gly
1				5				10						15	

35

Lys	Gly	Pro	Leu	Xaa
			20	

40

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

45

Met	Ile	Arg	Ala	Leu	Ser	Leu	Phe	Leu	Leu	Ile	Phe	Asp	Ala	Ala	Leu
1				5				10						15	

50

Phe	Ser	Leu	Ser	Val	Phe	Val	Phe	Ile	Gly	His	Leu	Leu	Pro	Met	Pro
			20				25						30		

55

Lys	Gly	Thr	Gly	Leu	His	Ser	Cys	Ala	Lys	His	Leu	Ile	Lys	Ser	Leu
			35				40					45			

60

Lys	Glu	Asn	Val	Leu	Pro	Leu	Met	Asn	Tyr	Pro	Asp	Cys	Lys	Leu	Lys
		50					55							60	

Ile Asn Ile Ser Pro Xaa  
65 70

5

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

15 Met Gly Lys Leu Ile Arg Leu Ser Val Met Val Met Ser Val Arg Arg  
1 5 10 15

Leu Phe Ser Ile Tyr Trp Val Leu Ser Thr Val Pro Asp Ala Val Gly  
20 25 30

20 Ser Arg Gly Gly Met Glu Glu Glu Cys Ser Arg Gly Leu Cys Cys Val  
35 40 45

25 Ala Gly Gln His Lys Gln Ala Lys Gly Lys Arg Gln Ala Trp Asn Lys  
50 55 60

Gly Gly Glu Tyr Gln Cys Val Thr Tyr Cys Xaa  
65 70 75

30

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

40 Met Pro Ala Leu Val Thr Leu Leu Leu Leu Phe Pro Leu Leu Pro Leu  
1 5 10 15

Met Glu Ala Ser Cys His Val Met Arg Cys Pro Met Glu Arg Pro Thr  
20 25 30

45

Xaa

50

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

60 Glu Ala Pro Trp Gly Leu Leu Lys Leu Leu Leu Leu Ala Val Phe  
1 5 10 15

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 287:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

15

Met	Gln	Gln	Lys	Gln	Lys	Lys	Ala	Asn	Glu	Lys	Lys	Glu	Glu	Pro	Lys
1				5					10					15	

Xaa

20

(2) INFORMATION FOR SEQ ID NO: 288:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

30

Met	Gln	Arg	Lys	Val	Ser	Asp	Phe	Ile	Ile	His	Gln	Arg	Leu	Thr	Val
1				5					10					15	

35

Asn	Leu	Cys	Val	Ile	Ser	Phe	Phe	Phe	Phe	Leu	Pro	Ile	Cys	Ile	Phe
			20					25					30		

Ser	Leu	Ala	Lys	Lys	Xaa
			35		

40

(2) INFORMATION FOR SEQ ID NO: 289:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

50

Met	Ala	Leu	Leu	Ile	Ser	Ser	Leu	Ile	Trp	Ser	Xaa
1				5				10			

55

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

Met Gln Met Phe Thr Val Ser Leu Leu Leu Ser Leu Leu Leu Arg Ser  
 1 5 10 15  
 5 Thr Asp Gln Asn His Leu Gln Leu Leu Val Gly Arg Glu Asp His Tyr  
 20 25 30  
 10 Gly Gly Xaa  
 35

(2) INFORMATION FOR SEQ ID NO: 291:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

Met Ser Glu Ser Ala Cys Ile Leu Asn Asn Gln Lys Glu Leu Xaa  
 1 5 10 15  
 25

(2) INFORMATION FOR SEQ ID NO: 292:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

Met Asp Leu Asp Arg Val Lys Ala Glu Ala Thr Glu Asp Ile Thr Ser  
 1 5 10 15  
 Gly Val Leu Cys Leu Leu Phe Leu Arg Leu Pro Pro Asn Ser Cys Ile  
 20 25 30  
 40 Phe Pro Ser Ala Val Leu Gly Ser Thr Arg Thr Xaa  
 35 40  
 45

(2) INFORMATION FOR SEQ ID NO: 293:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu  
 1 5 10 15  
 Leu Leu Phe Ala Gly Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr  
 20 25 30  
 60 Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val

516

35 40 45

Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys  
50 55 60

5 Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu  
65 70 75 80

10 Ala Leu Phe Ala Ser Gly Leu Ile His Arg Val Cys Val Thr Thr Cys  
85 90 95

Phe Ile Phe Ser Met Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser Ser  
100 105 110

15 Thr Leu Tyr Gln Ala Ala Ala Pro Val Leu Thr Pro Ala Lys Val Thr  
115 120 125

Gly Lys Ser Lys Lys Arg Asn Xaa  
130 135

20

(2) INFORMATION FOR SEQ ID NO: 294:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

30 Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln Glu  
1 5 10 15

35 Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys Leu  
20 25 30

Arg Xaa

40

(2) INFORMATION FOR SEQ ID NO: 295:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 137 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

50 Met Arg Thr Pro Gly Pro Leu Pro Val Leu Leu Leu Leu Ala Gly  
1 5 10 15

Ala Pro Ala Ala Arg Pro Thr Pro Thr Cys Tyr Ser Arg Met Arg  
20 25 30

55 Ala Leu Ser Gln Glu Ile Thr Arg Asp Phe Asn Leu Leu Gln Val Ser  
35 40 45

60 Glu Pro Ser Glu Pro Cys Val Arg Tyr Leu Pro Arg Leu Tyr Leu Asp  
50 55 60

517

Ile His Asn Tyr Cys Val Leu Asp Lys Leu Arg Asp Phe Val Ala Ser  
 65 70 75 80

5 Pro Pro Cys Trp Lys Val Ala Gln Val Asp Ser Leu Lys Asp Lys Ala  
 85 90 95

Arg Lys Leu Tyr Thr Ile Met Asn Ser Phe Cys Arg Arg Asp Leu Val  
 100 105 110

10 Phe Leu Leu Asp Asp Cys Asn Ala Leu Glu Tyr Pro Ile Pro Val Thr  
 115 120 125

Thr Val Leu Pro Asp Arg Gln Arg Xaa  
 15 130 135

20 (2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Met Trp Leu Leu Lys Pro Ser Ala His Ser Pro Val His Xaa Leu Val  
 1 5 10 15

30 Leu Leu Phe Pro Arg Gly Trp Ser Gln Pro Gly Thr His Lys Arg Gln  
 20 25 30

Ile Leu Val Asn Xaa Ala Ser Leu Pro Gly Gly Cys Leu Leu Pro Trp  
 35 40 45

Ile Trp Ser Gly Ala Ala Leu Arg Phe Xaa  
 50 55

40 (2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met Ser Arg Arg Ala Glu Ala Ser Ile Phe Val Leu Pro Lys Thr Leu  
 50 1 5 10 15

Leu Phe Val Leu Phe Pro Ala Phe Pro Ser Pro Ala Val Gly Cys Pro  
 20 25 30

55 Val Pro Xaa  
 35

60 (2) INFORMATION FOR SEQ ID NO: 298:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Ser Cys Tyr Ile Thr Pro Trp Ser Lys Ile Gln Ser Phe Ser Leu Ser  
 1 5 10 15  
 Leu Phe Gln Phe Ile Leu Gln Glu Val Asn Ile Thr Leu Pro Glu Asn  
 20 25 30  
 Ser Val Trp Tyr Glu Arg Tyr Lys Phe Asp Ile Pro Val Phe His Leu  
 35 40 45  
 Asn Gly Gln Phe Leu Met Met His Arg Val Asn Thr Ser Lys Leu Glu  
 50 55 60  
 Lys Gln Leu Leu Lys Leu Glu Gln Gln Ser Thr Gly Xaa Xaa  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO: 299:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

Met Phe Val Leu Phe Ser Leu Pro Lys Tyr Ala Gly Leu Arg Leu Pro  
 1 5 10 15  
 Ile Pro Gly Leu Ser Ala Leu Leu Val Phe Leu Leu Ser Leu Phe Ser  
 20 25 30  
 Arg Arg Ala Gln Val Glu Leu Thr Thr Gly Arg Glu Thr Leu Pro Lys  
 35 40 45  
 Asn Leu Gln Gly Tyr Phe Pro Glu Phe Gly Phe Gln Val Gln Asn Phe  
 50 55 60  
 Leu Ser Cys Lys Ile Tyr Ala Ala Ser Gln Lys Gln Pro Leu Pro Pro  
 65 70 75 80  
 Leu Tyr Gln Leu Arg Phe Tyr Leu Lys His Met Gly Leu Pro Xaa  
 85 90 95

## (2) INFORMATION FOR SEQ ID NO: 300:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

519

Met Ser Ser His Trp Thr Leu Lys Ile Leu Leu Val Pro Leu Phe Tyr  
 1 5 10 15

5 Leu Ser Leu Glu Phe Pro Ser Gly Phe Val Leu Cys Leu Ala Asn Asp  
 20 25 30

Leu Gly Tyr His Phe Ser Ser Arg Val Arg Ser Xaa  
 35 40

10

(2) INFORMATION FOR SEQ ID NO: 301:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

20 Met Leu Val Val Asn Ile Asn Leu Val Phe Leu Leu Phe Phe Ile Phe  
 1 5 10 15

25 Leu Cys Tyr Leu Asp Ala Cys Ile Asn Val Phe Cys Phe Tyr Xaa  
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 302:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

35 Met Pro Val Leu Pro Gly Arg Thr Thr Ala Leu Leu Ser Leu Thr Leu  
 1 5 10 15

40 Ala Phe Ala Val Pro Cys Ser Gly Val Glu Ala Gly Pro Cys Val Pro  
 20 25 30

Arg Ser His Gly Cys Ser Ser Trp Glu Ala Ser Val Cys Val Thr Ser  
 35 40 45

45 Ser Thr Pro Gly Gly Ser Trp Arg Ala Arg Ala Leu Phe Pro Ser Ala  
 50 55 60

50 Ala Trp His Arg Xaa Ala Ala Trp Asp Ser Pro Trp Thr Gln Thr Gly  
 65 70 75 80

Asp Phe Ala Arg Gly Ala Met Gly Gly Ala Gly Ala Leu Pro Gly Gly  
 85 90 95

55 Cys Val Cys Ile Ser Gly Arg Pro Arg Ala Gln Lys Leu Pro Ala Leu  
 100 105 110

Xaa

60

520

## (2) INFORMATION FOR SEQ ID NO: 303:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

5  
10 Thr His Ile His Thr His Ile Ile Ile Cys Ser Ser Val Xaa  
1 5 10

## 15 (2) INFORMATION FOR SEQ ID NO: 304:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

20 Met Glu Asn Phe Phe Phe Ser Phe Tyr Leu Phe Leu Ile Thr Leu Ile  
1 5 10 15

25 Pro Asn Gly Arg Thr Leu Ser Thr Thr Ala Asp His Cys Lys Ile Pro  
20 25 30

30 Cys Ile Xaa  
35

## 35 (2) INFORMATION FOR SEQ ID NO: 305:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

40 Met Glu Leu Trp Glu Leu Ala Leu Cys Leu Leu Val Ala Leu Ser Ala  
1 5 10 15

45 His Met Phe Thr Val Gln Leu Leu Ala Asp Leu Gly Phe Leu Phe Gly  
20 25 30

50 Gly Phe Xaa  
35

## (2) INFORMATION FOR SEQ ID NO: 306:

## 55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

60

521

Met Gly Ala Gly Ile Leu Ala Leu Leu Leu Pro Leu Glu Ser Val Leu  
 1 5 10 15  
 Thr Cys Ser Trp Ile Ser Val Ser Thr Ser Glu Arg Gln Leu Trp Gln  
 5 20 25 30  
 Ser Ser Gln Lys Ala Thr Ile Leu Ser Leu Lys Leu Asp Ser Cys Phe  
 35 40 45  
 Cys Gly His Ser Gly Leu Lys Gly Lys Asn Glu Asp Thr Asp Ser Ser  
 10 50 55 60  
 Val Pro Ile Ile Pro Ser Lys Thr His Thr His Leu Gly Lys His Leu  
 15 65 70 75 80  
 Ile Xaa

20

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 amino acids  
 (B) TYPE: amino acid  
 (C) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

25

Met Phe Tyr Phe Val Leu Phe Ile Tyr Ser Ser Ser Glu Thr Trp Ser  
 30 1 5 10 15  
 Gly Ser Val Ala Gln Asp Gly Val His Gly Val Ile Ile Gly His Cys  
 20 25 30  
 Ser Val Glu Leu Pro Gly Ser Gly Asp Pro Pro Ala Ser Ala Xaa Leu  
 35 35 40 45  
 Val Ala Gly Thr Ile Gly Thr Cys Pro Thr Met Pro Gly Phe Val Tyr  
 50 55 60  
 Phe Leu Asn Asp Val Xaa Asn Xaa  
 65 70

45

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

50

Met Asp Ser Thr Leu Arg Gln Gly Arg Xaa Leu Leu Thr Leu Val Pro  
 55 1 5 10 15  
 Ala Ser Leu Phe Ser Leu Thr Leu Gly Gly Pro Gly Pro Trp Lys Asp  
 20 25 30  
 Pro Xaa

60

## 5 (2) INFORMATION FOR SEQ ID NO: 309:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

15 Met Gln Val Val Gly Ser Trp Pro Gly Arg Val Gly Val Val Gly Leu  
 1 5 10 15  
 Ala Phe Ser Leu Val Ile Pro Pro Pro Ala Ile Cys Ile Ala Gly Pro  
 20 25 30  
 20 Ala Pro Gly Leu Gly Gly Gly Glu Arg Gln Gln Lys Gly Leu Gly Arg  
 35 40 45  
 Gly Gly Gly Gly Leu Arg Asn Cys Pro Gly Arg Val Gly Met Ala Ala  
 50 55 60  
 25 Glu Pro Gly Ala Leu Leu Cys Leu Thr Ser Arg Asp Gly Ser Leu Leu  
 65 70 75 80  
 Leu Ser Cys Val Arg Pro His His Val Ile Lys Pro Lys Gly Thr Ala  
 85 90 95  
 30 Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Xaa Xaa  
 100 105 110  
 35 Gly Gly Xaa  
 115

## 40 (2) INFORMATION FOR SEQ ID NO: 310:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

50 Met Asp Leu Pro Gln Phe Ile Tyr Leu Phe Ile Phe Cys Phe Cys Cys  
 1 5 10 15  
 Leu Ala Ile Val Asn Asn Ala Ser Ile Asn Ile His Ile Gln Val Ser  
 20 25 30  
 Met Trp Leu Tyr Val Phe Ile Ser Leu Gly Tyr Leu His Gly Ser Arg  
 35 40 45  
 55 Ile Leu Gly His Asn Ile Ile Leu Cys Leu Thr Ser Gln Arg Ile Ala  
 50 55 60  
 60 Lys Arg Phe Phe Ile Val Ala Ala Ser Phe Thr Phe Pro Pro Ala Met  
 65 70 75 80



Tyr Lys Asp Phe Tyr Phe Ser Ile Ser Leu His Leu Pro Thr Leu Leu  
                     85                    90                    95

5 Phe Xaa Xaa Xaa Phe Val Phe Ser Leu Leu Pro Pro  
                     100                    105

10 (2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Met Cys Ser Pro Ser Leu Ser Ser Ser Pro Pro Pro Leu Leu Gln Val  
     1                    5                    10                    15

20 Phe Phe Phe Phe Phe Phe Ser Pro His Trp Ala Ala Lys Val Val Pro  
                     20                    25                    30

25 Gln Trp Lys Xaa Arg His Pro Gln Val Ser Ser Gln Leu Leu Leu Cys  
                     35                    40                    45

Phe Leu Arg Val Asn Cys Gln Phe Leu Phe Leu Gln Glu Ile Leu Phe  
     50                    55                    60

30 Xaa  
     65

35 (2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Met Cys Leu Ser Arg Trp Lys Ile Phe Tyr Thr Leu Leu Ile Leu Phe  
     1                    5                    10                    15

45 Xaa Xaa Phe Ser Ile Thr Ser Glu Xaa Glu Thr Phe Tyr Met Ile Ile  
                     20                    25                    30

50 Ile His His Asn Pro Thr Gln Ile Thr Ala Ser Cys Ser Phe Thr Phe  
                     35                    40                    45

Leu Xaa  
     50

55

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 293 amino acids

524

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

5 Met Glu Arg Pro Asp Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser  
 1 5 10 15  
 Leu Pro Ala Gly Ser Gly Asn Ala Leu Ala Ala Ser Leu Asn His Tyr  
 20 25 30  
 10 Ala Gly Tyr Xaa Gln Val Thr Asn Glu Asp Leu Leu Thr Asn Cys Thr  
 35 40 45  
 Leu Leu Leu Cys Arg Arg Leu Leu Ser Pro Met Asn Leu Leu Ser Leu  
 15 50 55 60  
 His Thr Ala Ser Gly Leu Arg Leu Phe Ser Val Leu Ser Leu Ala Trp  
 65 70 75 80  
 20 Gly Phe Ile Ala Asp Val Asp Leu Glu Ser Glu Lys Tyr Arg Arg Leu  
 85 90 95  
 Gly Glu Met Arg Phe Thr Leu Gly Thr Phe Leu Arg Leu Ala Ala Leu  
 100 105 110  
 25 Arg Thr Tyr Arg Gly Arg Leu Ala Tyr Leu Pro Val Gly Arg Val Gly  
 115 120 125  
 Ser Lys Thr Pro Ala Ser Pro Val Val Val Gln Gln Gly Pro Val Asp  
 130 135 140  
 Ala His Leu Val Pro Leu Glu Glu Pro Val Pro Ser His Trp Thr Val  
 145 150 155 160  
 35 Val Pro Asp Glu Asp Phe Val Leu Val Leu Ala Leu Leu His Ser His  
 165 170 175  
 Leu Gly Ser Glu Met Phe Ala Ala Pro Met Gly Arg Cys Ala Ala Gly  
 180 185 190  
 40 Val Met His Leu Phe Tyr Val Arg Ala Gly Val Ser Arg Ala Met Leu  
 195 200 205  
 Leu Arg Leu Phe Leu Ala Met Glu Lys Gly Arg His Met Glu Tyr Glu  
 210 215 220  
 Cys Pro Tyr Leu Val Tyr Val Pro Val Val Ala Phe Arg Leu Glu Pro  
 225 230 235 240  
 50 Lys Asp Gly Lys Gly Val Phe Ala Val Asp Gly Glu Leu Met Val Ser  
 245 250 255  
 Glu Ala Val Gln Gly Gln Val His Pro Asn Tyr Phe Trp Met Val Ser  
 260 265 270  
 55 Gly Cys Val Glu Pro Pro Pro Ser Trp Lys Pro Gln Gln Met Pro Pro  
 275 280 285  
 Pro Glu Glu Pro Leu  
 290  
 60

## (2) INFORMATION FOR SEQ ID NO: 314:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Pro Leu Glu Gly Phe Cys Leu Val Leu Asp Ile Gly Phe Leu Leu  
 1 5 10 15

15

Val Met Leu Ile Ser Leu Ala Ser Glu Cys Phe Thr Thr Cys Leu Asp  
 20 25 30

20

Ser Phe Ser Thr Thr Glu Pro Gly Cys Lys Phe Tyr Lys Leu Leu His  
 35 40 45

Ser Val Ser Leu Leu Asn Ile Asn Phe Asn Val Lys Ser Leu Leu Cys  
 50 55 60

25

Ser His Ile Xaa  
 65

## (2) INFORMATION FOR SEQ ID NO: 315:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Met Pro Leu Gln Leu Ser Gly Gln Tyr Trp Ile Ser Leu Leu Val Phe  
 1 5 10 15

40

Leu Ser Leu Gln Pro Phe Pro Gln Ala Ala Ile Pro Cys Ala Leu Thr  
 20 25 30

Asp Val Gly Gly Ser Cys Val Ile Cys His Ile Leu Leu Asn Cys Leu  
 35 40 45

45

Cys Ile Leu Phe Thr Leu Thr Ala Pro Ser Leu Ser His Val Leu Leu  
 50 55 60

50

Ile Lys Met Ser Leu Ser Val Cys Tyr Glu Pro Gly Ala Asp Leu Ser  
 65 70 75 80

Asp Arg Ala Ala Thr Gly Asn Lys Lys Leu Thr Arg Ser Thr Cys Leu  
 85 90 95

55

Leu Met His Ser Asn Lys Leu Cys Xaa  
 100 105

60

## (2) INFORMATION FOR SEQ ID NO: 316:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Trp Gly Cys Ser Gly Leu Gly His Arg Thr Val Ser Phe Leu Leu  
 1 5 10 15  
 Leu Leu Pro Cys Ser Phe Pro Arg Pro Cys Xaa Leu Phe Gly Leu Ile  
 20 25 30  
 Pro Ile Ser Arg Pro Cys Lys Val Glu Ala Pro Arg Leu Ser Val Pro  
 35 40 45  
 Xaa Leu Ser Cys Ala Ser His Pro Tyr Cys Asn Cys Pro Met Ser Thr  
 50 55 60  
 Ser Cys Pro Leu Pro Arg Xaa  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 317:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Leu Asn Val Leu Ser Lys Val Gln Gln Leu Val Ser Xaa Leu Gly  
 1 5 10 15  
 Leu Val Thr Phe Leu Leu Asn His Ser Ala Ala Gly Gly Ser Pro Gln  
 20 25 30  
 His Arg Trp Leu Leu Leu Xaa  
 35

## (2) INFORMATION FOR SEQ ID NO: 318:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Lys Ala Ile Ala Arg Ala Cys Leu Leu Leu Ser Leu Leu Val Leu  
 1 5 10 15  
 Pro His Val Val Ser Glu His Leu Phe Trp His His Asn Pro Arg His  
 20 25 30  
 Pro Val Ile Trp Pro Phe Pro Pro Phe His Leu Ile Ser Cys Ser Val  
 35 40 45

527

Ser Ala Ser Thr Trp His Leu Gly Glu Xaa Leu Leu Leu Leu Val Pro  
 50 55 60

Ile Ala Pro Ser Val Trp Ser Xaa  
 65 70

5

10

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Glu Gln Gly Gly Gly Pro Arg Leu Leu Leu Ile Pro Gly Leu  
 1 5 10 15

20

Leu His Asn Thr Tyr Leu Ala Arg Pro Gly Asp Phe Pro Ala Gln Gly  
 20 25 30

Thr Thr Glu Asn Thr Glu Cys Gln Gly Ser Pro Ser Pro Ile Ser His  
 35 40 45

25

Leu Gly Lys Val Arg Ser Leu Asp Ser Asn Thr Gln Ile Xaa  
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Met Pro Leu Leu Phe Phe Ser Val Ser Thr Leu Phe Ser Gly Ser Val  
 1 5 10 15

40

Thr Leu Gln Gln Arg Gly Met Phe Leu Pro Trp Thr Gly Thr Gly Glu  
 20 25 30

45

Gln Val Leu Ala Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu Met  
 35 40 45

Asn Val Gln Ser Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly Leu  
 50 55 60

50

Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser Ser  
 65 70 75 80

55

Ala Leu Val Ser Ile Asn Gln Thr Ile Pro Asn Glu Arg Thr Met Gln  
 85 90 95

Leu Leu Gly Gln Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg Val  
 100 105 110

60

Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile Asn

528

115                      120                      125  
 Asn Tyr Asp Met Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp Asp  
 130                      135                      140  
 5 Ser Lys Glu Val Glu Ser Phe Gln Gln Leu Leu Asn Ala Arg Thr Gln  
 145                      150                      155                      160  
 10 Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro Phe Gly Gly Leu Val Ala  
 165                      170                      175  
 Phe Val Lys Glu Ala Glu Ala Leu Ile Glu Arg Gly Gln Ala Glu Arg  
 180                      185                      190  
 15 Leu Arg Gly Glu Glu Ala Arg Val Thr Gln Leu Ile Arg Gly Phe Gly  
 195                      200                      205  
 Ser Ser Trp Lys Ser Ser Val Glu Ser Leu Ser Gln Asp Val Met Arg  
 210                      215                      220  
 20 Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser Ile Ile Gln Gly Ala Leu  
 225                      230                      235                      240  
 25 Thr Gln Leu Ile Gln Leu Tyr His Arg Phe His Arg Val Leu Ser Gln  
 245                      250                      255  
 Pro Gln Leu Arg Ala Leu Pro Ala Arg Ala Glu Leu Ile Asn Ile His  
 260                      265                      270  
 30 His Leu Met Val Glu Leu Lys Lys His Lys Pro Asn Phe Xaa  
 275                      280                      285

35 (2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Phe Arg Ala Leu Arg Asp Leu Leu Thr His Tyr Pro Gln Gln Ile  
 1                      5                      10                      15  
 45 Leu Leu Gln Val Leu Val Val Met Tyr Gln Val Leu Gln Val Trp Glu  
 20                      25                      30  
 50 Leu Pro Trp Pro Glu Leu Ile His Leu Gln Gly Ile Val Pro Thr Asp  
 35                      40                      45  
 Gln Leu His Leu Lys Gln Xaa  
 50                      55

55

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

60

529

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

5 Asp Phe Val Pro Val Leu Val Phe Val Leu Ile Lys Ala Asn Pro Pro  
 1 5 10 15  
 Cys Leu Leu Ser Thr Val Gln Tyr Ile Ser Ser Phe Tyr Ala Ser Cys  
 20 25 30  
 10 Leu Ser Gly Glu Glu Ser Tyr Trp Trp Met Gln Phe Thr Ala Ala Val  
 35 40 45  
 15 Glu Phe Ile Lys Thr Ile Asp Asp Arg Lys Xaa  
 50 55

(2) INFORMATION FOR SEQ ID NO: 323:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Met His Pro Ala Arg Lys Leu Leu Ser Leu Leu Phe Leu Ile Leu Met  
 1 5 10 15  
 30 Gly Thr Glu Leu Thr Gln Asp Ser Ala Ala Pro Asp Ser Leu Leu Arg  
 20 25 30  
 Ser Ser Lys Gly Ser Thr Arg Gly Ser Leu Ala Ala Ile Val Ile Trp  
 35 40 45  
 35 Arg Gly Lys Ser Glu Ser Arg Ile Ala Lys Thr Pro Gly Ile Phe Arg  
 50 55 60  
 40 Gly Gly Gly Thr Leu Val Leu Pro Pro Thr His Thr Pro Glu Trp Leu  
 65 70 75 80  
 Ile Leu Pro Leu Gly Ile Thr Leu Pro Leu Gly Ala Pro Glu Thr Gly  
 85 90 95  
 45 Gly Gly Asp Cys Ala Ala Glu Thr Trp Lys Gly Ser Gln Arg Ala Gly  
 100 105 110  
 Gln Leu Cys Ala Leu Leu Ala Xaa  
 115 120  
 50

(2) INFORMATION FOR SEQ ID NO: 324:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

530

Phe Phe Leu Val Val Phe Ser Leu Ser Phe Xaa Pro Ser Val Leu Thr  
 1 5 10 15

5 Ser Pro Val His Xaa Pro His Cys Cys Gln Xaa Asp Xaa Ile Leu Phe  
 20 25 30

Lys Asn Thr Leu Xaa Xaa Phe Xaa Ala Lys Tyr Xaa  
 35 40

10

(2) INFORMATION FOR SEQ ID NO: 325:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

20 Met Phe Ser Arg Thr Ser Asn Phe Trp Thr Phe Phe Phe Gln Phe Leu  
 1 5 10 15

Ile Phe Lys Val Phe Leu Val Leu Lys Asn Xaa Phe Thr Ser Gln Lys  
 20 25 30

25

Ile Xaa Xaa Ile Xaa Xaa Glu Lys Pro Lys Lys Lys Lys Xaa Arg Gly  
 35 40 45

30 Gly Arg Ala Pro Ser Pro Gln Gly Gly Pro Xaa  
 50 55

35

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Gly Leu Leu Ile Phe Met Leu Leu Ile Gly Ile His Ser Gln Cys  
 1 5 10 15

45

Ser Xaa

50

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Val Leu Phe Cys Phe Val Leu Phe Cys Phe Val Phe Glu Met Asp  
 1 5 10 15

60



531

Ser Ser Ser Val Thr Gln Ala Gly Val Gln Trp Cys Asp Leu Gly Ser  
 20 25 30

5 Leu Gln Ala Pro Pro Pro Gly Phe Ser Pro Phe Ser Cys Leu Ser Leu  
 35 40 45

Pro Ser Ser Trp Asp Tyr Arg Arg Pro Pro Pro Arg Pro Ala Asn Phe  
 50 55 60

10 Leu Tyr Phe Leu Val Glu Thr Gly Phe His His Val Ser Gln Asp Gly  
 65 70 75 80

Leu Asp Leu Leu Thr Ser Xaa  
 85

15

(2) INFORMATION FOR SEQ ID NO: 328:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 538 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

25 Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile Leu Leu Val Phe  
 1 5 10 15

30 Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala Pro Gly Pro Thr  
 20 25 30

Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp Ala Arg Lys Asn  
 35 40 45

35 His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro Asn His Cys Asp  
 50 55 60

Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu Ile Glu Ala Asn  
 65 70 75 80

40 Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His Met Glu Met Ser  
 85 90 95

45 Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe  
 100 105 110

Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val  
 115 120 125

50 Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala  
 130 135 140

His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys  
 145 150 155 160

55 Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe  
 165 170 175

60 Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg  
 180 185 190

532

Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile  
 195 200 205

5 Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys  
 210 215 220

Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile  
 225 230 235 240

10 Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val  
 245 250 255

15 Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile  
 260 265 270

Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met  
 275 280 285

20 Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu  
 290 295 300

Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu  
 305 310 315 320

25 Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val  
 325 330 335

30 Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln  
 340 345 350

Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu  
 355 360 365

35 Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr  
 370 375 380

Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser  
 385 390 395 400

40 Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His  
 405 410 415

45 Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu  
 420 425 430

Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr  
 435 440 445

50 Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala  
 450 455 460

Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu  
 465 470 475 480

55 Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser  
 485 490 495

60 Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe  
 500 505 510

533

Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe  
 515 520 525

5 Ile Asn Asp Asn Ala Ala Ser Gly Ile Xaa  
 530 535

10 (2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Gly Ile Ala Leu Ala Val Leu Gly Trp Leu Ala Val Met Leu Cys  
 1 5 10 15

20 Cys Ala Leu Pro Met Trp Arg Val Thr Ala Phe Ile Gly Ser Asn Ile  
 20 25 30

25 Val Thr Ser Gln Thr Ile Trp Glu Gly Leu Trp Met Asn Cys Val Val  
 35 40 45

Gln Ser Thr Gly Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala  
 50 55 60

30 Leu Pro Gln Asp Leu Gln Ala Ala Arg Ala Leu Val Ile Ile Ser Ile  
 65 70 75 80

Ile Val Ala Ala Leu Gly Val Leu Leu Ser Val Val Gly Gly Lys Cys  
 85 90 95

35 Thr Asn Cys Leu Glu Asp Glu Ser Ala Lys Ala Lys Thr Met Ile Val  
 100 105 110

40 Ala Gly Val Val Phe Leu Leu Ala Gly Leu Met Val Ile Val Pro Val  
 115 120 125

Ser Trp Thr Ala His Asn Ile Ile Gln Asp Phe Tyr Asn Pro Leu Val  
 130 135 140

45 Ala Ser Gly Gln Lys Arg Glu Met Gly Ala Ser Leu Tyr Val Gly Trp  
 145 150 155 160

Ala Ala Ser Gly Leu Leu Leu Gly Gly Gly Leu Leu Cys Cys Asn  
 165 170 175

50 Cys Pro Pro Arg Thr Asp Lys Pro Tyr Ser Ala Lys Tyr Ser Ala Ala  
 180 185 190

55 Arg Ser Ala Ala Ala Ser Asn Tyr Val Xaa  
 195 200

60 (2) INFORMATION FOR SEQ ID NO: 330:

534

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Ala Thr Val Thr Ala Thr Thr Lys Val Pro Glu Ile Arg Asp Val  
 1 5 10 15

10 Thr Arg Ile Glu Arg Ile Gly Ala His Ser His Ile Arg Gly Leu Gly  
 20 25 30

Leu Asp Asp Ala Leu Glu Pro Arg Gln Ala Ser Gln Gly Met Val Gly  
 35 40 45

15 Gln Leu Ala Ala Arg Arg Ala Ala Gly Val Val Leu Glu Met Ile Arg  
 50 55 60

Glu Gly Lys Ile Ala Gly Arg Ala Val Leu Ile Ala Gly Gln Pro Gly  
 20 65 70 75 80

Thr Gly Lys Thr Ala Ile Ala Met Gly Met Ala Gln Ala Leu Gly Pro  
 85 90 95

25 Asp Thr Pro Phe Thr Ala Ile Ala Gly Ser Glu Ile Phe Ser Leu Glu  
 100 105 110

Met Ser Lys Thr Glu Ala Leu Thr Gln Ala Phe Arg Arg Ser Ile Gly  
 115 120 125

30 Val Arg Ile Lys Glu Glu Thr Glu Ile Ile Glu Gly Glu Val Val Glu  
 130 135 140

Ile Gln Ile Asp Arg Pro Ala Thr Gly Thr Gly Ser Lys Val Gly Lys  
 35 145 150 155 160

Leu Thr Leu Lys Thr Thr Glu Met Glu Thr Ile Tyr Asp Leu Gly Thr  
 165 170 175

40 Lys Met Ile Xaa Ser Leu Thr Lys Asp Lys Val Gln Ala Gly Asp Val  
 180 185 190

Ile Thr Ile Asp Lys Ala Thr Gly Lys Ile Ser Lys Leu Gly Arg Ser  
 195 200 205

45 Phe Thr Arg Ala Arg Glu Leu Arg Arg Tyr Gly Leu Pro Asp Gln Val  
 210 215 220

Arg Ala Val Pro Arg Trp Gly Ala Pro Glu Thr Gln Gly Gly Gly Ala  
 50 225 230 235 240

His Arg Val Pro Ala Arg Asp Arg Arg His Gln Leu Ser His Pro Gly  
 245 250 255

55 Leu Pro Gly Ala Leu Leu Arg  
 260

## 60 (2) INFORMATION FOR SEQ ID NO: 331:

535

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

5 Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu Asn Ile Leu Leu Gly  
 1 5 10 15  
 10 Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys Glu Lys Gly  
 20 25 30  
 15 Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr  
 35 40 45  
 Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg Thr Tyr Asn  
 50 55 60  
 20 Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val Ser Gln Arg Leu Tyr  
 65 70 75 80  
 Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser Met Ala  
 85 90 95  
 25 Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln Thr Gly Asp  
 100 105 110  
 30 Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn Ser Ile Tyr Glu Leu  
 115 120 125  
 Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val Leu Glu Tyr Ala Thr  
 130 135 140  
 35 Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr Ser Gln Ala Gly Phe  
 145 150 155 160  
 Ser Gly Glu Asp Arg Leu Glu Gln Ala Lys Leu Phe Cys Arg Thr Leu  
 165 170 175  
 40 Glu Asp Ile Leu Ala Asp Ala Pro Glu Ser Gln Asn Asn Cys Arg Leu  
 180 185 190  
 45 Ile Ala Tyr Gln Glu Pro Ala Asp Asp Ser Ser Phe Ser Leu Ser Gln  
 195 200 205  
 Glu Val Leu Arg His Leu Arg Gln Glu Glu Lys Glu Glu Val Thr Val  
 210 215 220  
 50 Gly Ser Leu Lys Thr Ser Ala Val Pro Ser Thr Ser Thr Met Ser Gln  
 225 230 235 240  
 Glu Pro Glu Leu Leu Ile Ser Gly Met Glu Lys Pro Leu Pro Leu Arg  
 245 250 255  
 55 Thr Asp Phe Ser  
 260  
 60

## (2) INFORMATION FOR SEQ ID NO: 332:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

5 Met Thr Pro Gln Lys Pro Ala Leu Ala Val Leu Leu Leu Glu Val Pro  
1 5 10 15

Leu Leu Leu Thr Leu Ser Val Leu Lys Lys Arg Cys Leu Val Thr Cys  
20 25 30

15 Glu Pro Thr Ser Arg Phe Val Ser Cys Asp Leu Pro Leu Ser Val Xaa  
35 40 45

20

## (2) INFORMATION FOR SEQ ID NO: 333:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

25 Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu  
1 5 10 15

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala  
35 20 25 30

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser  
35 40 45

40 Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr  
50 55 60

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile  
65 70 75 80

45 Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe  
85 90 95

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg  
50 100 105 110

Gly Leu Ser Gly Lys Tyr Gln Thr Ser Ser Lys Leu Phe Gln Asn Cys  
115 120 125

55 Ser Glu Leu Phe Lys Thr Gln Thr Phe Ser Gly Asp Phe Met His Arg  
130 135 140

Leu Pro Leu Leu Gly Glu Lys Gln Glu Ala Lys Glu Asn Gly Thr Asn  
145 150 155 160

60

537

Leu Thr Phe Ile Gly Asp Lys Thr Ala Met His Glu Pro Leu Gln Thr  
 165 170 175

5 Trp Gln Asp Ala Pro Tyr Ile Phe Ile Val His Ile Gly Ile Ser Ser  
 180 185 190

Ser Lys Glu Ser Ser Lys Glu Asn Ser Leu Ser Asn Leu Phe Thr Met  
 195 200 205

10 Thr Val Glu Val Lys Gly Pro Tyr Glu Tyr Leu Thr Leu Glu Asp Tyr  
 210 215 220

Pro Leu Met Ile Phe Phe Met Val Met Cys Ile Val Tyr Val Leu Phe  
 225 230 235 240

15 Gly Val Leu Trp Leu Ala Trp Ser Ala Cys Tyr Trp Arg Asp Leu Leu  
 245 250 255

20 Arg Ile Gln Phe Trp Ile Gly Ala Val Ile Phe Leu Gly Met Leu Glu  
 260 265 270

Lys Ala Val Phe Tyr Ala Glu Phe Gln Asn Ile Arg Tyr Lys Gly Xaa  
 275 280 285

25 Ser Val Gln Gly Ala Leu Ile Leu Ala Glu Leu Leu Ser Ala Val Lys  
 290 295 300

Arg Ser Leu Ala Arg Thr Leu Val Ile Ile Val Ser Leu Gly Tyr Gly  
 305 310 315 320

30 Ile Val Lys Pro Arg Leu Glu Ser Leu Phe Ile Arg Leu Xaa  
 325 330

35 (2) INFORMATION FOR SEQ ID NO: 334:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 200 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

40 Met Val Leu Xaa Val Val Thr Leu Gly Leu Ala Leu Phe Thr Leu Cys  
 1 5 10 15

Gly Lys Phe Lys Arg Trp Lys Leu Asn Gly Ala Phe Leu Leu Ile Thr  
 20 25 30

50 Ala Phe Leu Ser Val Leu Ile Trp Val Ala Trp Met Thr Met Tyr Leu  
 35 40 45

Phe Gly Asn Val Lys Leu Gln Gln Gly Asp Ala Trp Asn Asp Pro Thr  
 50 55 60

55 Leu Ala Ile Thr Leu Ala Ala Ser Ala Gly Ser Ser Ser Ser Ser Thr  
 65 70 75 80

60 Pro Ser Leu Arg Ser Thr Ala Pro Phe Cys Gln Pro Cys Arg Arg Thr  
 85 90 95

538

Arg Pro Thr Thr Ser Thr Arg Arg Ser Pro Gly Cys Gly Arg Arg Pro  
 100 105 110

5 Ser Arg Arg Thr Cys Ser Cys Arg Gly Pro Ile Trp Arg Thr Arg Pro  
 115 120 125

Ser Pro Trp Met Asn Thr Met Gln Leu Ser Glu Gln Gln Asp Phe Pro  
 130 135 140

10 Thr Ala Ala Trp Glu Lys Asp Pro Val Ala Ala Trp Gly Lys Asp Pro  
 145 150 155 160

15 Ala Leu Arg Leu Glu Ala Thr Cys Ile Ser Gln Leu Arg Trp Pro Ser  
 165 170 175

Cys Ser Thr Val Gly Pro Ser Gln Leu Leu Arg Gln Val Thr Gln Glu  
 180 185 190

20 Xaa Thr Phe Gly Glu Arg Leu Xaa  
 195 200

25 (2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met Leu Leu His His Gln Leu Leu Ile Val Thr Leu His Leu Val Leu  
 1 5 10 15

35 Leu Leu Ala Thr Leu Leu Val Xaa  
 20

40 (2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 143 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala Leu  
 1 5 10 15

Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val Leu Gln  
 20 25 30

55 Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser Asp Trp Leu  
 35 40 45

Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser Lys Ile Asn Glu  
 50 55 60

60



539

Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe Gln Ile Asn Ser His  
 65 70 75 80  
 Tyr Trp Cys Asn Xaa Tyr Lys Ser Tyr Ser Glu Asn Leu Cys His Val  
 5 85 90 95  
 Asp Cys Gln Asp Leu Leu Asn Pro Asn Leu Leu Ala Gly Ile His Cys  
 100 105 110  
 Ala Lys Arg Ile Val Ser Gly Ala Arg Gly Met Asn Asn Trp Val Arg  
 115 120 125  
 Met Glu Xaa Cys Thr Val Gln Ala Gly His Ser Ser Thr Gly Xaa  
 130 135 140  
 15

(2) INFORMATION FOR SEQ ID NO: 337:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 95 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:  
 25 Met Leu Val Ile Ala Gly Gly Ile Leu Ala Ala Leu Leu Leu Ile  
 1 5 10 15  
 Val Val Val Leu Cys Leu Tyr Phe Lys Ile His Asn Ala Leu Lys Ala  
 30 20 25 30  
 Ala Lys Glu Pro Glu Ala Val Ala Val Lys Asn His Asn Pro Asp Lys  
 35 35 40 45  
 Val Trp Trp Ala Lys Asn Ser Gln Ala Lys Thr Ile Ala Thr Glu Ser  
 50 55 60  
 Cys Pro Ala Leu Gln Cys Cys Glu Gly Tyr Arg Met Cys Ala Ser Phe  
 65 70 75 80  
 40 Asp Ser Leu Pro Pro Cys Cys Cys Asp Ile Asn Glu Gly Leu Xaa  
 85 90 95  
 45

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:  
 50 Met Leu Leu Lys Ser Asn Ile Leu Met Leu Asn Leu Phe Ala Ala Asn  
 55 1 5 10 15  
 Val Gly Ala Asn Phe Ala Leu Thr Val Glu Lys Ile Gly Met Ile Leu  
 20 25 30  
 60 Leu Asn Val Ser Gly Xaa

540

35

## 5 (2) INFORMATION FOR SEQ ID NO: 339:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala  
 1 5 10 15  
 Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Pro  
 20 25 30  
 Leu Leu His Asp Gly Glu Xaa  
 35

## 25 (2) INFORMATION FOR SEQ ID NO: 340:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Ser Asp Pro Leu Ala Ser Ala Ser Gln Asn Ala Gly Ile Val Ser Val  
 1 5 10 15  
 Gly Leu Cys Thr Arg Pro Gly Pro Gln Phe Lys Asn Ala Gln Pro Pro  
 20 25 30  
 Phe Pro Xaa Gln Lys Ala Pro Arg Cys Leu Trp Glu Asn Gln Pro Pro  
 35 40 45  
 Pro Trp Arg Lys Ala Trp Asp Leu Pro Ser His Leu Gly Arg Arg Gly  
 50 55 60  
 Ile Cys Gly Lys Ser Phe Xaa  
 65 70

## 50 (2) INFORMATION FOR SEQ ID NO: 341:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Tyr Val Met Ile Phe Lys Lys Glu Phe Ala Pro Ser Asp Glu Glu Leu  
 1 5 10 15  
 Asp Ser Tyr Arg Arg Gly Glu Glu Trp Asp Pro Gln Lys Ala Glu Glu

541

20 25 30

Lys Arg Asn Xaa Lys Glu Leu Ala Gln Arg Gln Xaa Gly Gly Gly Ser  
35 40 45

5 Pro Ala Gly Ala Cys Gly Gly Glu Pro Cys Gln Arg Leu Gln Gly Gln  
50 55 60

10 Val Gln Pro Pro His Arg Gln Gly Ser Ser Gln Arg Arg Ser Pro His  
65 70 75 80

Ala Thr Gly Gln Xaa  
85

15

(2) INFORMATION FOR SEQ ID NO: 342:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

25 Met Trp Asp Trp Asp Trp Ser Ala Pro Trp Ser Trp Pro Leu Trp Leu  
1 5 10 15

Ser Leu Ala Leu Val Cys Leu Ser Ala Gly Ala Lys Gly His Arg Ala  
20 25 30

30 Ser Glu Ala Gly His Ala Arg Ala Leu Thr Cys Glu Met Gly Ser Glu  
35 40 45

35 Phe Xaa Thr Ala Xaa Gly Leu Val Leu Gly Xaa Xaa Xaa Trp Thr Xaa  
50 55 60

Xaa Asn Gly Ser Ala Gly Pro Glu Arg Arg Gly Trp Arg Pro Ala Ala  
65 70 75 80

40 Phe Leu Ala Val Phe Leu Leu Gly Asp Xaa  
85 90

45 (2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

55 Met Phe Gly Pro Thr Phe His Ser Leu Val Leu Val Pro Pro Trp Pro  
1 5 10 15

Asn Leu Ser Leu Leu His Phe Thr Ser Pro Val Gly Gln His Ser Ser  
20 25 30

60 Phe Leu Pro Thr Ser Leu Arg Leu Xaa Lys Lys Lys Lys Lys Lys  
35 40 45

5

(2) INFORMATION FOR SEQ ID NO: 344:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

15

Met Cys Ser Lys Asn Gly Phe Leu Leu Ala Trp Ser Trp Asn Ser Pro  
 1 5 10 15

20

Trp Leu Pro Gln Ala Ser Leu Ala His Gly Cys Trp Gly Arg Trp Met  
 20 25 30

Ser Asp Leu Val Gly Cys Ser Arg Glu Asn Lys Cys Ala Leu Arg Asp  
 35 40 45

25

His Ser Glu Arg Val Gln Gly Xaa  
 50 55

30

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Ser Pro Leu Xaa Phe Cys Val Val Leu Leu Leu Gln Ala Ala Arg Gly  
 1 5 10 15

40

Tyr Val Val Arg Lys Pro Ala Gln Ser Arg Leu Asp Asp Asp Pro Pro  
 20 25 30

45

Pro Ser Thr Leu Leu Lys Asp Tyr Gln Asn Val Pro Gly Ile Glu Lys  
 35 40 45

Val Asp Asp Val Val Lys Arg Leu Leu Ser Leu Glu Met Ala Asn Lys  
 50 55 60

50

Lys Glu Met Leu Lys Ile Lys Gln Glu Gln Phe Met Lys Lys Ile Val  
 65 70 75 80

Ala Asn Pro Glu Asp Thr Arg Ser Leu Glu Ala Arg Ile Ile Ala Leu  
 85 90 95

55

Ser Val Lys Ile Arg Ser Tyr Glu Glu His Leu Glu Lys His Arg Lys  
 100 105 110

Asp Lys Ala His Lys Arg Tyr Leu Leu Met Ser Ile Asp Gln Arg Lys  
 115 120 125

60

543

Lys Met Leu Lys Asn Leu Arg Asn Thr Asn Tyr Asp Val Phe Glu Lys  
 130 135 140  
 5 Ile Cys Trp Gly Leu Gly Ile Glu Tyr Thr Phe Pro Pro Leu Tyr Tyr  
 145 150 155 160  
 Arg Arg Ala His Arg Arg Phe Val Thr Lys Lys Ala Leu Cys Ile Arg  
 165 170 175  
 10 Val Phe Gln Glu Thr Gln Lys Leu Lys Lys Arg Arg Arg Ala Leu Lys  
 180 185 190  
 Ala Ala Ala Ala Ala Gln Lys Gln Ala Lys Arg Arg Asn Pro Asp Ser  
 195 200 205  
 15 Pro Ala Lys Ala Ile Pro Lys Thr Leu Lys Asp Ser Gln Xaa  
 210 215 220

20 (2) INFORMATION FOR SEQ ID NO: 346:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 amino acids  
 25 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

30 Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala  
 1 5 10 15  
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
 20 25 30  
 35 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Xaa  
 50 55 60

40  
 45 (2) INFORMATION FOR SEQ ID NO: 347:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 amino acids  
 50 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

55 Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly  
 1 5 10 15  
 Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly  
 20 25 30  
 60 Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala

544

35 40 45

Gln Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro  
50 55 60

5 Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala  
65 70 75 80

Gln Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val  
10 85 90 95

Ile Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Xaa His  
100 105 110

15 Leu Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Xaa Xaa Glu Glu Lys  
115 120 125

Gln Ala Arg Lys Ala Gln Xaa Glu Ala Glu Glu Ala Glu Arg Glu Xaa  
20 130 135 140

Arg Lys Arg Leu Glu Ser Gln Arg Glu Xaa  
145 150

25

(2) INFORMATION FOR SEQ ID NO: 348:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

30

35 Met Gln Lys Cys Met Leu Ser Ala Leu Val Phe His Ile Gln Trp Ser  
1 5 10 15

Xaa

40

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

45

50 Met Leu Val Cys Ser Phe Leu Phe Leu Xaa  
1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

60

545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Val Ile Glu Leu Cys Val Ser Leu Arg Ser Leu Asn Phe Xaa  
 1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 351:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

15

Met Cys Glu Phe Xaa Xaa Xaa Ile Met Xaa Leu Ala Gly Tyr Phe Ala  
 1 5 10 15

Cys Xaa

20

(2) INFORMATION FOR SEQ ID NO: 352:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

30

Met Val Gly Gly Tyr Val Ser Ser Phe Ser Phe Pro Pro Val Ser Ser  
 1 5 10 15

35

Ser Leu Leu Leu Pro Ala Ser Phe Ala Phe Pro Phe Leu Pro Gly Thr  
 20 25 30

Pro Cys Pro Phe Leu Tyr Phe Leu Pro Ser Pro Phe Ser Pro Leu Pro  
 35 40 45

40

Leu Ser Leu Thr Arg Ser Asn Ser Phe Leu Leu Asn Gly Xaa  
 50 55 60

45

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

50

55

Glu Lys Lys Ser Met Ser Val Ser Asp Ile Tyr Ala Leu Glu Ser Leu  
 1 5 10 15

Gly Arg Ser Leu Phe Thr Leu Asn Ser Met Cys Leu Pro Leu Ser Phe  
 20 25 30

60

Xaa

## 5 (2) INFORMATION FOR SEQ ID NO: 354:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Gly Gly Ala Ser Arg Arg Val Glu Ser Gly Ala Trp Ala Tyr Leu  
 1 5 10 15  
 Ser Pro Leu Val Leu Arg Lys Glu Leu Glu Ser Leu Val Glu Asn Glu  
 20 25 30  
 Gly Ser Glu Val Leu Ala Leu Pro Glu Leu Pro Ser Ala His Pro Ile  
 35 40 45  
 Ile Phe Trp Asn Leu Leu Trp Tyr Phe Gln Arg Leu Arg Leu Pro Ser  
 50 55 60  
 Ile Leu Pro Gly Leu Val Leu Ala Ser Cys Asp Gly Pro Ser Xaa Ser  
 65 70 75 80  
 Gln Ala Pro Ser Pro Trp Leu Thr Pro Asp Pro Ala Ser Val Gln Val  
 85 90 95  
 Arg Leu Leu Trp Asp Val Leu Thr Pro Asp Pro Asn Ser Cys Pro Pro  
 100 105 110  
 Leu Tyr Val Leu Trp Arg Val His Ser Gln Ile Pro Gln Arg Val Val  
 115 120 125  
 Trp Pro Gly Pro Val Pro Ala Ser Leu Ser Leu Ala Leu Leu Glu Ser  
 130 135 140  
 Val Leu Arg His Val Gly Leu Asn Glu Val His Lys Ala Val Gly Leu  
 145 150 155 160  
 Leu Leu Glu Thr Leu Gly Pro Pro Pro Thr Gly Leu His Leu Gln Arg  
 165 170 175  
 Gly Ile Tyr Arg Glu Ile Leu Phe Leu Thr Met Ala Ala Leu Gly Lys  
 180 185 190  
 Asp His Val Asp Ile Val Ala Phe Asp Lys Lys Tyr Lys Ser Ala Phe  
 195 200 205  
 Asn Lys Leu Ala Ser Ser Met Gly Lys Glu Glu Leu Arg His Arg Arg  
 210 215 220  
 Ala Gln Met Pro Thr Pro Lys Ala Ile Asp Cys Arg Lys Cys Phe Gly  
 225 230 235 240  
 Ala Pro Pro Glu Cys  
 245

60



## (2) INFORMATION FOR SEQ ID NO: 355:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

10

Met Lys Phe Ser Leu Leu Phe Leu Pro Met Leu Leu Ile Leu Lys Pro  
 1 5 10 15

15

Asp Leu Phe His Ile Ser Ile Cys Thr Leu Ala Ala Cys Gly Leu Thr  
 20 25 30

Phe Pro Xaa  
 35

20

## (2) INFORMATION FOR SEQ ID NO: 356:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

30

Met Leu Phe Phe Phe Ile Leu His Leu Leu Ser Ile Met Ser Phe Leu  
 1 5 10 15

Ser Pro Asp Ile Met Xaa  
 20

35

## (2) INFORMATION FOR SEQ ID NO: 357:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

45

Met Phe Gly Leu Leu Val Glu Ser Gln Thr Leu Leu Glu Glu Asn Ala  
 1 5 10 15

50

Val Gln Gly Thr Glu Arg Thr Leu Gly Leu Asn Ile Ala Pro Phe Ile  
 20 25 30

Asn Gln Phe Gln Val Pro Ile Arg Val Phe Leu Asp Leu Ser Ser Leu  
 35 40 45

55

Pro Cys Ile Pro Leu Ser Lys Pro Val Glu Leu Leu Arg Leu Asp Leu  
 50 55 60

60

Met Thr Pro Tyr Leu Asn Thr Ser Asn Arg Glu Val Lys Val Tyr Val  
 65 70 75 80

548

Cys Xaa Ile Trp Glu Asp Leu Thr Ala Ile Pro Phe Trp Val Ser Tyr  
85 90 95

Val Pro

5

(2) INFORMATION FOR SEQ ID NO: 358:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Phe Gly Ala His Arg Xaa Trp Gln Gly Ser Val Leu Leu Phe Leu  
1 5 10 15

20

Ser Phe Ala Trp Gly Asn Gly Gly Ser Val Thr Phe Ser Asp Val Pro  
20 25 30

Arg Val Met Pro Leu Ala Gly Gly Pro Xaa Xaa Gln Val Ser Ser Thr  
35 40 45

25

Pro Arg Pro Pro Pro His Gln Val Thr Ser Ser Pro Gly Leu Glu Ser  
50 55 60

30

Ala His Ile Val Cys Pro Glu Arg Lys Lys Lys Lys Lys Lys  
65 70 75

(2) INFORMATION FOR SEQ ID NO: 359:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Thr Leu Leu Xaa Phe Leu Xaa Leu Leu Thr Thr Glu Gly Gly Arg Glu  
1 5 10 15

45

Asn Ile Phe Xaa Gly Arg Ile Leu Xaa Leu Gln Xaa Ser Pro Xaa  
20 25 30

50

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Leu Ser Phe Phe Ile Cys Leu Leu Ile Phe Val His Leu Leu Leu  
1 5 10 15

60

Leu Ser Phe Leu Ile Ser Asp Trp Pro Pro Pro Thr Gly Ser Ala Xaa  
                   20                  25                  30  
 5 His Lys Ile Leu Arg Leu Met Val Val Gln Arg Leu Ser Leu Leu Asp  
                   35                  40                  45  
 Gln Arg Lys Arg Trp Ser Glu Ala Xaa  
           50                  55

10

(2) INFORMATION FOR SEQ ID NO: 361:

15 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 3 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

20 Lys Tyr Xaa  
      1

25 (2) INFORMATION FOR SEQ ID NO: 362:

30 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 32 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Trp Ser Ser Ala Ser Ser Ser Trp Val Thr Thr Pro Glu Arg Ile Arg  
      1                  5                  10                  15  
 35 Pro Arg Met Asp Thr Leu Pro Val Lys Gly His Phe Leu Ser Met Xaa  
                   20                  25                  30

40

45 (2) INFORMATION FOR SEQ ID NO: 363:

50 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 28 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Asp Ile Phe Val Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile  
      1                  5                  10                  15  
 55 Asn Leu Thr Ala Xaa Asp Thr Val His Phe Leu Xaa  
                   20                  25

60 (2) INFORMATION FOR SEQ ID NO: 364:

550

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Thr Leu Thr Ser Phe Leu Glu Leu Pro Leu Ala Pro Glu Pro Xaa  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO: 365:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met His Arg Tyr Ile Thr Phe Phe Lys Cys Phe Arg Ser Val Ile Leu  
1 5 10 15

Asp Leu Leu Phe Ile Leu Ser Pro Leu Ser Gln Gly Cys Phe Ile Leu  
20 25 30

Phe Xaa

## (2) INFORMATION FOR SEQ ID NO: 366:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Phe Gly Phe Ile Phe Leu Leu Leu Ile Phe Cys Ile Xaa Leu Cys  
1 5 10 15

Ser Arg Thr Leu Ser Thr Phe Ile Pro Lys Leu Val Gly Phe Leu Tyr  
20 25 30

Trp Lys Phe Ser Ile Asn Leu Ser Leu Leu Thr Leu Ile Lys Lys  
35 40 45

Lys Lys Lys Lys Lys Lys Thr Pro Arg Gly Gly Pro Gly Xaa Gln Ser  
50 55 60

Pro Pro  
65

## (2) INFORMATION FOR SEQ ID NO: 367:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

551

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

5 Met Pro Gly Leu Gly Arg Pro Arg Gln Ala Arg Trp Thr Leu Met Leu  
 1 5 10 15  
 Leu Leu Ser Thr Ala Met Tyr Gly Ala His Ala Pro Leu Leu Ala Leu  
 20 25 30  
 10 Cys His Val Asp Gly Arg Val Pro Phe Arg Pro Ser Ser Ala Val Leu  
 35 40 45  
 Leu Thr Glu Leu Thr Lys Leu Leu Cys Ala Phe Ser Leu Leu Val  
 15 50 55 60  
 Gly Trp Gln Ala Trp Pro Gln Gly Pro Pro Pro Trp Arg Gln Ala Ala  
 65 70 75 80  
 20 Pro Phe Ala Leu Ser Ala Leu Leu Tyr Gly Ala Asn Asn Asn Leu Val  
 85 90 95  
 Ile Tyr Leu Gln Arg Tyr Met Asp Pro Ser Thr Tyr Gln Val Leu Ser  
 100 105 110  
 25 Asn Leu Lys Ile Gly Ser Thr Ala Val Leu Tyr Cys Leu Cys Leu Arg  
 115 120 125  
 His Arg Leu Ser Val Arg Gln Gly Leu Ala Leu Leu Leu Met Ala  
 130 135 140  
 Ala Gly Ala Cys Tyr Ala Ala Gly Gly Leu Gln Val Pro Gly Asn Thr  
 145 150 155 160  
 35 Leu Pro Ser Pro Pro Pro Ala Ala Ala Ala Ser Pro Met Pro Leu His  
 165 170 175  
 Ile Thr Pro Leu Gly Leu Leu Leu Leu Ile Leu Tyr Cys Leu Ile Ser  
 180 185 190  
 40 Gly Leu Ser Ser Val Tyr Thr Glu Leu Leu Met Lys Arg Gln Xaa Leu  
 195 200 205  
 Pro Leu Ala Leu Gln Asn Leu Phe Leu Tyr Thr Phe Gly Val Leu Leu  
 210 215 220  
 Asn Leu Gly Leu His Ala Gly Gly Gly Ser Gly Pro Gly Leu Leu Glu  
 225 230 235 240  
 50 Gly Phe Ser Gly Trp Ala Ala Leu Val Val Leu Ser Gln Ala Leu Asn  
 245 250 255  
 Gly Leu Leu Met Ser Ala Val Met Lys His Gly Ser Ser Ile Thr Arg  
 260 265 270  
 55 Leu Phe Val Val Ser Cys Ser Leu Val Val Asn Ala Val Leu Ser Ala  
 275 280 285  
 Val Leu Leu Arg Leu Gln Leu Thr Ala Ala Phe Phe Leu Ala Thr Leu  
 290 295 300  
 60

552

Leu Ile Gly Leu Ala Met Arg Leu Tyr Tyr Gly Ser Arg  
 305 310 315

5

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

15 Met Gly Glu Gln Pro His Phe Ser Leu Cys Val Leu Leu Ala Ala Val  
 1 5 10 15

Arg Glu Asp Xaa Asp Pro Xaa Val Phe Pro Cys Cys Phe Leu Xaa  
 20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 369:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 43 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

30 Met Ser Phe Ile Ala Leu His Pro Leu Leu Pro Glu Ala Ala Leu Gly  
 1 5 10 15

35 Val Pro Gly Gln Ser Pro His Arg Pro Leu Trp Gln Thr Gln Cys Cys  
 20 25 30

Val Ala Pro Pro Gln Pro Arg Ala Glu Phe Xaa  
 35 40

40

(2) INFORMATION FOR SEQ ID NO: 370:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 255 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

50 Met Val Thr Ala Leu Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His  
 1 5 10 15

Ala Glu Arg Ile Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe  
 20 25 30

55

Leu Leu Leu His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly  
 35 40 45

60 Pro Phe Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala  
 50 55 60

553

Thr Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile  
 65 70 75 80  
 5 His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser Cys  
 85 90 95  
 Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala Ser His  
 100 105 110  
 10 Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp Pro Phe Leu  
 115 120 125  
 Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro Pro Gly Asn Glu  
 130 135 140  
 15 Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu Glu Pro Leu Met Glu  
 145 150 155 160  
 20 Met Arg Leu Arg Asp Ala Pro Gln His Phe Tyr Ala Ala Leu Leu Gln  
 165 170 175  
 Leu Gly Leu Lys Tyr Leu Phe Ile Leu Gly Ile Gln Ile Leu Ala Cys  
 180 185 190  
 25 Ala Leu Ala Ala Ser Ile Leu Arg Arg His Leu Met Val Trp Lys Val  
 195 200 205  
 Phe Ala Pro Lys Phe Ile Phe Glu Ala Val Gly Phe Ile Val Ser Ser  
 210 215 220  
 30 Val Gly Leu Leu Leu Gly Ile Ala Leu Val Met Arg Val Asp Gly Ala  
 225 230 235 240  
 35 Val Ser Ser Trp Phe Arg Gln Leu Phe Leu Ala Gln Gln Arg Xaa  
 245 250 255

40 (2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Xaa Gly Pro Trp Gly Glu Glu Ala Leu Ile Arg Leu Pro Thr Pro  
 1 5 10 15  
 50 Ser Gly Leu Xaa  
 20

55

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

60 (B) TYPE: amino acid

554

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

5 Met Ala Thr Leu Glu Xaa Asn Gln Arg Glu Val Asp Arg Glu Ile Arg  
 1 5 10 15  
 Ser Leu Leu Leu Trp Phe Leu Leu Cys Glu Ile Val Ser Gly Trp Leu  
 20 25 30  
 10 Cys Pro Glu Gly Pro Trp Phe Ser Gln Gly Cys Gln Ile Tyr Lys Asn  
 35 40 45  
 Leu Ser Ser Ser Ser Ser Tyr Asn Leu Ser Phe Leu Leu Ser Leu Xaa  
 50 55 60  
 15

20

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

30 Met Ile His Ser Gly Cys Thr Ser Gln Cys Leu Glu Gly Phe Phe Leu  
 1 5 10 15  
 Ile Phe Leu Leu Asp Phe Asn Pro Val Leu Ala Leu Asp Leu Ile Gly  
 20 25 30  
 35 Ile Met Arg Lys Ala Ser His Xaa  
 35 40

40

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 35 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

50 Met Val Phe Ser Ala Arg Val Ser Leu Tyr Thr Arg Phe Lys Val Ile  
 1 5 10 15  
 Leu Leu Ser Leu Leu Ile Met Ile Leu His Val Cys Trp Val Trp Val  
 20 25 30  
 55 Ile Leu Xaa  
 35

60

(2) INFORMATION FOR SEQ ID NO: 375:



555

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Gly Leu Leu Tyr Ile Met Tyr Cys Asn Ile Xaa  
1 5 10

10

## (2) INFORMATION FOR SEQ ID NO: 376:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

20 Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu Pro  
1 5 10 15

Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser  
20 25 30

25

Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys  
35 40 45

30

Ser Gly Gly Arg Asp His Thr Gly Gly Asn Lys Asp Arg Gly Ile Xaa  
50 55 60

35

## (2) INFORMATION FOR SEQ ID NO: 377:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

45 Met Arg Lys Gln Arg Leu Val Pro Met Tyr Leu Gly Leu Ile Tyr Ile  
1 5 10 15

Leu Leu Xaa

50

## (2) INFORMATION FOR SEQ ID NO: 378:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

60

556

Met Arg Gln His Xaa  
1 5

5

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

15 Leu Leu Leu Pro Val Leu Ala Ser Ser Val Pro Ser His Ser Ala Thr  
1 5 10 15  
Xaa

20

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

30 Met Leu Pro Leu Leu Leu Phe Thr Tyr Leu Asn Ser Phe Leu His Gln  
1 5 10 15  
Arg Ile Pro Gln Ser Val Arg Ile Leu Gly Ser Leu Val Ala Ile Leu  
20 25 30  
35 Leu Val Phe Leu Ile Thr Ala Ile Leu Val Lys Val Gln Leu Asp Ala  
35 40 45  
40 Leu Pro Phe Phe Val Ile Thr Met Ile Lys Ile Val Leu Ile Asn Ser  
50 55 60  
Phe Gly Ala Ile Leu Gln Gly Ser Leu Phe Gly Leu Ala Gly Leu Leu  
65 70 75 80  
45 Pro Ala Ser Xaa

50

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

55 Met Lys Leu Ser Leu Phe Leu Ile Leu Ser Asp Val Phe Tyr Leu Gly  
1 5 10 15  
60

Ser Pro Xaa Thr Xaa  
20

5

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

15

Met Gly Thr Arg Arg Lys Gly Val Ala Trp Leu Ser Leu Ala Pro Leu  
1 5 10 15

Ile Thr Gly Leu Ala Pro Ala His Ile Thr Ala Val Xaa  
20 25

20

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

30

Met Lys Asp Leu Leu Gln Arg Asn Pro Trp Lys Asn Ser Leu Leu Leu  
1 5 10 15

Leu Gln Val Cys Gln Ala Phe Leu Val Cys Ser Leu Thr Gln Leu Ala  
20 25 30

35

Val Xaa

40

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

50

Met Ser Glu Ser His Lys Ile Trp Trp Cys Tyr Arg His Leu Ala Phe  
1 5 10 15

Pro Leu Leu Thr Leu Ile Leu Tyr Pro Ala Thr Leu Gly Arg Ser Val  
20 25 30

55

Phe Cys His Asp Cys Lys Phe Pro Glu Ala Ser Pro Ala Met Xaa  
35 40 45

60

(2) INFORMATION FOR SEQ ID NO: 385:

558

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Leu Asn Arg Ile Met Val Ala Ser Phe Gly Ala Val Leu Val Gln  
1 5 10 15  
Val Cys Arg Gly Xaa Gly Gln Gly Xaa  
20 25

## (2) INFORMATION FOR SEQ ID NO: 386:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Gln Leu Leu Leu Leu Gly Leu Ile Arg Ser Gln Pro Ser Pro Pro  
1 5 10 15  
Pro Ser Leu Cys Leu Met Leu Cys Pro Cys Leu Pro Cys Leu Arg Tyr  
20 25 30  
Ser Pro Phe Val Pro Gln His Pro Cys Pro Leu Pro Leu Asp Leu Cys  
35 40 45  
Leu Ala Gly Cys Ser Ser Leu Ser Val Gln Asp Lys Cys Ser Trp Pro  
50 55 60  
Tyr Pro Ile Xaa  
65

## (2) INFORMATION FOR SEQ ID NO: 387:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

Lys Glu Phe Phe Val Phe Leu Phe Val Cys Leu Phe Trp Leu Leu Ser  
1 5 10 15  
Asn Thr Pro Leu Thr Phe Ile Ser Ile Ile Leu Gln Arg Lys Glu Thr  
20 25 30  
Asn Xaa

## (2) INFORMATION FOR SEQ ID NO: 388:

559

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Ser Phe Leu Met Val Leu Val Ile Leu Ala Ala Ser Pro Xaa  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

1 5 10

## (2) INFORMATION FOR SEQ ID NO: 390:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Thr Lys Ala Arg Leu Phe Arg Leu Trp Leu Val Leu Gly Ser Val  
 1 5 10 15

Phe Met Ile Leu Leu Ile Ile Val Tyr Trp Asp Ser Ala Gly Ala Ala  
 20 25 30

His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr Gly Pro Pro  
 35 40 45

Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu Thr Ala Asp Ser  
 50 55 60

Asp Val Asp Xaa Phe Leu Asp Xaa Phe Leu Ser Ala Gly Val Lys Gln  
 65 70 75 80

Ser Asp Xaa Pro Arg Lys Glu Thr Glu Gln Pro Pro Ala Pro Gly Ser  
 85 90 95

Met Glu Glu Ser Val Arg Xaa Tyr Asp Trp Ser Pro Arg Xaa Ala Arg  
 100 105 110

Arg Thr Gln Thr Arg Ala Gly Ser Xaa Arg Xaa Gly Gly Xaa Cys Cys  
 115 120 125

Gly Ala Ser Ala Pro Xaa Pro Ala Trp Pro Ser Pro Pro Arg Ser Ala  
 130 135 140

560

His Ser Thr Thr Ser Pro Thr Arg Ser Xaa  
145 150

5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Val Leu Leu Gly Leu Leu Ser Xaa  
1 5

20

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Cys Ile His Val Phe Met Xaa Val Leu Trp Val Leu Phe Leu Leu  
1 5 10 15

30

Asn Pro Leu Cys Thr Gly Leu Trp Pro Leu Xaa Asn Cys Phe Ser Val  
20 25 30

Leu Arg His Ala Asp Trp Val Leu Gly Ala Asp Tyr Lys Gly Glu Glu  
35 40 45

35

Leu Asn Arg His Gln Gly Pro Met Lys Pro Lys Asp Xaa  
50 55 60

40

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

45

Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser  
1 5 10 15

50

His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser  
20 25 30

55

Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp  
35 40 45

Ala Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu  
50 55 60

60

561

Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu  
 65 70 75 80

5 Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg  
 85 90 95

Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr  
 100 105 110

10 Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu  
 115 120 125

Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg  
 130 135 140

15 Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn  
 145 150 155 160

Val Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys  
 165 170 175

Phe Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe  
 180 185 190

25 Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu  
 195 200 205

Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu  
 210 215 220

30 Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser  
 225 230 235 240

Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln  
 245 250 255

Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys  
 260 265 270

40 Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala  
 275 280 285

Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu  
 290 295 300

45 Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu  
 305 310 315 320

Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu Glu Ala Glu  
 325 330 335

50 Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln Gln Tyr Arg Gln Val  
 340 345 350

55 His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp Cys Glu Ile Thr Ala  
 355 360 365

His Leu Leu Ala Leu Pro Glu His Asp Ala Arg Glu Lys Val Leu Gln  
 370 375 380

60

562

Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp Arg Tyr Arg Gln Asp  
 385 390 395 400

5 Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln Ala Glu Tyr Gln Val  
 405 410 415

Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp Glu Gly Tyr Phe Gln  
 420 425 430

10 Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys Glu Leu Arg Xaa  
 435 440 445

15 (2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Val Ile Ser Tyr Val Thr Phe Thr Pro Val Ser Ala Asp Cys Phe  
 1 5 10 15

25 Phe Asn Val Leu Val Cys Phe Xaa  
 20

30 (2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Glu Leu Leu Phe Leu Leu Ile Ile Ile Leu Gly Glu Ser Leu Ser Asp  
 1 5 10 15

Val Ile Leu Leu Ile Cys Phe Xaa  
 20

45 (2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Phe Tyr Trp Gly Gly Leu Ser Phe Tyr Phe Leu Leu Ser Ser Gly  
 1 5 10 15

Val Gly Phe Tyr Cys Phe Leu Phe Gly Phe Gly Met Glu Ile Trp Ile  
 20 25 30

60



Ala Ala Xaa  
35

5

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Gly Arg Xaa  
1

15

(2) INFORMATION FOR SEQ ID NO: 398:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Lys Leu Ser Leu Leu Ile Leu Thr Leu Met Gln Arg Tyr Phe Arg  
1 5 10 15

30

Thr Ile Thr Asn Ser Leu Cys Lys Xaa  
20 25

35

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Pro Ala Val Ser Gly Pro Gly Pro Leu Phe Cys Leu Leu Leu  
1 5 10 15

45

Leu Leu Asp Pro His Ser Pro Glu Thr Gly Cys Pro Pro Leu Arg Arg  
20 25 30

50

Phe Glu Tyr Lys Leu Ser Phe Lys Gly Pro Arg Leu Ala Leu Pro Gly  
35 40 45

Ala Gly Ile Pro Phe Trp Ser His His Gly Gly Glu Gly Gln Gly Trp  
50 55 60

55

Gly Pro Leu Cys Pro Gly Ser Leu Lys Val Leu Glu Gly Leu Xaa  
65 70 75

60

(2) INFORMATION FOR SEQ ID NO: 400:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Lys Val Phe Leu Ser Met Pro Phe Leu Val Leu Phe Gln Ser Leu  
 1 5 10 15  
 Ile Gln Glu Asp Xaa  
 20

## (2) INFORMATION FOR SEQ ID NO: 401:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Ala Ala Leu Thr Ser His Leu Gln Asn Gln Ser Asn Asn Ser Asn  
 1 5 10 15  
 Trp Asn Leu Arg Thr Arg Ser Lys Cys Lys Lys Asp Val Phe Met Pro  
 20 25 30  
 Pro Ser Ser Ser Ser Glu Leu Gln Glu Ser Arg Gly Leu Ser Asn Phe  
 35 40 45  
 Thr Ser Thr His Leu Leu Leu Lys Glu Asp Glu Gly Val Asp Asp Val  
 50 55 60  
 Asn Phe Arg Lys Val Arg Lys Pro Lys Gly Lys Val Thr Ile Leu Lys  
 65 70 75 80  
 Gly Ile Pro Ile Lys Lys Thr Lys Lys Gly Cys Arg Lys Ser Cys Ser  
 85 90 95  
 Gly Phe Val Xaa Ser Asp Ser Lys Arg Glu Ser Val Cys Asn Lys Ala  
 100 105 110  
 Asp Ala Glu Ser Glu Pro Val Ala Gln Lys Ser Gln Leu Asp Arg Thr  
 115 120 125  
 Val Cys Ile Ser Asp Ala Gly Ala Cys Gly Glu Thr Leu Ser Val Thr  
 130 135 140  
 Ser Glu Glu Asn Ser Leu Val Lys Lys Lys Glu Arg Ser Leu Ser Ser  
 145 150 155 160  
 Gly Ser Asn Phe Cys Ser Glu Gln Lys Thr Ser Gly Ile Ile Asn Lys  
 165 170 175  
 Phe Cys Ser Ala Lys Asp Ser Glu His Asn Glu Lys Tyr Glu Asp Thr  
 180 185 190  
 Phe Leu Glu Ser Glu Glu Ile Gly Thr Lys Val Glu Val Val Glu Arg

565

	195		200		205
	Lys Glu His Leu His Thr Asp Ile Leu Lys Arg Gly Ser Glu Met Asp				
5	210		215		220
	Asn Asn Cys Ser Pro Thr Arg Lys Asp Phe Thr Glu Asp Thr Ile Pro				
	225		230		235 240
10	Arg Asn Thr Asp Arg Lys Lys Glu Asn Lys Pro Val Phe Phe Gln Gln				
	245		250		255
	Ile				

15

(2) INFORMATION FOR SEQ ID NO: 402:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 424 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

25	Met Glu Lys Gln Cys Cys Ser His Pro Val Ile Cys Ser Leu Ser Thr	
	1                                5                                10                                15	
	Met Tyr Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser Ser Ser	
	20                                25                                30	
30	Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn Lys Tyr Asp	
	35                                40                                45	
	Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu Val Lys Leu Val	
35	50                                55                                60	
	Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys Lys Asp His Gln Ser	
	65                                70                                75                                80	
40	Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu Phe Ser Asp Phe Met Lys	
	85                                90                                95	
	Trp Ser Ile Pro Ala Phe Leu Tyr Phe Leu Asp Asn Leu Ile Val Phe	
	100                                105                                110	
45	Tyr Val Leu Ser Tyr Leu Gln Pro Ala Met Ala Val Ile Phe Ser Asn	
	115                                120                                125	
	Phe Ser Ile Ile Thr Thr Ala Leu Leu Phe Arg Ile Val Leu Lys Xaa	
50	130                                135                                140	
	Arg Leu Asn Trp Ile Gln Trp Ala Ser Leu Leu Thr Leu Phe Leu Ser	
	145                                150                                155                                160	
55	Ile Val Ala Leu Thr Ala Gly Thr Lys Thr Leu Gln His Asn Leu Ala	
	165                                170                                175	
	Gly Arg Gly Phe His His Asp Ala Phe Phe Ser Pro Ser Asn Ser Cys	
	180                                185                                190	
60		

566

Leu Leu Phe Arg Asn Glu Cys Pro Arg Lys Asp Asn Cys Thr Ala Lys  
 195 200 205  
 5 Glu Trp Thr Phe Pro Glu Ala Lys Trp Asn Thr Thr Ala Arg Val Phe  
 210 215 220  
 Ser His Ile Arg Leu Gly Met Gly His Val Leu Ile Ile Val Gln Cys  
 225 230 235 240  
 10 Phe Ile Ser Ser Met Ala Asn Ile Tyr Asn Glu Lys Ile Leu Lys Glu  
 245 250 255  
 Gly Asn Gln Leu Thr Glu Xaa Ile Phe Ile Gln Asn Ser Lys Leu Tyr  
 260 265 270  
 15 Phe Phe Gly Ile Leu Phe Asn Gly Leu Thr Leu Gly Leu Gln Arg Ser  
 275 280 285  
 Asn Arg Asp Gln Ile Lys Asn Cys Gly Phe Phe Tyr Gly His Ser Ala  
 290 295 300  
 20 Phe Ser Val Ala Leu Ile Phe Val Thr Ala Phe Gln Gly Leu Ser Val  
 305 310 315 320  
 25 Ala Phe Ile Leu Lys Phe Leu Asp Asn Met Phe His Val Leu Met Ala  
 325 330 335  
 Gln Val Thr Thr Val Ile Ile Thr Thr Val Ser Val Leu Val Phe Asp  
 340 345 350  
 30 Phe Arg Pro Ser Leu Glu Phe Phe Leu Glu Ala Pro Ser Val Leu Leu  
 355 360 365  
 Ser Ile Phe Ile Tyr Asn Ala Ser Lys Pro Gln Val Pro Glu Tyr Ala  
 370 375 380  
 Pro Arg Gln Glu Arg Ile Arg Asp Leu Ser Gly Asn Leu Trp Glu Arg  
 385 390 395 400  
 40 Ser Ser Gly Asp Gly Glu Glu Leu Glu Arg Leu Thr Lys Pro Lys Ser  
 405 410 415  
 Asp Glu Ser Asp Glu Asp Thr Phe  
 420  
 45

(2) INFORMATION FOR SEQ ID NO: 403:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Trp Gly Gln Gly Ser Gln Lys Ser His Phe Ser Asp Leu Val Phe  
 1 5 10 15  
 Gly Val Arg Glu Leu Cys Ala Gln Pro Ser Asp Pro Gly Ser Pro His  
 20 25 30  
 60

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 404:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

15

Met Val Gln His Ile Gln Pro Ala Ala Leu Ser Leu Leu Ala Gln Trp  
 1 5 10 15

20

Ser Thr Leu Val Gln Glu Leu Glu Ala Ala Leu Gln Leu Ala Phe Tyr  
 20 25 30

Pro Asp Ala Val Glu Glu Trp Leu Glu Glu Asn Val His Pro Ser Leu  
 35 40 45

25

Gln Arg Leu Gln Xaa Leu Leu Gln Asp Leu Ser Glu Val Ser Ala Pro  
 50 55 60

Pro Leu Pro Pro Thr Ser Pro Gly Arg Asp Val Ala Gln Asp Pro Xaa  
 65 70 75 80

30

35

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

45

Met Leu Asn Gln Gly Tyr Ile Arg Lys Ile Ile Leu Ile Ile Ile Leu  
 1 5 10 15

Gly Ser Phe Ser Ser Pro Lys Lys Ala Ile Leu Met Gly Phe Gln Asn  
 20 25 30

50

Gln Lys Lys Ala Leu Asn Glu Glu Gln Thr Thr Gly Val Pro Met Ser  
 35 40 45

Ile Ser Gly Lys Leu Arg Pro Ser Arg Ser Leu Asp Phe Val Gln Pro  
 50 55 60

55

Pro Arg Phe Gln Ser Gln Gln Pro Ser Ala Val Val Asp Arg Arg Gly  
 65 70 75 80

Phe Xaa Xaa Lys Ala Ala Arg Gly Gln Glu Phe Ser Glu Ser Xaa  
 85 90 95

60

## (2) INFORMATION FOR SEQ ID NO: 406:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

10

Met Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln  
 1 5 10 15

15

Ala Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Val  
 20 25 30

Ser Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro  
 35 40 45

20

Thr Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr  
 50 55 60

His Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu  
 65 70 75 80

25

Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro  
 85 90 95

30

His Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu  
 100 105 110

Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro  
 115 120 125

35

Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp  
 130 135 140

Tyr Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Asp Thr  
 145 150 155 160

40

Leu Glu Glu Asn Arg Gly Tyr Met Glu Ile Glu Gln Ser Val Lys Ser  
 165 170 175

45

Phe Lys Met Pro Ser Ser Asn Ile Glu Glu Glu Asp Ser His Phe Phe  
 180 185 190

Phe His Leu Ile Ile Phe Ala Phe Cys Ile Ala Val Val Tyr Ile Thr  
 195 200 205

50

Tyr His Asn Lys Arg Lys Ile Phe Leu Leu Val Gln Ser Arg Lys Trp  
 210 215 220

Arg Asp Gly Leu Cys Ser Lys Thr Val Glu Tyr His Arg Leu Asp Gln  
 225 230 235 240

55

Asn Val Asn Glu Ala Met Pro Ser Leu Lys Ile Thr Asn Asp Tyr Ile  
 245 250 255

60

Phe

## (2) INFORMATION FOR SEQ ID NO: 407:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

Met Phe Met Arg Ile Ala Lys Ala Tyr Ala Ala Leu Thr Asp Glu Glu  
 1 5 10 15  
 Ser Arg Lys Asn Trp Glu Glu Phe Gly Asn Pro Asp Gly Pro Gln Ala  
 20 25 30  
 Thr Ser Phe Gly Ile Ala Leu Pro Ala Trp Ile Val Asp Gln Lys Asn  
 35 40 45  
 Ser Ile Leu Val Leu Leu Val Tyr Gly Leu Ala Phe Met Val Ile Leu  
 50 55 60  
 Pro Val Val Val Gly Ser Trp Trp Tyr Arg Ser Ile Arg Tyr Ser Gly  
 65 70 75 80  
 Asp Gln Ile Leu Ile Arg Thr Thr Gln Ile Tyr Thr Tyr Phe Val Tyr  
 85 90 95  
 Lys Thr Arg Asn Met Asp Met Lys Arg Leu Ile Met Val Leu Xaa Gly  
 100 105 110  
 Ala Ser Glu Phe Asp Pro Gln Tyr Asn Lys Asp Ala Thr Ser Arg Pro  
 115 120 125  
 Thr Asp Asn Ile Leu Ile Pro Gln Leu Ile Arg Glu Ile Gly Ser Ile  
 130 135 140  
 Asn Leu Lys Lys Asn Glu Pro Pro Leu Thr Cys Pro Tyr Ser Leu Lys  
 145 150 155 160  
 Ala Arg Val Leu Leu Leu Ser His Leu Ala Arg Met Lys Ile Pro Glu  
 165 170 175  
 Thr Leu Glu Glu Asp Gln Gln Phe Met Leu Lys Lys Cys Pro Ala Leu  
 180 185 190  
 Leu Gln Glu Met Val Asn Val Ile Cys Gln Leu Ile Val Met Ala Arg  
 195 200 205  
 Asn Arg Glu Glu Arg Glu Phe Arg Ala Pro Thr Leu Ala Ser Leu Glu  
 210 215 220  
 Asn Cys Met Lys Leu Ser Gln Met Ala Val Gln Gly Leu Gln Gln Phe  
 225 230 235 240  
 Lys Ser Pro Leu Leu Gln Leu Pro His Ile Glu Glu Asp Asn Leu Arg  
 245 250 255  
 Arg Val Ser Asn His Lys Lys Tyr Lys Ile Lys Thr Ile Gln Asp Leu

570

	260	265	270
5	Val Ser Leu Lys Glu Ser Asp Arg His Thr Leu Leu His Phe Leu Glu 275 280 285		
	Asp Glu Lys Tyr Glu Glu Val Met Ala Val Leu Gly Ser Phe Pro Tyr 290 295 300		
10	Val Thr Met Asp Ile Lys Ser Gln Val Leu Asp Asp Glu Asp Ser Asn 305 310 315 320		
	Asn Ile Thr Val Gly Ser Leu Val Thr Val Leu Val Lys Leu Thr Arg 325 330 335		
15	Gln Thr Met Ala Glu Val Phe Glu Lys Glu Gln Ser Ile Cys Ala Ala 340 345 350		
20	Glu Glu Gln Pro Ala Glu Asp Gly Gln Gly Glu Thr Asn Lys Asn Arg 355 360 365		
	Thr Lys Gly Gly Trp Gln Gln Lys Ser Lys Gly Pro Lys Lys Thr Ala 370 375 380		
25	Lys Ser Lys Lys Lys Lys Pro Leu Lys Lys Lys Pro Thr Pro Val Leu 385 390 395 400		
	Leu Pro Gln Ser Lys Gln Gln Lys Gln Lys Gln Ala Asn Gly Val Val 405 410 415		
30	Gly Asn Glu Ala Ala Val Lys Glu Asp Glu Glu Glu Val Ser Asp Lys 420 425 430		
35	Gly Ser Asp Ser Glu Glu Glu Glu Thr Asn Arg Asp Ser Gln Ser Glu 435 440 445		
	Lys Asp Asp Gly Ser Asp Arg Asp Ser Asp Arg Glu Gln Asp Glu Lys 450 455 460		
40	Gln Asn Lys Asp Asp Glu Ala Glu Trp Gln Glu Leu Gln Gln Ser Ile 465 470 475 480		
	Gln Arg Lys Glu Arg Ala Leu Leu Glu Thr Lys Ser Lys Ile Thr His 485 490 495		
45	Pro Val Tyr Ser Leu Tyr Phe Pro Glu Glu Lys Gln Glu Trp Trp Trp 500 505 510		
50	Leu Tyr Ile Ala Asp Arg Lys Glu Gln Thr Leu Ile Ser Met Pro Tyr 515 520 525		
	His Val Cys Thr Leu Lys Asp Thr Glu Glu Val Glu Leu Lys Phe Pro 530 535 540		
55	Ala Pro Gly Lys Pro Gly Asn Tyr Gln Tyr Thr Val Phe Leu Arg Ser 545 550 555 560		
	Asp Ser Tyr Met Gly Leu Asp Gln Ile Lys Pro Leu Glu Val Xaa Lys 565 570 575		
60	Phe Met Arg Leu Lys Pro Val Pro Glu Asn His Pro Gln Trp Asp Thr		



571

580 585 590

Ala Ile Glu Gly Asp Glu Asp Gln Glu Asp Ser Glu Gly Phe Glu Asp  
595 600 605

5 Ser Phe Glu Gly Gly Arg Gly Arg Glu Glu Gly Arg Trp Trp Thr  
610 615 620

10

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

15

20 Met Lys Ala Ser Gln Cys Cys Cys Cys Leu Ser His Leu Leu Ala Ser  
1 5 10 15

Val Leu Leu Leu Leu Leu Pro Glu Leu Ser Gly Xaa Leu Xaa Val  
20 25 30

25 Leu Leu Gln Ala Ala Glu Ala Ala Pro Gly Leu Gly Pro Pro Asp Pro  
35 40 45

Arg Pro Arg Thr Leu Pro Pro Leu Pro Pro Gly Pro Thr Pro Ala Gln  
50 55 60

30 Gln Pro Gly Arg Gly Leu Ala Glu Ala Ala Gly Pro Arg Gly Ser Glu  
65 70 75 80

35 Gly Gly Asn Gly Ser Asn Pro Val Ala Gly Leu Glu Thr Asp Asp His  
85 90 95

Gly Gly Lys Ala Gly Glu Gly Ser Val Gly Gly Gly Leu Ala Val Ser  
100 105 110

40 Pro Asn Pro Gly Asp Lys Pro Met Thr Gln Arg Ala Leu Thr Val Leu  
115 120 125

Met Val Val Ser Gly Ala Val Leu Val Tyr Phe Val Val Arg Thr Val  
130 135 140

45 Arg Met Arg Arg Arg Asn Arg Lys Thr Arg Arg Tyr Gly Val Leu Asp  
145 150 155 160

50 Thr Asn Ile Glu Asn Met Glu Leu Thr Pro Leu Glu Gln Asp Asp Glu  
165 170 175

Asp Asp Asp Asn Thr Leu Phe Asp Ala Asn His Pro Arg Arg  
180 185 190

55

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

60

572

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

5 Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile  
 1 5 10 15

Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser  
 20 25 30

10 Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp  
 35 40 45

Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro  
 15 50 55 60

Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly  
 65 70 75 80

20 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Lys Ser Thr Lys  
 85 90 95

Ala Ala His Pro Thr Asp Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser  
 100 105 110

25 Pro Ser Thr Asp Val Gln Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly  
 115 120 125

Phe His Glu Asp Asp Pro Phe Phe Tyr Asp Glu His Thr Leu Arg Lys  
 130 135 140

Arg Gly Leu Leu Val Ala Ala Val Leu Phe Ile Thr Gly Ile Ile Ile  
 145 150 155 160

35 Leu Thr Ser Gly Lys Cys Arg Gln Leu Ser Arg Leu Cys Arg Asn His  
 165 170 175

Cys Arg Xaa

40

(2) INFORMATION FOR SEQ ID NO: 410:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

50

Met Phe Lys Cys Leu Gln Thr Thr Phe Leu Phe Ile Xaa Xaa  
 1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

60

573

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

5 Met Leu Ala Gly Lys Leu Ile Pro Val His Gln Val Arg Gly Leu Lys  
 1 5 10 15  
 Glu Lys Ile Val Arg Ser Phe Glu Val Ser Pro Asp Gly Ser Phe Leu  
 20 25 30  
 10 Leu Ile Asn Gly Ile Ala Gly Tyr Leu His Leu Leu Ala Met Lys Thr  
 35 40 45  
 Lys Glu Leu Ile Gly Ser Met Lys Ile Asn Gly Arg Val Ala Ala Ser  
 50 55 60  
 15 Thr Phe Ser Ser Asp Ser Lys Lys Val Tyr Ala Ser Ser Gly Asp Gly  
 65 70 75 80  
 20 Glu Val Tyr Val Trp Asp Val Asn Ser Arg Lys Cys Leu Asn Arg Phe  
 85 90 95  
 Val Asp Glu Gly Ser Leu Tyr Gly Leu Ser Ile Ala Thr Ser Arg Asn  
 100 105 110  
 25 Gly Gln Tyr Val Ala Cys Gly Ser Asn Cys Gly Val Val Asn Ile Tyr  
 115 120 125  
 Asn Gln Asp Ser Cys Leu Gln Glu Thr Asn Pro Lys Pro Ile Lys Ala  
 130 135 140  
 30 Ile Met Asn Leu Val Thr Gly Val Thr Ser Leu Thr Phe Asn Pro Thr  
 145 150 155 160  
 35 Thr Glu Ile Leu Ala Ile Ala Ser Glu Lys Met Lys Glu Ala Val Arg  
 165 170 175  
 Leu Val His Leu Pro Ser Cys Thr Val Phe Ser Asn Phe Pro Val Ile  
 180 185 190  
 40 Lys Asn Lys Asn Ile Ser His Val His Thr Met Asp Phe Ser Pro Arg  
 195 200 205  
 Ser Gly Tyr Phe Ala Leu Gly Asn Glu Lys Gly Lys Ala Leu Met Tyr  
 210 215 220  
 45 Arg Leu His His Tyr Ser Asp Phe  
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

60 Ile Leu Leu Cys Ser Trp Pro Thr Gly Leu Val Gly Gly Arg Asp Pro  
 1 5 10 15

Gly Ser Ser Arg Gly Ser Ser Ala Ser Leu Thr Pro Ser Pro Gly Arg  
20 25 30

5 Gln Pro Cys Ser Arg Arg Arg Gly Tyr Ser Val Gly Arg Arg Ser Ser  
35 40 45

Pro Pro Asp Gly Ser Xaa  
50

10

(2) INFORMATION FOR SEQ ID NO: 413:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

20

Met Ser Leu Gln Ser Asn Ala Trp Ser Lys Xaa Leu Phe Ile Val Phe  
1 5 10 15

25

Leu Phe Leu Arg Val Leu Phe Lys Thr Gly Val Ser Ser Glu Glu Ser  
20 25 30

Xaa

30

(2) INFORMATION FOR SEQ ID NO: 414:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

40

Met Ala Val Val Leu Leu Ala Asn Leu Ala Gln Gly Asp Ser Leu Ala  
1 5 10 15

Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile Gly Asn Leu Leu Gly  
20 25 30

45

Phe Leu Glu Asp Ser Leu Ala Ala Thr Gln Phe Gln Gln Ser Gln Ala  
35 40 45

50

Ser Leu Leu His Met Gln Asn Pro Pro Phe Glu Pro Xaa Ser Val Asp  
50 55 60

Met Met Arg Arg Ala Ala Arg Ala Leu Leu Ala Leu Ala Lys Val Asp  
65 70 75 80

55

Glu Asn His Ser Glu Phe Thr Leu Tyr Glu Ser Arg Leu Leu Asp Ile  
85 90 95

Ser Val Ser Pro Leu Met Asn Ser Xaa Val Ser Gln Val Ile Cys Asp  
100 105 110

60

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575

Val Leu Phe Leu Xaa Trp Pro Val Met Thr Ala Val Gly His Leu Pro  
 115 120 125

5 Pro Pro Cys Val Cys Ala Cys Val Glu Asn Leu Glu Thr Asp Cys Cys  
 130 135 140

Pro Leu Phe Met Gln Asn His Leu Arg Ile Gln Phe Thr Leu Cys Cys  
 145 150 155 160

10 Pro Ala Ser Pro Leu Gly Lys Ser Leu Ser Cys Phe Ser Leu Leu Leu  
 165 170 175

Pro Pro Pro Leu Pro Pro Ser Pro His Ala Phe Leu Phe Leu Val Leu  
 180 185 190

15 Thr Leu Leu Pro Ser Gly Pro Tyr Pro Thr Leu Phe Glu Lys Thr Lys  
 195 200 205

20 Leu Cys Leu His Arg Arg Leu Phe Leu Phe Xaa  
 210 215

25 (2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Leu Pro Asp Glu Ser Phe Gly Leu Leu Leu Ser Ile Pro Ser Leu  
 1 5 10 15

35 Thr Pro Ser Ala Ala Ala Pro Ser Phe Cys Val His Leu Met Gln Ala  
 20 25 30

Ser Arg Ser Ser Lys Arg Ala Ser His Val Pro Val His Leu Leu Trp  
 35 40 45

40 Gly Asp Xaa  
 50

45 (2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Arg Pro Gly Ser Phe Ser Phe Ile Ala Phe Leu Ala Thr Glu Val  
 55 1 5 10 15

Ser Ser Cys Phe Pro Gly Arg Pro Asp Cys Xaa Thr Gly Met Trp Leu  
 20 25 30

60 Leu Gln Leu Gln Lys Lys Gln Arg Thr Leu Leu Ala Met Ala Pro Arg

576

35 40 45

Arg Xaa  
50

5

(2) INFORMATION FOR SEQ ID NO: 417:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

15 Asp Arg Pro Cys Pro Ser Ser Leu Trp Lys Val Phe Pro Leu Leu Leu  
 1 5 10 15

20 Leu Leu Met Arg Leu Phe Pro Leu Pro Val Pro Gly Asn Gln Arg Ala  
 20 25 30

Xaa Leu Pro His Pro Phe Xaa Ala Pro Arg Leu Pro Cys Leu Leu Cys  
 35 40 45

25 Leu Cys Thr Gln Gln Phe Xaa Val Cys Ser His Tyr Leu Pro Ala Gly  
 50 55 60

Tyr Arg Val Asn Ser Xaa  
 65 70

30

(2) INFORMATION FOR SEQ ID NO: 418:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

40 Met His Glu Lys Ala Trp Asn Leu Ile Leu Leu Trp Trp Leu Ser Leu  
 1 5 10 15

45 Asp Leu Leu Gly Val Ala Lys Thr Ala Met Trp Ala Gln Trp Cys Gly  
 20 25 30

Leu Asn Asp His Lys Gly Lys Xaa  
 35 40

50

(2) INFORMATION FOR SEQ ID NO: 419:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

60 Met Ala Phe Val Leu Leu Xaa Cys Phe Val Xaa Leu Gln Ser Ser Xaa

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEC ID NO: 422:

25

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

45

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

60

## 5 (2) INFORMATION FOR SEQ ID NO: 423:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

15 Met Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys  
 1 5 10 15  
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly  
 20 25 30  
 Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn Tyr Ile  
 20 35 40 45  
 His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His Ile Val Leu  
 50 55 60  
 25 Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu Leu Cys Glu Ala  
 65 70 75 80  
 Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys Ile Met Cys Val Ala  
 85 90 95  
 30 Gly Ile Gly Leu Val Val Leu Phe Phe Ser Trp Met Leu Ser Ile Phe  
 100 105 110  
 Arg Ser Lys Tyr His Gly Tyr Pro Tyr Ser Phe Leu Met Ser Xaa  
 35 115 120 125

## 40 (2) INFORMATION FOR SEQ ID NO: 424:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

50 Met Thr Trp His Ser Arg Glu Ser Phe Xaa Leu Leu Arg Val Val Ala  
 1 5 10 15  
 Pro Ser Gln Ala Pro Gly Met Gln Val Ser Pro Ser Gln Arg Ala Trp  
 20 25 30  
 Arg Arg Pro Leu His Arg Cys His Val Ala Ala Pro Arg Pro His His  
 35 40 45  
 55 Phe Ala Phe Phe Arg Asn Pro Phe Ser Trp Ser Phe Ile Lys Leu Leu  
 50 55 60  
 60 Tyr Arg Tyr Leu Xaa  
 65



## (2) INFORMATION FOR SEQ ID NO: 425:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Gly Leu Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val  
 1 5 10 15  
 Gln Ile Ala Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp  
 20 25 30  
 Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Thr  
 35 40 45  
 Trp Pro Thr Thr Arg Ser Leu Gly Arg Gln Asp Glu His Gln Asp Arg  
 50 55 60  
 Val His Ile Leu Gly Gly Phe Pro Gln Leu His Gly His Ser Pro Tyr  
 65 70 75 80  
 Gly Leu Pro Gly Arg Gly Glu Arg Tyr Val Gly Xaa  
 85 90

## (2) INFORMATION FOR SEQ ID NO: 426:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser  
 1 5 10 15  
 Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln  
 20 25 30  
 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
 35 40 45  
 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
 50 55 60  
 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile  
 65 70 75 80  
 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln  
 85 90 95  
 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly  
 100 105 110

580

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro  
 115 120 125  
 5 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln  
 130 135 140  
 Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu  
 145 150 155 160  
 10 Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr  
 165 170 175  
 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys  
 180 185 190  
 15 Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His  
 195 200 205  
 20 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys  
 210 215 220  
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn  
 225 230 235 240  
 25 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys  
 245 250 255  
 Phe Tyr Pro Gly Lys Cys Ile Xaa Pro Pro Gly Leu Glu Gly Glu Gln  
 260 265 270  
 30 Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys  
 275 280 285  
 35 Ile Gly Lys Ser Lys Cys Lys Xaa Ser Lys Gly Tyr Gln Gly Asp Leu  
 290 295 300  
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys  
 305 310 315 320  
 40 His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His  
 325 330 335  
 Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala  
 340 345 350  
 45 Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
 355 360 365  
 50 Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp Xaa  
 370 375 380

- 55 (2) INFORMATION FOR SEQ ID NO: 427:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 24 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

581

Met Thr Ser Asn Leu Leu Leu Thr Leu Leu Leu Lys Asp Thr Leu  
1 5 10 15

5 Xaa Leu Ala Lys Xaa Asn Xaa Xaa  
20

10 (2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Arg His His Thr Gln Leu Asn Phe Ile Phe Leu Val Glu Met Val  
1 5 10 15

20 Phe Leu His Val Gly Gln Ala Gly Leu Lys Leu Pro Thr Ser Gly Asp  
20 25 30

25 Xaa Ala Cys Phe Gly Leu Pro Lys Val Leu Gly Leu Gln Ala Xaa  
35 40 45

30 (2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met Cys Ser Asp Xaa  
1 5

40

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

50 Leu Leu Ser Ile Leu Leu Cys Leu Leu Ala Ser Gly Leu Val Val Phe  
1 5 10 15

Phe Leu Phe Pro His Ser Val Leu Val Asp Asp Asp Gly Ile Lys Val  
20 25 30

55

Val Lys Val Thr Phe Asn Lys Gln Asp Ser Leu Val Ile Leu Thr Ile  
35 40 45

60 Met Ala Thr Leu Lys Ile Arg Asn Ser Asn Phe Tyr Thr Val Ala Val  
50 55 60

582

Thr Ser Leu Ser Ser Gln Ile Gln Tyr Met Asn Thr Val Val Asn Phe  
 65 70 75 80  
 5 Thr Gly Lys Ala Glu Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe  
 85 90 95  
 Cys Thr Val Pro Glu Ile Leu Val His Asn Ile Val Ile Phe Met Arg  
 100 105 110  
 10 Thr Ser Val Lys Ile Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu  
 115 120 125  
 15 Glu Thr His His Tyr Val Asp Cys Gly Gly Asn Ser Thr Ala Ile Xaa  
 130 135 140

20

(2) INFORMATION FOR SEQ ID NO: 431:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

30 Met Phe Phe Phe Leu Tyr Val Tyr Ser Val Leu Cys Gly Leu Leu Val  
 1 5 10 15  
 Tyr Pro Ser Leu Pro Ser His Ser Val Ser Leu Val Thr Ser Leu Val  
 20 25 30  
 35 Ala Ser Ala Leu Xaa  
 35

40

(2) INFORMATION FOR SEQ ID NO: 432:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

50 Met Ala Ser Ile Asn Ala Val Tyr Ile His Val Phe Leu Gly Val Cys  
 1 5 10 15  
 Val Gln Ala Thr Ala Ala Cys Pro Trp Cys Ser Gln Cys Arg Xaa Gly  
 20 25 30  
 55 Ser Val Pro Ser Xaa  
 35

60 (2) INFORMATION FOR SEQ ID NO: 433:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

5 Met Met Ala Ala Met Val Leu Thr Ser Leu Ser Cys Ser Pro Val Val  
 1 5 10 15  
 10 Gln Ser Pro Pro Gly Thr Glu Ala Asn Phe Ser Ala Ser Arg Ala Ala  
 20 25 30  
 15 Cys Asp Pro Trp Lys Glu Ser Gly Asp Ile Ser Asp Ser Gly Xaa Ser  
 35 40 45  
 Thr Thr Ser Gly His Trp Ser Gly Ser Ser Gly Val Ser Thr Pro Ser  
 50 55 60  
 20 Pro Pro His Pro Gln Ala Ser Pro Lys Tyr Leu Gly Asp Ala Phe Gly  
 65 70 75 80  
 Ser Pro Gln Thr Asp His Gly Phe Glu Thr Asp Pro Asp Pro Phe Leu  
 85 90 95  
 25 Leu Asp Glu Pro Ala Pro Arg Lys Arg Lys Asn Ser Val Lys Val Met  
 100 105 110  
 30 Tyr Lys Cys Leu Trp Pro Asn Cys Gly Lys Val Leu Arg Ser Ile Val  
 115 120 125  
 Gly Ile Lys Arg His Val Lys Ala Leu His Leu Gly Asp Thr Val Asp  
 130 135 140  
 35 Ser Asp Gln Phe Lys Arg Glu Glu Asp Phe Tyr Tyr Thr Glu Val Gln  
 145 150 155 160  
 Leu Lys Glu Glu Ser Ala Ala Ala Ala Ala Ala Ala Ala Asp Pro  
 165 170 175  
 40 Gln Ser Leu Gly Leu Pro Pro Pro Ser Gln Leu Pro Pro Pro Ala Xaa  
 180 185 190  
 45

## (2) INFORMATION FOR SEQ ID NO: 434:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

50 Met Ser Thr Asn Tyr Leu Thr Asp Val Cys Ser Leu Phe Ser Tyr Leu  
 1 5 10 15  
 60 Asn Tyr Leu Tyr Phe His His His Leu Pro Val Pro Asn Thr Xaa

584

20

25

30

## 5 (2) INFORMATION FOR SEQ ID NO: 435:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Gly Phe Phe Phe Val Leu Phe Phe Leu Tyr Leu Ala Leu Ser Arg  
 1 5 10 15

15 Asp Trp Ser Ile Asn Phe Leu Lys Asp His Arg Ile Asn Phe Phe Val  
 20 25 30

20 Ala Thr Ser Tyr Phe Ser Val Tyr Val Arg Gly Xaa Pro Xaa Val Pro  
 35 40 45

Ala Asp Thr Pro Leu Gly Pro Leu Leu Ser Leu Trp Leu His His Asn  
 50 55 60

25 Ala Phe Phe Ser Ile Leu Pro Lys Phe Pro Glu Asn Xaa Xaa Phe Leu  
 65 70 75 80

Ile Leu Lys Lys Leu Val Val Glu Met Gly Trp Asp Leu Phe Ile Ser  
 85 90 95

30 Pro Glu Asn Lys Xaa  
 100

35

## (2) INFORMATION FOR SEQ ID NO: 436:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

40 (B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

45 Met Ala Arg Tyr Phe Ile Phe Phe Ile Leu Val Phe Met Lys Val Ser  
 1 5 10 15

Leu Asn Thr Thr Trp Pro Ala Pro Arg Pro Ala Thr Leu Arg Thr Ala  
 20 25 30

50 Asn Lys Ser Lys Xaa  
 35

## 55 (2) INFORMATION FOR SEQ ID NO: 437:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

60 (B) TYPE: amino acid

(D) TOPOLOGY: linear

585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

5 Phe Ser Thr Ile Arg Ser Gly Leu Thr Asp Arg Ser Val Asn Phe Leu  
    1                  5                  10                  15  
 Phe Leu Phe Leu Asp Val Pro Asp Cys Arg Leu Val Asn Ile Glu Leu  
           20                  25                  30  
 10 Met Ala Asn Ser Thr Val Thr His Ala Xaa  
           35                  40

(2) INFORMATION FOR SEQ ID NO: 438:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Leu

1

25

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

35 Met Pro Trp Arg Arg Ala Gly Leu Met Met Leu Pro Ile Ile Thr Gly  
    1                  5                  10                  15  
 Cys Cys Pro Cys Ser Ala Ser Ile Xaa  
           20                  25

40

(2) INFORMATION FOR SEQ ID NO: 440:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

50

Met Tyr Leu Cys Lys Thr Val Lys Val Leu Ile Cys Tyr Asp Trp Ile  
    1                  5                  10                  15

55

Leu Gly Leu Val Ser Ser Gly Gln His Trp Val Val Ser Leu Ser Tyr  
           20                  25                  30

Ser Ile Arg Val Tyr Pro Ala Met His Phe Thr Leu Cys Val His Ile  
           35                  40                  45

60

Tyr Ser Lys Glu Pro Cys

50

## 5 (2) INFORMATION FOR SEQ ID NO: 441:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

Met Thr Ala Leu Val Trp Arg Lys Gly Pro Asp Gly Gly Ser Arg Lys  
 1 5 10 15  
 Pro Ile Leu Leu Leu Phe Phe Phe Leu Pro Leu Ile Leu Cys Phe His  
 20 25 30  
 Ser Phe Ile His Ser Ser Asn Ile Cys Xaa  
 35 40

## 25 (2) INFORMATION FOR SEQ ID NO: 442:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

Met Phe Leu Thr Thr Trp Phe Leu Leu Leu Ser Val Ala Trp Xaa Ala  
 1 5 10 15  
 Leu Thr Arg Ser Gly Arg Ser Cys Leu Pro Leu Val Gly Arg Pro Arg  
 20 25 30  
 Glu Gln Ser Pro Arg Thr His Cys Ala Ala Ser Ser Thr Lys Glu Arg  
 35 40 45  
 Asn Ser Asp Pro Gln Pro Ser Pro Pro Glu Val Val Gly Pro Leu Trp  
 50 55 60  
 Ser Xaa  
 65

## 50 (2) INFORMATION FOR SEQ ID NO: 443:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Lys Ala Ile Gly Ile Glu Pro Ser Leu Ala Thr Tyr His His Ile  
 1 5 10 15  
 Ile Arg Leu Phe Asp Gln Pro Gly Asp Pro Leu Lys Arg Ser Ser Phe



587

20 25 30

Ile Ile Tyr Asp Ile Met Asn Glu Leu Met Gly Lys Arg Phe Ser Pro  
35 40 45

5 Lys Asp Pro Asp Asp Asp Lys Phe Phe Gln Ser Ala Met Ser Ile Cys  
50 55 60

10 Ser Ser Leu Arg Asp Leu Glu Leu Ala Tyr Gln Val His Gly Leu Leu  
65 70 75 80

Lys Thr Gly Asp Asn Trp Lys Phe Ile Gly Pro Asp Gln His Arg Asn  
85 90 95

15 Phe Tyr Tyr Ser Lys Phe Phe Asp Leu Ile Cys Leu Met Glu Gln Ile  
100 105 110

Asp Val Thr Leu Lys Trp Tyr Glu Asp Leu Ile Pro Ser Ala Tyr Phe  
115 120 125

20 Pro His Ser Gln Thr Met Ile His Leu Leu Gln Ala Leu Asp Val Ala  
130 135 140

25 Asn Arg Leu Glu Val Ile Pro Lys Ile Trp Glu Arg  
145 150 155

(2) INFORMATION FOR SEQ ID NO: 444:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr Leu Trp Gly Leu  
1 5 10 15

40 Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr Glu Glu Val Lys  
20 25 30

Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys Thr Ser Lys Lys  
35 40 45

45

Gly Asp Leu Leu Lys Cys Pro Leu Xaa  
50 55

50

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 416 amino acids

55

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

60 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro  
1 5 10 15

Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys  
 20 25 30  
 5 Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg  
 35 40 45  
 Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His  
 50 55 60  
 10 Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp  
 65 70 75 80  
 Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr  
 85 90 95  
 15 Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln  
 100 105 110  
 20 Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp  
 115 120 125  
 Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu  
 130 135 140  
 25 His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe  
 145 150 155 160  
 Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr  
 165 170 175  
 30 Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu  
 180 185 190  
 35 Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met  
 195 200 205  
 Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu  
 210 215 220  
 40 Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met  
 225 230 235 240  
 Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe  
 245 250 255  
 45 Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn  
 260 265 270  
 50 Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys  
 275 280 285  
 Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met  
 290 295 300  
 55 Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg  
 305 310 315 320  
 60 Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser  
 325 330 335

589

Gln Xaa Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg  
 340 345 350

5 His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu  
 355 360 365

Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Ala Arg  
 370 375 380

10 Ala Trp Thr Thr Ser Thr Thr Cys Ser Arg Trp Ala Leu Arg Pro Pro  
 385 390 395 400

Arg Trp Thr Cys Ser Phe Leu Ser His Gly Val Ser Glu Gln Val Xaa  
 15 405 410 415

20

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 64 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

30 Met Ala Pro Gly Pro Leu Ser Ala Thr Gln Ala Val Val Ile His Thr  
 1 5 10 15

Thr His Cys Leu Gln Leu Pro Val Trp Cys Leu Ser Leu Val Ser Glu  
 20 25 30

35 Leu Leu Gly Arg Ala Pro Pro His Asn Lys Asp Ala Leu Arg Pro Ser  
 35 40 45

Lys Lys Lys Lys Lys Lys Leu Xaa Gly Gly Pro Val Pro Ile Pro Pro  
 40 50 55 60

45

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 206 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

55 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser Pro  
 1 5 10 15

Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly Trp Ala  
 20 25 30

60

590

Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys Leu Val Val  
 35 40 45

5 Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly Gly Ala Ala Leu  
 50 55 60

Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala Ala Val Arg Ser Xaa  
 65 70 75 80

10 His His Glu Pro Ala Gly Glu Thr Gly Asn Gly Thr Xaa Gly Ala Ile  
 85 90 95

Tyr Phe Asp Gln Val Leu Val Asn Glu Gly Gly Gly Phe Asp Arg Ala  
 100 105 110

15 Ser Gly Ser Phe Val Ala Pro Val Arg Gly Val Tyr Ser Phe Arg Phe  
 115 120 125

20 His Val Val Lys Val Tyr Asn Arg Gln Thr Val Gln Val Ser Leu Met  
 130 135 140

Leu Asn Thr Trp Pro Val Ile Ser Ala Phe Ala Asn Asp Pro Asp Val  
 145 150 155 160

25 Thr Arg Glu Ala Ala Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly  
 165 170 175

Asp Arg Val Ser Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp  
 180 185 190

30 Lys Tyr Ser Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu Xaa  
 195 200 205

35

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

45 Met Ser Ser Leu Leu Ser Ala Gly Leu Gln Ala Ser Leu Cys Gly Lys  
 1 5 10 15

Xaa Leu Trp Ala Ser Thr Trp Tyr Leu Val Cys Cys Leu Leu Pro Phe  
 20 25 30

50 Phe His Gln Gly Cys Cys Asp His Lys Ser Lys Gln Gln Tyr Ile Pro  
 35 40 45

Asn Leu Lys Ser Tyr Cys Gly Leu Ser Thr Ile Glu Ile Xaa  
 50 55 60

55

60

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

591

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

5 Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile Leu Leu Val Phe  
 1 5 10 15  
 10 Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala Pro Gly Pro Thr  
 20 25 30  
 Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp Ala Arg Lys Asn  
 35 40 45  
 15 His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro Asn His Cys Asp  
 50 55 60  
 Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu Ile Glu Ala Asn  
 65 70 75 80  
 20 Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His Met Glu Met Ser  
 85 90 95  
 Pro Trp Phe Gln Phe Met Xaa Phe Ile Leu Gln Leu Asp Ile Ala Phe  
 100 105 110  
 Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val  
 115 120 125  
 30 Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala  
 130 135 140  
 His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys  
 145 150 155 160  
 35 Thr Pro Glu His Gly Gly Pro Val Thr Met Asn Val Met Ser Phe Leu  
 165 170 175  
 Ser Trp Lys Leu Gly Leu Trp Pro Met Lys Phe Tyr Leu Leu Asn Ile  
 180 185 190  
 Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu  
 195 200 205  
 45 Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr  
 210 215 220  
 Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile  
 225 230 235 240  
 50 Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro  
 245 250 255  
 Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe  
 260 265 270  
 55 Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp  
 275 280 285  
 60 Met Leu Leu Phe Gly Asp Ile Arg Gln Ala Ser Ser Met Xaa Cys Phe

592

290 295 300  
Xaa Pro Ser Gly Ser Ser Ser Val Ala Ser Thr Xaa  
305 310 315

5

(2) INFORMATION FOR SEQ ID NO: 450:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

15 Met Leu Ala Leu Leu Gly Leu Leu Ala Gly Thr Glu His Pro Pro Gly  
1 5 10 15

20 Pro Gln Gly Pro Gly Pro Ser Xaa  
20

(2) INFORMATION FOR SEQ ID NO: 451:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

30 Met Pro Ser Gly Ala Cys Cys Ser Pro Xaa  
1 5 10

35

(2) INFORMATION FOR SEQ ID NO: 452:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

45 Met Leu Pro Ala Leu Ser Thr Val Leu Leu Pro Thr Pro Ser Leu Cys  
1 5 10 15

Ser Gly Asn Pro Arg Glu Gly Trp Ala Xaa  
20 25

50

(2) INFORMATION FOR SEQ ID NO: 453:

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 172 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

60

593

Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala Val Ile Cys Tyr  
 1 5 10 15

Leu Leu Gln Leu Leu Ser Gly Phe Ser Val Phe Leu Leu Pro Trp Ala  
 5 20 25 30

Pro Leu Ser Leu Arg Ala Phe Leu Met Pro Ile His Val Tyr Ser Gly  
 35 40 45

10 Ile Val Ile Phe Gly Thr Val Ile Ala Thr Ala Leu Met Gly Leu Thr  
 50 55 60

Glu Lys Leu Ile Phe Ser Leu Arg Asp Pro Ala Tyr Ser Thr Phe Pro  
 65 70 75 80

15 Pro Glu Gly Val Phe Val Asn Thr Leu Gly Leu Leu Ile Leu Val Phe  
 85 90 95

Gly Ala Leu Ile Phe Trp Ile Val Thr Arg Pro Gln Trp Lys Arg Pro  
 20 100 105 110

Lys Glu Pro Asn Ser Thr Ile Leu His Pro Asn Gly Gly Thr Glu Gln  
 115 120 125

25 Gly Ala Arg Gly Ser Met Pro Ala Tyr Ser Gly Asn Asn Met Asp Lys  
 130 135 140

Ser Asp Ser Glu Leu Asn Xaa Glu Val Ala Ala Arg Lys Arg Asn Leu  
 145 150 155 160

30 Ala Leu Asp Glu Ala Gly Gln Arg Ser Thr Met Xaa  
 165 170

35

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

45 Met Phe His Val Leu Met Ala Gln Val Thr Xaa Val Ile Ile Thr Thr  
 1 5 10 15

Val Ser Val Leu Val Phe Asp Phe Arg Pro Ser Leu Glu Phe Phe Leu  
 20 25 30

50 Glu Ala Xaa Ser Val Xaa Leu Ser Ile Phe Ile Tyr Asn Ala Ser Lys  
 35 40 45

Pro Gln Val Pro Glu Tyr Ala Pro Arg Gln Glu Arg Ile Arg Asp Leu  
 50 55 60

55 Ser Gly Asn Leu Trp Glu Arg Ser Ser Gly Asp Gly Glu Glu Leu Glu  
 65 70 75 80

60 Arg Leu Thr Lys Pro Lys Ser Asp Glu Ser Asp Glu Asp Thr Phe Xaa  
 85 90 95

5

(2) INFORMATION FOR SEQ ID NO: 455:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

15

Met Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln  
 1 5 10 15

20

Ala Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Val  
 20 25 30

Ser Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro  
 35 40 45

25

Thr Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr  
 50 55 60

His Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu  
 65 70 75 80

30

Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro  
 85 90 95

His Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu  
 100 105 110

35

Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro  
 115 120 125

40

Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp  
 130 135 140

Tyr Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Xaa His  
 145 150 155 160

45

Leu Gly Arg Lys Gln Gly Leu His Gly Asn Xaa  
 165 170

50

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Lys Ala Ser Gln Cys Cys Cys Cys Leu Ser His Leu Leu Ala Ser.  
 1 5 10 15

60



595

Val Leu Leu Leu Leu Leu Leu Pro Glu Leu Ser Gly Xaa Leu Xaa Val  
 20 25 30  
 Leu Leu Gln Ala Ala Glu Ala Ala Pro Gly Xaa Gly Pro Pro Asp Pro  
 5 35 40 45  
 Arg Pro Gly His Tyr Arg Arg Cys His Arg Ala Leu Thr Pro Ala Gln  
 50 55 60  
 10 Gln Pro Gly Arg Gly Leu Ala Glu Ala Ala Gly Ala Ala Gly Leu Arg  
 65 70 75 80  
 Gly Arg Gln Trp Gln Gln Pro Cys Gly Arg Ala Xaa  
 85 90  
 15  
 (2) INFORMATION FOR SEQ ID NO: 457:  
 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 206 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:  
 25 Ile Ser Val Leu Xaa Tyr Pro His Cys Val Val His Glu Leu Pro Glu  
 1 5 10 15  
 Leu Thr Ala Glu Ser Leu Glu Ala Gly Asp Ser Asn Gln Phe Cys Trp  
 30 20 25 30  
 Arg Asn Leu Phe Ser Cys Ile Asn Leu Leu Arg Ile Leu Asn Lys Leu  
 35 35 40 45  
 Thr Lys Trp Lys His Ser Arg Thr Met Met Leu Val Val Phe Lys Ser  
 50 55 60  
 Ala Pro Ile Leu Lys Arg Ala Leu Lys Val Lys Gln Ala Met Met Gln  
 40 65 70 75 80  
 Leu Tyr Val Leu Lys Leu Leu Lys Val Gln Thr Lys Tyr Leu Gly Arg  
 85 90 95  
 Gln Trp Arg Lys Ser Asn Met Lys Thr Met Ser Ala Ile Tyr Gln Lys  
 45 100 105 110  
 Val Arg His Arg Leu Asn Asp Asp Trp Ala Tyr Gly Asn Asp Leu Asp  
 115 120 125  
 50 Ala Arg Pro Trp Asp Phe Gln Ala Glu Glu Cys Ala Leu Arg Ala Asn  
 130 135 140  
 Ile Glu Arg Phe Asn Ala Arg Arg Tyr Asp Arg Ala His Ser Asn Pro  
 145 150 155 160  
 55 Asp Phe Leu Pro Val Asp Asn Cys Leu Gln Ser Val Leu Gly Gln Arg  
 165 170 175  
 Val Asp Leu Pro Glu Asp Phe Gln Met Asn Tyr Asp Leu Trp Leu Glu  
 60 180 185 190

Arg Glu Val Phe Ser Lys Pro Ile Ser Trp Glu Glu Leu Leu  
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

15 Met Ala Pro Pro Ala Pro Gly Pro Ala Ser Gly Gly Ser Gly Glu Val  
 1 5 10 15

Asp Glu Leu Phe Asp Val Lys Asn Ala Phe Tyr Ile Gly Ser Tyr Gln  
 20 25 30

20 Gln Cys Ile Asn Glu Ala Xaa Xaa Val Lys Leu Ser Ser Pro Glu Arg  
 35 40 45

Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln Arg  
 25 50 55 60

Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro Glu  
 65 70 75 80

30 Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser Arg  
 85 90 95

Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser Xaa  
 100 105 110

35 Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr Leu  
 115 120 125

His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly Asp  
 40 130 135 140

Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu Asp  
 145 150 155 160

45 Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu Asp  
 165 170 175

Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu Ala  
 180 185 190

50 Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu Met  
 195 200 205

Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu Asn Gly Gln Ala Ala  
 55 210 215 220

Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu Gln  
 225 230 235 240

60 Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn Leu

597

245                      250                      255  
 Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn Arg  
                          260                      265                      270  
 5 Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser His Pro Phe Ile Lys  
                          275                      280                      285  
 10 Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln Tyr  
                          290                      295                      300  
 Ala Pro Ser Ala Glu Ala Gly Pro Glu Leu Ser Gly Pro  
 305                      310                      315  
 15  
 (2) INFORMATION FOR SEQ ID NO: 459:  
 (i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 261 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:  
 25 Arg Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln  
       1                      5                      10                      15  
 Arg Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro  
                          20                      25                      30  
 30 Glu Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser  
                          35                      40                      45  
 Arg Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser  
 35                      50                      55                      60  
 Xaa Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr  
       65                      70                      75                      80  
 40 Leu His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly  
                          85                      90                      95  
 Asp Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu  
                          100                      105                      110  
 45 Asp Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu  
                          115                      120                      125  
 Asp Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu  
 50                      130                      135                      140  
 Ala Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu  
       145                      150                      155                      160  
 55 Met Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Asn Gly Gln Ala  
                          165                      170                      175  
 Ala Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu  
                          180                      185                      190  
 60

598

Gln Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn  
 195 200 205  
 5 Leu Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn  
 210 215 220  
 Arg Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser His Pro Phe Ile  
 225 230 235 240  
 10 Lys Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln  
 245 250 255  
 Tyr Ala Pro Ser Ala  
 260  
 15

(2) INFORMATION FOR SEQ ID NO: 460:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:  
 25 Met Lys Ala Ile Gly Ile Glu Pro Ser Leu Ala Thr Tyr His His Ile  
 1 5 10 15  
 Ile Arg Leu Phe Asp Gln Pro Gly Asp Pro Leu Lys Arg Ser Ser Phe  
 30 20 25 30  
 Ile Ile Tyr Asp Ile Met Asn Glu Leu Met Gly Lys Arg Phe Ser Pro  
 35 40 45  
 35 Lys Asp Pro Asp Asp Asp Lys Phe Phe Gln Ser Ala Met Ser Ile Cys  
 50 55 60  
 Ser Ser Leu Arg Asp Leu Glu Leu Ala Tyr Gln Val His Gly Leu Leu  
 40 65 70 75 80  
 Lys Thr Gly Asp Asn Trp Lys Phe Ile Gly Pro Asp Gln His Arg Asn  
 85 90 95  
 45 Phe Tyr Tyr Ser Lys Phe Phe Asp Leu Ile Cys Leu Met Glu Gln Ile  
 100 105 110  
 Asp Val Thr Leu Lys Trp Tyr Glu Asp Leu Ile Pro Ser Ala Tyr Phe  
 115 120 125  
 50 Pro His Ser Gln Thr Met Ile His Leu Leu Gln Ala Leu Asp Val Ala  
 130 135 140  
 Asn Arg Leu Glu Val Ile Pro Lys Ile Trp Glu Arg  
 145 150 155  
 55

(2) INFORMATION FOR SEQ ID NO: 461:

60 (i) SEQUENCE CHARACTERISTICS:

599

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

5

Lys Asp Ser Lys Glu Tyr Gly His Thr Phe Arg Ser Asp Leu Arg Glu  
 1 5 10 15

10

Glu Ile Leu Met Leu Met Ala Arg Asp Lys His Pro Pro Glu Leu Gln  
 20 25 30

Val Ala Phe Ala Asp Cys Ala Ala Asp Ile Lys Ser Ala Tyr Glu Ser  
 35 40 45

15

Gln Pro Ile Arg Gln Thr Ala Gln Asp Trp Pro Ala Thr Ser Leu Asn  
 50 55 60

Cys Ile Ala Ile Leu Phe Leu Arg Ala Gly Arg Thr Gln Glu Ala Trp  
 65 70 75 80

20

Lys Met Leu Gly Leu Phe Arg Lys His Asn Lys Ile Pro Arg Ser Glu  
 85 90 95

25

Leu Leu Asn Glu Leu Met Asp Ser Ala Lys Val Ser Asn Ser Pro Ser  
 100 105 110

Gln Ala Ile Glu Val Val Glu Leu Ala Ser Ala Phe Ser Leu Pro Ile  
 115 120 125

30

Cys Glu Gly Leu Thr Gln Arg Val Met Ser Asp Phe Ala Ile Asn Gln  
 130 135 140

Glu Gln Lys Glu Ala Leu Ser Asn Leu Thr Ala Leu Thr Ser Asp Ser  
 145 150 155 160

35

Asp Thr Asp Ser Ser Ser Asp Ser Asp Ser Asp Thr Ser Glu Gly Lys  
 165 170 175

40

(2) INFORMATION FOR SEQ ID NO: 462:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ser Ser Asp Asn Glu Ser Asp Ile Glu Asp Glu Asp Leu Lys Leu  
 1 5 10 15

55

Glu Leu Arg Arg Leu Arg Asp Lys His Leu Lys Glu Ile Gln Asp Leu  
 20 25 30

Gln Ser Arg Gln Lys His Glu Ile Glu Ser Leu Tyr Thr Lys Leu Gly  
 35 40 45

60

600

Lys Val Pro Pro Ala Val Ile Ile Pro Pro Ala Ala Pro Leu Ser Gly  
 50 55 60  
 5 Arg Arg Arg Arg Pro Thr Lys Ser Lys Gly Ser Lys Ser Ser Arg Ser  
 65 70 75 80  
 Ser Ser Leu Gly Asn Lys Ser Pro Gln Leu Ser Gly Asn Leu Ser Gly  
 85 90 95  
 10 Gln Ser Ala Ala Ser Val Leu His Pro Gln Gln Thr Leu His Pro Pro  
 100 105 110  
 Gly Asn Ile Pro Glu Ser Gly Gln Asn Gln Leu Leu Gln Pro Leu Lys  
 115 120 125  
 15 Pro Ser Pro Ser Ser Asp Asn Leu Tyr Ser Ala Phe Thr Ser Asp Gly  
 130 135 140  
 20 Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly Gln Gly Thr Ser Ser  
 145 150 155 160  
 Thr Asn Thr Val Gly Ala Thr Val Asn Ser Gln Ala Ala Gln Ala Gln  
 165 170 175  
 25 Pro Pro Ala Met Thr Ser Ser Arg Lys Gly Thr Phe Thr Asp Asp Leu  
 180 185 190  
 His Lys Leu Val Asp Asn Trp Ala Arg Asp Ala Met Asn Leu Ser Gly  
 195 200 205  
 30 Arg Arg Gly Ser Lys Gly His Met Asn Tyr Glu Gly Pro Gly Met Ala  
 210 215 220  
 35 Arg Lys Phe Ser Ala Pro Gly Gln Leu Cys Ile Ser Met Thr Ser Asn  
 225 230 235 240  
 Leu Gly Gly Ser Ala Pro Ile Ser Ala Ala Ser Ala Thr Ser Leu Gly  
 245 250 255  
 40 His Phe Thr Lys Ser Met Cys Pro Pro Gln Gln Tyr Gly Phe Pro Ala  
 260 265 270  
 Thr Pro Phe Gly Ala Gln Trp Ser Gly Thr Gly Gly Pro Ala Pro Gln  
 275 280 285  
 45 Pro Leu Gly Gln Phe Gln Pro Val Gly Thr Ala Ser Leu Gln Asn Phe  
 290 295 300  
 50 Asn Ile Ser Asn Leu Gln Lys Ser Ile Ser Asn Pro Pro Gly Ser Asn  
 305 310 315 320  
 Leu Arg Thr Thr

55

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 133 amino acids

601

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

5 Ile Gln Asp Leu Gln Ser Arg Gln Lys His Glu Ile Glu Ser Leu Tyr  
 1 5 10 15

Thr Lys Leu Gly Lys Val Pro Pro Ala Val Ile Ile Pro Pro Ala Ala  
 20 25 30

10 Pro Leu Ser Gly Arg Arg Arg Arg Pro Thr Lys Ser Lys Gly Ser Lys  
 35 40 45

15 Ser Ser Arg Ser Ser Ser Leu Gly Asn Lys Ser Pro Gln Leu Ser Gly  
 50 55 60

Asn Leu Ser Gly Gln Ser Ala Ala Ser Val Leu His Pro Gln Gln Thr  
 65 70 75 80

20 Leu His Pro Pro Gly Asn Ile Pro Glu Ser Gly Gln Asn Gln Leu Leu  
 85 90 95

Gln Pro Leu Lys Pro Ser Pro Ser Ser Asp Asn Leu Tyr Ser Ala Phe  
 100 105 110

25 Thr Ser Asp Gly Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly Gln  
 115 120 125

30 Gly Thr Ser Ser Thr  
 130

(2) INFORMATION FOR SEQ ID NO: 464:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

Thr Ser Asp Gly Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly Gln  
 1 5 10 15

45 Gly Thr Ser Ser Thr Asn Thr Val Gly Ala Thr Val Asn Ser Gln Ala  
 20 25 30

Ala Gln Ala Gln Pro Pro Ala Met Thr Ser Ser Arg Lys Gly Thr Phe  
 35 40 45

50 Thr Asp Asp Leu His  
 50

55

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

60

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

5 Lys Gly His Met Asn Tyr Glu Gly Pro Gly Met Ala Arg Lys Phe Ser  
 1 5 10 15  
 Ala Pro Gly Gln Leu Cys Ile Ser Met Thr Ser Asn Leu Gly Gly Ser  
 20 25 30  
 10 Ala Pro Ile Ser Ala Ala Ser Ala Thr Ser Leu Gly His Phe Thr Lys  
 35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 466:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

25

Gln Pro Leu Lys Pro Ser Pro Ser Ser Asp Asn Leu Tyr Ser Ala Phe  
 1 5 10 15

30

Thr Ser Asp Gly Ala Ile Ser Val Pro Ser Leu Ser Ala Pro Gly  
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 467:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Val Arg Val Ala Ala Ala Glu Ser Met Xaa Leu Leu Leu Glu Cys Ala  
 1 5 10 15

45

Xaa Val Arg Gly Pro Glu Tyr Leu Thr Gln Met Trp His Phe Met Cys  
 20 25 30

Asp Ala Leu Ile Lys Ala Ile Gly Thr Glu Pro Asp Ser Asp Val Leu  
 35 40 45

50

Ser Glu Ile Met His Ser Phe Ala Lys  
 50 55

55

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

60

(B) TYPE: amino acid



603

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

5 Met Glu Ile Asn Asn Gln Asn Cys Phe Ile Val Ile Asp Leu Val Arg  
 1 5 10 15

Thr Val Met Glu Asn Gly Val Glu Gly Leu Leu Ile Phe Gly Ala Phe  
 20 25 30

10 Leu Pro Glu Ser Trp Leu Ile Gly Val Arg Cys Ser Ser Glu Pro Pro  
 35 40 45

Lys Ala Leu Leu Leu Ile Leu Ala His Ser Gln Lys Arg Arg Leu Asp  
 50 55 60

15 Gly Trp Ser Phe Ile Arg His Leu Arg Val His Tyr Cys Val Ser Leu  
 65 70 75 80

20 Thr Ile His Phe Ser  
 85

(2) INFORMATION FOR SEQ ID NO: 469:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

Gln Asp Lys His Ala Glu Glu Val Arg Lys Asn Lys Glu Leu Lys Glu  
 1 5 10 15

35 Glu Ala Ser Arg  
 20

40 (2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

Gln Gln Asp Leu Ser Pro Trp Ala Ala Pro Val Gly Cys Pro Leu Xaa  
 1 5 10 15

50 Xaa Ala Ser Xaa Thr Cys His Xaa Leu Pro Leu Ser Gly Cys Leu Arg  
 20 25 30

Arg Gln Ser Xaa Ser Leu Pro Val Val Ala Xaa Leu Cys Phe Trp Phe  
 35 40 45

Ser Cys Pro Leu Ala Ser Leu Phe Val Pro Gly Gln Pro Cys Val Thr  
 50 55 60

60 Cys Pro Phe Pro Ser Leu Pro Phe Gln Asp Lys His Ala Glu Glu Val

604

55                      70                      75                      80  
 Arg Lys Asn Lys Glu Leu Lys Glu Glu Ala Ser Arg  
                                  35                      90

5

(2) INFORMATION FOR SEQ ID NO: 471:

10

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

15

Pro Thr Arg Cys Cys Thr Thr Gln Pro Cys Arg Ser Ser Ala Arg Arg  
   1                                  5                                  10                                  15

20

Pro Cys Trp Val Pro Met Val Pro Ser Pro Glu Gly Arg Glu Xaa Gln  
                   20                                  25                                  30

Pro Thr Cys Pro Ser  
                   35

25

(2) INFORMATION FOR SEQ ID NO: 472:

30

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(2) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

35

Met Lys Arg Ser Leu Asn Glu Asn Ser Ala Arg Ser Thr Ala Gly Cys  
   1                                  5                                  10                                  15

Leu Pro Val Pro Leu Phe Asn Gln Lys Lys Arg Asn Arg Gln Pro Leu  
                   20                                  25                                  30

40

Thr Ser Asn Pro Leu Lys Asp Asp Ser Gly Ile Ser Thr Pro Ser Asp  
                   35                                  40                                  45

45

Asn Tyr Asp Phe Pro Pro Leu Pro Thr Asp Trp Ala Trp Glu Ala Val  
                   50                                  55                                  60

Asn Pro Glu Xaa Ala Pro Val Met Lys Thr Val Asp Thr Gly Gln Ile  
                   55                                  70                                  75                                  80

50

Pro His Ser Val Ser Arg Pro Leu Arg Ser Gln Asp Ser Val Phe Asn  
                                   85                                  90                                  95

Ser Ile Gln Ser Asn Thr Gly Arg Ser Gln Gly Gly Trp Ser Tyr Arg  
                   100                                  105                                  110

55

Asp Gly Asn Lys Asn Thr Ser Leu Lys Thr Trp Xaa Lys Asn Asp Phe  
                   115                                  120                                  125

60

Lys Pro Gln Cys Lys Arg Thr Asn Leu Val Ala Asn Asp Gly Lys Asn  
                   130                                  135                                  140

605

Ser Cys Pro Met Ser Ser Gly Ala Gln Gln Gln Lys Gln Leu Arg Thr  
 145 150 155 160  
 5 Pro Glu Pro Pro Asn Leu Ser Arg Asn Lys Glu Thr Glu Leu Leu Arg  
 165 170 175  
 Gln Thr His Ser Ser Lys Ile Ser Gly Cys Thr Met Arg Gly Leu Asp  
 180 185 190  
 10 Lys Asn Ser Ala Leu Gln Thr Leu Lys Pro Asn Phe Gln Gln Asn Gln  
 195 200 205  
 Tyr Lys Xaa Gln Met Leu Asp Asp Ile Pro Glu Asp Asn Thr Leu Lys  
 210 215 220  
 15 Glu Thr Ser Leu Tyr Gln Leu Gln Phe Lys Glu Lys Ala Ser Ser Leu  
 225 230 235 240  
 20 Arg Ile Ile Ser Ala Val Ile Glu Ser Met Lys Tyr Trp Arg Glu His  
 245 250 255  
 Ala Gln Lys Thr Val Leu Leu Phe Glu Val Leu Ala Val Leu Asp Ser  
 260 265 270  
 25 Ala Val Thr Pro Gly Pro Tyr Tyr Ser Lys Thr Phe Leu Met Arg Asp  
 275 280 285  
 Gly Lys Asn Thr Leu Pro Cys Val Phe Tyr Glu Ile Asp Arg Glu Leu  
 290 295 300  
 30 Pro Arg Leu Ile Arg Gly Arg Val His Arg Cys Val Gly Asn Tyr Asp  
 305 310 315 320  
 35 Gln Lys Lys Asn Ile Phe Gln Cys Val Ser Val Arg Pro Ala Ser Val  
 325 330 335  
 Ser Glu Gln Lys Thr Phe Gln Ala Phe Val Lys Ile Ala Asp Val Glu  
 340 345 350  
 40 Met Gln Tyr Tyr Ile Asn Val Met Asn Glu Thr  
 355 360  
 45  
 (2) INFORMATION FOR SEQ ID NO: 473:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:  
 55 Ser Gln Asp Ser Val Phe Asn Ser Ile Gln Ser Asn Thr Gly Arg Ser  
 1 5 10 15  
 Gln Gly Gly Trp Ser Tyr Arg Asp Gly Asn Lys Asn Thr Ser Leu Lys  
 20 25 30  
 60 Thr Trp Xaa Lys Asn Asp Phe Lys Pro Gln Cys Lys Arg

35

40

45

## 5 (2) INFORMATION FOR SEQ ID NO: 474:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Asn Lys Glu Thr Glu Leu Leu Arg Gln Thr His Ser Ser Lys Ile Ser  
 1 5 10 15  
 Gly Cys Thr Met Arg Gly Leu Asp Lys Asn Ser Ala Leu Gln Thr Leu  
 20 25 30  
 Lys Pro Asn Phe  
 35

## 25 (2) INFORMATION FOR SEQ ID NO: 475:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Ser Ser Leu Arg Ile Ile Ser Ala Val Ile Glu Ser Met Lys Tyr Trp  
 1 5 10 15  
 Arg Glu His Ala Gln Lys Thr Val Leu Leu Phe Glu Val Leu Ala Val  
 20 25 30  
 Leu Asp Ser Ala Val Thr Pro Gly Pro Tyr Tyr Ser Lys Thr Phe Leu  
 35 40 45  
 Met

## 45 (2) INFORMATION FOR SEQ ID NO: 476:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

50 (B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Pro Arg Leu Ile Arg Gly Arg Val His Arg Cys Val Gly Asn Tyr Asp  
 55 1 5 10 15  
 Gln Lys Lys Asn Ile Phe Gln Cys Val Ser Val Arg Pro Ala Ser Val  
 20 25 30  
 Ser Glu Gln Lys Thr Phe Gln Ala Phe Val

607

35

40

## 5 (2) INFORMATION FOR SEQ ID NO: 477:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

Gly Val Phe Arg Pro Cys Val Cys Gly Arg Pro Ala Ser Leu Thr Cys  
 1 5 10 15  
 Ser Pro Leu Asp Pro Glu Val Gly Pro Tyr Cys Asp Thr Pro Thr Met  
 20 25 30  
 Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro Val  
 35 40 45  
 His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys Thr  
 50 55 60  
 Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg Gly  
 65 70 75 80  
 Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His Arg  
 85 90 95  
 Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp Val  
 100 105 110  
 Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr Lys  
 115 120 125  
 Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln Leu  
 130 135 140  
 Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp Val  
 145 150 155 160  
 Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu His  
 165 170 175  
 Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe Arg  
 180 185 190  
 Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr Val  
 195 200 205  
 Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu Val  
 210 215 220  
 Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met Leu  
 225 230 235 240  
 Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu Leu  
 245 250 255

60

608

Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met Phe  
260 265 270

5 Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe Ser  
275 280 285

Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn Ala  
290 295 300

10 Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys Xaa  
305 310 315 320

Lys Trp Arg Thr Lys Ser Ser Trp Gly Ser Thr Ser Met Xaa Trp Thr  
325 330 335

15 Xaa Arg Xaa Pro Xaa Asp Ala Arg Xaa Pro Val Val Gly Xaa Arg Xaa  
340 345 350

Ile Gln Xaa Leu Lys Asp His Xaa Pro Arg Met Val Leu Asp Ser Lys  
20 355 360 365

Pro Gln  
370

25

(2) INFORMATION FOR SEQ ID NO: 478:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

35 Thr Cys Ser Pro Leu Asp Pro Glu Val Gly Pro Tyr Cys Asp Thr Pro  
1 5 10 15

Thr Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser  
20 25 30

40 Pro Val His Thr Thr Leu Ser  
35

45

(2) INFORMATION FOR SEQ ID NO: 479:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

55 Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His Arg  
1 5 10 15

Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp Val  
20 25 30

60 Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr Lys

35 40 45  
Val Phe Gly Ser Lys Phe  
50  
5

## (2) INFORMATION FOR SEQ ID NO: 480:

## 10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

Arg Glu Met Phe Glu Val Thr Gly Leu His Asp Val Asp Gln Gly Trp  
1 5 10 15  
Met Arg Ala Val Arg Lys His Ala Lys Gly Leu His Ile Val Pro Arg  
20 25 30  
Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp  
35 40 45  
25 Ser Glu Asp Glu  
50

## 30 (2) INFORMATION FOR SEQ ID NO: 481:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

## 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

His Phe Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln  
1 5 10 15  
40 Lys Arg Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu  
20 25 30  
His Gln Ala Arg Leu Leu Ala Leu Val Ile Pro Pro Ala Ile Thr  
45 35 40 45  
Pro Gly Thr Asp Gln Leu Gly Met  
50 55

50

## (2) INFORMATION FOR SEQ ID NO: 482:

## 55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

60 Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro

610

1                    5                    10                    15  
 Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu  
                     20                    25                    30  
 5 Asp Pro Lys Xaa Lys Trp Arg Thr Lys Ser Ser Trp Gly Ser Thr  
                     35                    40                    45

10

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 152 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

20 Glu Arg Gly Val Ser Ile Asn Gln Phe Cys Lys Glu Phe Asn Glu Arg  
     1                    5                    10                    15  
 Thr Lys Asp Ile Lys Glu Gly Ile Pro Leu Pro Thr Lys Ile Leu Val  
                     20                    25                    30  
 25 Lys Pro Asp Arg Thr Phe Glu Ile Lys Ile Gly Gln Pro Thr Val Ser  
                     35                    40                    45  
 Tyr Phe Leu Lys Ala Ala Ala Gly Ile Glu Lys Gly Ala Arg Gln Thr  
                     50                    55                    60  
 30 Gly Lys Glu Val Ala Gly Leu Val Thr Leu Lys His Val Tyr Glu Ile  
                     65                    70                    75                    80  
 Ala Arg Ile Lys Ala Gln Asp Glu Ala Phe Ala Leu Gln Asp Val Pro  
                     85                    90                    95  
 35 Leu Ser Ser Val Val Arg Ser Ile Ile Gly Ser Ala Arg Ser Leu Gly  
                     100                    105                    110  
 40 Ile Arg Val Val Lys Asp Leu Ser Ser Glu Glu Leu Ala Ala Phe Gln  
                     115                    120                    125  
 Lys Glu Arg Ala Ile Phe Leu Ala Ala Gln Lys Glu Ala Asp Leu Ala  
                     130                    135                    140  
 45 Ala Gln Glu Glu Ala Ala Lys Lys  
                     145                    150

50

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 270 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

60 Ala Val Tyr Thr Tyr His Glu Lys Lys Lys Asp Thr Ala Ala Ser Gly  
     1                    5                    10                    15



611

Tyr Gly Thr Gln Asn Ile Arg Leu Ser Arg Asp Ala Val Lys Asp Phe  
                     20                    25                    30  
 5 Asp Cys Cys Cys Leu Ser Leu Gln Pro Cys His Asp Pro Val Val Thr  
                     35                    40                    45  
 Pro Asp Gly Tyr Leu Tyr Glu Arg Glu Ala Ile Leu Glu Tyr Ile Leu  
                     50                    55                    60  
 10 His Gln Lys Lys Glu Ile Ala Arg Gln Met Lys Ala Tyr Glu Lys Gln  
                     65                    70                    75                    80  
 Arg Gly Thr Arg Arg Glu Glu Gln Lys Glu Leu Gln Arg Ala Ala Ser  
                     85                    90                    95  
 15 Gln Asp His Val Arg Gly Phe Leu Glu Lys Glu Ser Ala Ile Val Ser  
                     100                    105                    110  
 20 Arg Pro Leu Asn Pro Phe Thr Ala Lys Ala Leu Ser Gly Thr Ser Pro  
                     115                    120                    125  
 Asp Asp Val Gln Pro Gly Pro Ser Val Gly Pro Pro Ser Lys Asp Lys  
                     130                    135                    140  
 25 Asp Lys Val Leu Pro Ser Phe Trp Ile Pro Ser Leu Thr Pro Glu Ala  
                     145                    150                    155                    160  
 Lys Ala Thr Lys Leu Glu Lys Pro Ser Arg Thr Val Thr Cys Pro Met  
                     165                    170                    175  
 30 Ser Gly Lys Pro Leu Arg Met Ser Asp Leu Thr Pro Val His Phe Thr  
                     180                    185                    190  
 35 Pro Leu Asp Ser Ser Val Asp Arg Val Gly Leu Ile Thr Arg Ser Glu  
                     195                    200                    205  
 Arg Tyr Val Cys Ala Val Thr Arg Asp Ser Leu Ser Asn Ala Thr Pro  
                     210                    215                    220  
 40 Cys Ala Val Leu Arg Pro Ser Gly Ala Val Val Thr Leu Glu Cys Val  
                     225                    230                    235                    240  
 Glu Lys Leu Ile Arg Lys Asp Met Val Asp Pro Val Thr Gly Asp Lys  
                     245                    250                    255  
 45 Leu Thr Asp Arg Asp Ile Ile Val Leu Gln Arg Gly Gly Thr  
                     260                    265                    270  
 50

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 54 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

60 Tyr Leu Tyr Glu Arg Glu Ala Ile Leu Glu Tyr Ile Leu His Gln Lys

612

1                      5                      10                      15  
 Lys Glu Ile Ala Arg Gln Met Lys Ala Tyr Glu Lys Gln Arg Gly Thr  
                     20                      25                      30  
 5 Arg Arg Glu Glu Gln Lys Glu Leu Gln Arg Ala Ala Ser Gln Asp His  
                     35                      40                      45  
 10 Val Arg Gly Phe Leu Glu  
                     50

(2) INFORMATION FOR SEQ ID NO: 486:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

Phe Thr Ala Lys Ala Leu Ser Gly Thr Ser Pro Asp Asp Val Gln Pro  
                     1                      5                      10                      15  
 25 Gly Pro Ser Val Gly Pro Pro Ser Lys Asp Lys Asp Lys Val Leu Pro  
                     20                      25                      30  
 Ser Phe Trp Ile Pro Ser Leu Thr Pro Glu Ala Lys Ala Thr Lys Leu  
                     35                      40                      45  
 30 Glu Lys Pro Ser Arg Thr Val Thr Cys Pro Met Ser Gly Lys Pro Leu  
                     50                      55                      60

35

(2) INFORMATION FOR SEQ ID NO: 487:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

Val His Phe Thr Pro Leu Asp Ser Ser Val Asp Arg Val Gly Leu Ile  
                     1                      5                      10                      15  
 50 Thr Arg Ser Glu Arg Tyr Val Cys Ala Val Thr Arg Asp Ser Leu Ser  
                     20                      25                      30  
 Asn Ala Thr Pro Cys Ala Val Leu Arg Pro Ser Gly Ala Val Val Thr  
                     35                      40                      45  
 55 Leu Glu Cys Val Glu Lys Leu Ile  
                     50                      55

60

## (2) INFORMATION FOR SEQ ID NO: 488:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

5 Met Asp Thr Ser Glu Asn Arg Pro Glu Asn Asp Val Pro Glu Pro Pro  
 10 1 5 10 15  
 Met Pro Ile Ala Asp Gln Val Ser Asn Asp Asp Arg Pro Glu Gly Ser  
 20 25 30  
 15 Val Glu Asp Glu Glu Lys Lys Glu Ser Ser Leu Pro Lys Ser Phe Lys  
 35 40 45  
 Arg Lys Ile Ser Val Val Ser Ala Thr Lys Gly Val Pro Ala Gly Asn  
 50 55 60  
 20 Ser Asp Thr Glu Gly Gly Gln Pro Gly Arg Lys Arg Arg Trp Gly Ala  
 65 70 75 80  
 Ser Thr Ala Thr Thr Gln Lys Lys Pro Ser Ile Ser Ile Thr Thr Glu  
 25 85 90 95  
 Ser Leu Lys Ser Leu Ile Pro Asp Ile Lys Pro Leu Ala Gly Gln Glu  
 100 105 110  
 30 Ala Val Val Asp Leu His Ala Asp Asp Ser Arg Ile Ser Glu Asp Glu  
 115 120 125  
 Thr Glu Arg Asn Gly Asp Asp Gly Thr His Asp Lys Gly Leu Lys Ile  
 130 135 140  
 35 Cys Arg Thr Val Thr Gln Val Val Pro Ala Glu Gly Gln Glu Asn Gly  
 145 150 155 160  
 Gln Arg Glu Glu Glu Glu Glu Lys Glu Pro Glu Ala Glu Pro Pro  
 40 165 170 175  
 Val Pro Pro Gln Val Ser Val Glu Val Ala Leu Pro Pro Pro Ala Glu  
 180 185 190  
 45 His Glu Val Lys Lys Val Thr Leu Gly Asp Thr Leu Thr Arg Arg Ser  
 195 200 205  
 Ile Ser Gln Gln Lys Ser Gly Val Ser Ile Thr Ile Asp Asp Pro Val  
 210 215 220  
 50 Arg Thr Ala Gln Val Pro Ser Pro Pro Arg Gly Lys Ile Ser Asn Ile  
 225 230 235 240  
 Val His Ile Ser Asn Leu Val Arg Pro Phe Thr Leu Gly Gln Leu Lys  
 245 250 255  
 Glu Leu Leu Gly Arg Thr Gly Thr Leu Val Glu Glu Ala Phe Trp Ile  
 260 265 270  
 60 Asp Lys Ile Lys Ser His Cys Phe Val Thr Tyr Ser Thr Val Glu Glu

275                      280                      285  
 Ala Val Ala Thr Arg Thr Ala Leu His Gly Val Lys Trp Pro Gln Ser  
 290                      295                      300  
 5 Asn Pro Lys Phe Leu Cys Ala Asp Tyr Ala Glu Gln Asp Glu Leu Asp  
 305                      310                      315                      320  
 10 Tyr His Arg Gly Leu Leu Val Asp Arg Pro Ser Glu Thr Lys Thr Glu  
 325                      330                      335  
 Glu Gln Gly Ile Pro Arg Pro Leu His Pro Pro Pro Pro Pro Val  
 340                      345                      350  
 15 Gln Pro Pro Gln His Pro Arg Ala Glu Gln Arg Glu Gln Glu Arg Ala  
 355                      360                      365  
 Val Arg Glu Gln Trp Ala Glu Arg Glu Arg Glu Met Glu Arg Arg Glu  
 370                      375                      380  
 20 Arg Thr Arg Ser Glu Arg Glu Trp Asp Arg Asp Lys Val Arg Glu Gly  
 385                      390                      395                      400  
 25 Pro Arg Ser Arg Ser Arg Ser Arg Xaa Arg Arg Arg Lys Glu Arg Ala  
 405                      410                      415  
 Lys Ser Lys Glu Lys Lys Ser Glu Lys Lys Glu Lys Ala Gln Glu Glu  
 420                      425                      430  
 30 Pro Pro Ala Lys Leu Leu Asp Asp Leu Phe Arg Lys Thr Lys Ala Ala  
 435                      440                      445  
 Pro Cys Ile Tyr Trp Leu Pro Leu Thr Asp Ser Gln Ile Val Gln Lys  
 450                      455                      460  
 35 Glu Ala Glu Arg Ala Glu Arg Ala Lys Glu Arg Glu Lys Arg Arg Lys  
 465                      470                      475                      480  
 40 Glu Gln Glu Glu Glu Glu Gln Lys Glu Arg Glu Lys Glu Ala Glu Arg  
 485                      490                      495  
 Glu Arg Asn Arg Gln Leu Glu Arg Glu Lys Arg Arg Glu His Ser Arg  
 500                      505                      510  
 45 Glu Arg Asp Arg Glu Arg Glu Arg Glu Arg Glu Arg Asp Arg Gly Asp  
 515                      520                      525  
 Arg Asp Arg Asp Arg Glu Arg Asp Arg Glu Arg Gly Arg Glu Arg Asp  
 530                      535                      540  
 50 Arg Arg Asp Thr Lys Arg His Ser Arg Ser Arg Ser Arg Ser Thr Pro  
 545                      550                      555                      560  
 55 Val Arg Asp Arg Gly Gly Arg  
 565

(2) INFORMATION FOR SEQ ID NO: 489:

615

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Gly Cys Asp Ser Cys Pro Pro His Leu Pro Arg Glu Ala Phe Ala Gln  
 1 5 10 15

10 Asp Thr Gln Ala Glu Gly Glu Cys Ser Ser Arg Ala Glu Arg Ala Asp  
 20 25 30

Met Cys Pro Asp Ala Pro Pro Ser Gln Glu Val Pro Glu Gly Pro Gly  
 35 40 45

15 Ala Ala Pro  
 50

20

## (2) INFORMATION FOR SEQ ID NO: 490:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

30 Pro Gln Leu Pro Ser Cys Gly Arg Pro Trp Pro Gly Thr Ala Ser Val  
 1 5 10 15

Phe Gln Ser His Thr Gln Gly Pro Arg Glu Asp Pro Asp Pro Cys Arg  
 20 25 30

35 Ala Gln Gly Ser Ala Gly Thr His Cys Pro Ile Ser Leu Ser Pro Pro  
 35 40 45

Arg Gln  
 50

40

## (2) INFORMATION FOR SEQ ID NO: 491:

45

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

Pro Gly Phe Arg Gly Pro Ser Gly Ser Leu Gly Cys Ser Phe Phe Pro  
 1 5 10 15

55 Arg Ser Leu Gly Arg Val Leu Pro Pro Gly Cys Gln Arg Pro Gly Ala  
 20 25 30

His Ala Asp Ser Ser Pro Pro Pro Thr Pro  
 35 40

60

## (2) INFORMATION FOR SEQ ID NO: 492:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

5  
 10 Glu Asp Leu Lys Lys Pro Asp Pro Ala Ser Leu Arg Ala Ala Ser Cys  
     1                    5                    10                    15  
 Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys Thr Cys Gly Leu  
                     20                    25                    30  
 15 Ala Glu Glu Leu Glu Lys Glu Lys Ser Arg Glu Gln Met Ser Ser Gln  
                     35                    40                    45  
 20 Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe Arg Cys  
                     50                    55                    60  
 Ala Ser Cys Pro Tyr Leu Gly Met Pro Ala Phe Lys Pro Gly Glu Lys  
                     65                    70                    75                    80  
 25 Val Leu Leu Ser

## 30 (2) INFORMATION FOR SEQ ID NO: 493:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

35  
 40 Glu Asp Leu Lys Lys Pro Asp Pro Ala Ser Leu Arg Ala Ala Ser Cys  
     1                    5                    10                    15  
 Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys Thr Cys Gly Leu  
                     20                    25                    30  
 45 Ala Glu Glu Leu Glu Lys Glu Lys Ser Arg Glu Gln Met Ser Ser Gln  
                     35                    40                    45  
 Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe Arg Cys  
                     50                    55                    60  
 50 Ala Ser Cys Pro Tyr Leu Gly Met Pro Ala Phe Lys Pro Gly Glu Lys  
                     65                    70                    75                    80  
 Val Leu Leu Ser Asp Ser Asn Leu His Asp  
                     85                    90

55

## (2) INFORMATION FOR SEQ ID NO: 494:

60

## (i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO: 495:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

25 Ser Cys Gly Glu Gly Lys Lys Arg Lys Ala Cys Lys Asn Cys Thr Cys  
1 5 10 15  
Gly Leu Ala Glu Glu Leu Glu Lys Glu  
20 25  
30

(2) INFORMATION FOR SEQ ID NO: 496:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Ser Gln Pro Lys Ser Ala Cys Gly Asn Cys Tyr Leu Gly Asp Ala Phe  
 1 5 10 15  
 Arg Cys Ala Ser Cys  
 20

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Arg Glu Ala Gly Gln Asn Ser Glu Arg Gln Tyr Val Ser Leu Ser Arg  
1 5 10 15  
Asp

## 5 (2) INFORMATION FOR SEQ ID NO: 498:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

Glu Ser Ser Gly Gln Ala Arg Thr Leu Ala Asp Pro Gly Pro Gly Trp  
 1 5 10 15  
 Pro Arg Gln Gln Gly Met Cys Phe Gly Ser Leu Thr Gly Leu Ser Thr  
 20 25 30  
 Thr Pro His Gly Phe Leu Thr Val Ser Ala Glu Ala Asp Pro Arg Leu  
 35 40 45  
 Ile Glu Ser Leu Ser Gln Met Leu Ser Met Gly Phe Ser Asp Glu Gly  
 50 55 60  
 Gly Trp Leu Thr Arg Leu Leu Gln Thr Lys Asn Tyr Asp Ile Gly Ala  
 65 70 75 80  
 Ala Leu Asp Thr Ile Gln Tyr Ser Lys His  
 85 90

## 30 (2) INFORMATION FOR SEQ ID NO: 499:

## 35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys Leu Val Val  
 1 5 10 15  
 Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly Gly Ala Ala Leu  
 20 25 30  
 Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Xaa Ala Val Arg Ser His  
 35 40 45  
 His His Glu Pro Ala Gly Glu Thr Gly Asn Gly Thr Ser Gly Ala Ile  
 50 55 60  
 Tyr Phe Asp Gln Val Leu Val Asn Glu Gly Gly Gly Phe Asp Arg Ala  
 65 70 75 80  
 Ser Gly Ser Phe Val Ala Pro Val Arg Gly Val Tyr Ser Phe Arg Phe  
 85 90 95  
 His Val Val Lys Val Tyr Asn Arg Gln Thr Val Gln Val Ser Leu Met  
 100 105 110



Leu Asn Thr Trp Pro Val Ile Ser Ala Phe Ala Asn Asp Pro Asp Val  
 115 120 125

5 Thr Arg Glu Ala Ala Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly  
 130 135 140

10 Asp Arg Val Ser Leu Arg Leu Arg Arg Gly Xaa Ser Thr Gly Trp  
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 500:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

20 Pro Arg Ser Arg Pro Ala Leu Arg Pro Gly Arg Gln Arg Pro Pro Ser  
 1 5 10 15

25 His Ser Ala Thr Ser Gly Val Leu Arg Pro Arg Lys Lys Pro Asp Pro  
 20 25 30

30

(2) INFORMATION FOR SEQ ID NO: 501:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

40 Met Thr Leu Ile Thr Pro Ser Xaa Lys Leu Thr Phe Xaa Lys Gly Asn  
 1 5 10 15

45 Lys Ser Trp Ser Ser Arg Ala Cys Ser Ser Thr Leu Val Asp Pro  
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 502:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

55 Gly His Pro Ser Pro Ala Leu Ser Ile Ala Pro Ser Asp Gly Ser Gln  
 1 5 10 15

60 Leu Pro Cys Asp Glu Val Pro Tyr Gly Glu Ala His Val Thr Arg Tyr  
 20 25 30

Cys Lys Lys Pro Leu Thr Asn Ser His Leu Glu Thr Glu Ala Gln Ser  
 35 40 45

5 Ser Ser Leu  
 50

10 (2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

20 GCTTCGTGTC CAACCTCTT GCCCTTCGCC TGTGTGCCTG GAGCCAGTCC CACCACGCTC 60  
 GCGTTTCCTC CTGTAGTGCT CACAGGTCCC AGCACCGATG GCATTCCCTT TGCCCTGAGT 120  
 CTGCAGCGGG TCCCTTTTGT GCTTCCTTCC CCTCAGGTAG CCTCTCTCCC CCTGGGCCAC 180  
 25 TCCCGGGGGT GAGGGGGTTA CCCCTTCCCA GTGTTTTTTA TTCCTGTGGG GCTCACCCCA 240  
 AAGTATTAAA AGTAGCTTTG TAA 263

30

(2) INFORMATION FOR SEQ ID NO: 504:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

GCTTCGTGTC CAACCTCTT GCCCTTCGCC TGTGTGCCTG GAGCCAGTCC CACCACGCTC 60  
 45 GCGTTTCCTC CTGTAGTGCT CACAGGTCCC AGCACCGATG GCATTCCCTT TGCCCTGAGT 120  
 CTGCAGCGGG TCCCTTTTGT GCTTCCTTCC CCTCAGGTAG CCTCTCTCCC CCTGGGCCAC 180  
 TCCCGGGGGT GAGGGGGTTA CCCCTTCCCA GTGTTTTTTA TTCCTGTGGG GCTCACCCCA 240  
 50 AAGTATTAAA AGTAGCTTTG TAA 263

55

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
 (B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

5 GCTTCGTGTC CAACCCTCTT GCCCTTCGCC TGTGTGCCTG GAGCCAGTCC CACCAGCTC 60  
GCGTTTCCTC CTGTAGTGCT CACAGGTCCC AGCACCGATG GCATTCCCTT TGCCCTGAGT 120  
10 CTGCAGCGGG TCCCTTTTGT GCTTCCTTCC CCTCAGGTAG CCTCTCTCCC CCTGGGCCAC 180  
TCCCGGGGGT GAGGGGGTTA CCCCTTCCCA GTGTMTTTTA TTCCTGTGGG GCTCACCCCA 240  
AAGTATTAAA AGTAGCTTTG TAA 263  
15

(2) INFORMATION FOR SEQ ID NO: 506:

20

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

30 TGGCTCACTG TCTTACAATC ACTGCTGTGG AATCATGATA CCACTTTTAG CTCCTTGCCAT 60  
CTTCCTTCAG TGTATTTTGG TTTTCAAGA GGAAGTAGAT TTAACTGGA CAACTTTGAG 120  
TACTGACATC ATTGATAAAT AAACGGCTT GTGGTTTCAA 160  
35

(2) INFORMATION FOR SEQ ID NO: 507:

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 292 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

45

Leu Asp Glu Leu Met Ala His Leu Thr Glu Met Gln Ala Lys Val Ala  
1 5 10 15

50

Val Arg Ala Asp Ala Gly Lys Lys His Leu Pro Asp Lys Gln Asp His  
20 25 30

Lys Ala Ser Leu Asp Ser Met Leu Gly Gly Leu Glu Gln Glu Leu Gln  
35 40 45

55

Asp Leu Gly Ile Ala Thr Val Pro Lys Gly His Cys Ala Ser Cys Gln  
50 55 60

Lys Pro Ile Ala Gly Lys Val Ile His Ala Leu Gly Gln Ser Trp His  
65 70 75 80

60

622

Pro Glu His Phe Val Cys Thr His Cys Lys Glu Glu Ile Gly Ser Ser  
85 90 95

5 Pro Phe Phe Glu Arg Ser Gly Leu Xaa Tyr Cys Pro Asn Asp Tyr His  
100 105 110

Gln Leu Phe Ser Pro Arg Cys Ala Tyr Cys Ala Ala Pro Ile Leu Asp  
115 120 125

10 Lys Val Leu Thr Ala Met Asn Gln Thr Trp His Pro Glu His Phe Phe  
130 135 140

Cys Ser His Cys Gly Glu Val Phe Gly Ala Glu Gly Phe His Glu Lys  
145 150 155 160

15 Asp Lys Lys Pro Tyr Cys Arg Lys Asp Phe Leu Ala Met Phe Ser Pro  
165 170 175

Lys Cys Gly Gly Cys Asn Arg Pro Val Leu Glu Asn Tyr Leu Ser Ala  
180 185 190

20 Met Asp Thr Val Trp His Pro Glu Cys Phe Val Cys Gly Asp Cys Phe  
195 200 205

25 Thr Ser Phe Ser Thr Gly Ser Phe Phe Glu Leu Asp Gly Arg Pro Phe  
210 215 220

Cys Glu Leu His Tyr His His Arg Arg Gly Thr Leu Cys His Gly Cys  
225 230 235 240

30 Gly Gln Pro Ile Thr Gly Arg Cys Ile Ser Ala Met Gly Tyr Lys Phe  
245 250 255

His Pro Glu His Phe Val Cys Ala Phe Cys Leu Thr Gln Leu Ser Lys  
260 265 270

35 Gly Ile Phe Arg Glu Gln Asn Asp Lys Thr Tyr Cys Gln Pro Cys Phe  
275 280 285

40 Asn Lys Leu Phe  
290

45 (2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Lys Ala Ser Leu Asp Ser Met Leu Gly Gly Leu Glu Gln Glu Leu Gln  
1 5 10 15

55 Asp Leu Gly Ile Ala Thr Val Pro Lys Gly His Cys Ala Ser Cys Gln  
20 25 30

Lys Pro Ile Ala Gly Lys Val Ile His Ala Leu  
35 40

60

## (2) INFORMATION FOR SEQ ID NO: 509:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Cys Pro Asn Asp Tyr His Gln Leu Phe Ser Pro Arg Cys Ala Tyr Cys  
 1 5 10 15  
 Ala Ala Pro Ile Leu Asp Lys Val Leu Thr Ala Met Asn Gln Thr Trp  
 20 25 30  
 His Pro Glu His Phe Phe Cys Ser His Cys Gly Glu Val Phe Gly Ala  
 35 40 45  
 Glu Gly  
 50

## (2) INFORMATION FOR SEQ ID NO: 510:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Asp Lys Lys Pro Tyr Cys Arg Lys Asp Phe Leu Ala Met Phe Ser Pro  
 1 5 10 15  
 Lys Cys Gly Gly Cys Asn Arg Pro Val Leu Glu Asn Tyr Leu Ser Ala  
 20 25 30  
 Met Asp Thr Val Trp His Pro Glu Cys Phe Val Cys Gly Asp Cys Phe  
 35 40 45  
 Thr Ser Phe Ser Thr Gly Ser Phe Phe Glu Leu Asp Gly Arg Pro Phe  
 50 55 60  
 Cys Glu Leu  
 65

## (2) INFORMATION FOR SEQ ID NO: 511:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Cys Gly Gln Pro Ile Thr Gly Arg Cys Ile Ser Ala Met Gly Tyr Lys  
 1 5 10 15

Phe His Pro Glu His Phe Val Cys Ala Phe Cys Leu Thr Gln Leu Ser  
20 25 30

5 Lys Gly Ile Phe Arg Glu Gln Asn Asp Lys Thr Tyr Cys Gln  
35 40 45

10 (2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Gly Ser Ser Gln Ser Val Glu Ile Pro Gly Gly Gly Thr Glu Gly  
1 5 10 15

20 Tyr His Val Leu Arg Val Gln Glu Asn Ser Pro Gly His Arg Ala Gly  
20 25 30

25 Leu Glu Pro Phe Phe Asp Phe Ile Val Ser Ile Asn Gly Ser Arg Leu  
35 40 45

Asn Lys Asp Asn Asp Thr Leu Lys Asp Leu Leu Lys Xaa Asn Val Glu  
50 55 60

30 Lys Pro Val Lys Met Leu Ile Tyr Ser Ser Lys Thr Leu Glu Leu Arg  
65 70 75 80

Glu Thr Ser Val Thr Pro Ser Asn Leu Trp Gly Gly Gln Gly Leu Leu  
85 90 95

35 Gly Val Ser Ile Arg Phe Cys Ser Phe Asp Gly Ala Asn Glu Asn Val  
100 105 110

40 Trp His Val Leu Glu Val Glu Ser Asn Ser Pro Ala Ala Leu Ala Gly  
115 120 125

Leu Arg Pro His Ser Asp Tyr Ile Ile Gly Ala Asp Thr Val Met Asn  
130 135 140

45 Glu Ser Glu Asp Leu Phe Ser Leu Ile Glu Thr His Glu Ala Lys Pro  
145 150 155 160

Leu Lys Leu Tyr Val Tyr Asn Thr Asp Thr Asp Asn Cys Arg Glu Val  
165 170 175

50 Ile Ile Thr Pro Asn Ser Ala Trp Gly Gly Glu Gly Ser Leu Gly Cys  
180 185 190

55 Gly Ile Gly Tyr Gly Tyr Leu His Arg Ile Pro Thr Arg Pro Phe Glu  
195 200 205

Glu Gly Lys Lys Ile Ser Leu Pro Gly Gln Met Ala Gly Thr Pro Ile  
210 215 220

60 Thr Pro Leu Lys Asp Gly Phe Thr Glu Val Gln Leu Ser Ser Val Asn

625

225                      230                      235                      240  
 Pro Pro Ser Leu Ser Pro Pro Gly Thr Thr Gly Ile Glu Gln Ser Leu  
                                  245                      250                      255  
 5 Thr Gly Leu Ser Ile Ser Ser Thr Pro Pro Ala Val Ser Ser Val Leu  
                                  260                      265                      270  
 Ser Thr Gly Val Pro Thr Val Pro Leu Leu Pro Pro Gln Val Asn Gln  
 10                      275                      280                      285  
 Ser Leu Thr Ser Val Pro Pro Met Asn Pro Ala Thr Thr Leu Pro Gly  
                                  290                      295                      300  
 15 Leu Met Pro Leu Pro Ala Gly Leu Pro Asn Leu Pro Asn Leu Asn Leu  
                                  305                      310                      315                      320  
 Asn Leu Pro Ala Pro His Ile Met Pro Gly Val Gly Leu Pro Glu Leu  
                                  325                      330                      335  
 20 Val Asn Pro Gly Leu Pro Pro Leu Pro Ser Met Pro Pro Arg Asn Leu  
                                  340                      345                      350  
 Pro Gly Ile Ala Pro Leu Pro Leu Pro Ser Glu Phe Leu Pro Ser Phe  
 25                      355                      360                      365  
 Pro Leu Val Pro Glu Ser Ser Ser Ala Ala Ser Ser Gly Glu Leu Leu  
                                  370                      375                      380  
 30 Ser Ser Leu Pro Pro Thr Ser Asn Ala Pro Ser Asp Pro Ala Thr Thr  
                                  385                      390                      395                      400  
 Thr Ala Lys Ala Asp Ala Ala Ser Ser Leu Thr Val Asp Val Thr Pro  
                                  405                      410                      415  
 35 Pro Thr Ala Lys Ala Pro Thr Thr Val Glu Asp Arg Val Gly Asp Ser  
                                  420                      425                      430  
 Thr Pro Val Ser Glu Lys Pro Val Ser Ala Ala Val Asp Ala Asn Ala  
 40                      435                      440                      445  
 Ser Glu Ser Pro  
                                  450

45

(2) INFORMATION FOR SEQ ID NO: 513:

50 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 109 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

55 Ser Val Glu Ile Pro Gly Gly Gly Thr Glu Gly Tyr His Val Leu Arg  
       1                      5                      10                      15  
 Val Gln Glu Asn Ser Pro Gly His Arg Ala Gly Leu Glu Pro Phe Phe  
                                  20                      25                      30

60

626

Asp Phe Ile Val Ser Ile Asn Gly Ser Arg Leu Asn Lys Asp Asn Asp  
 35 40 45

5 Thr Leu Lys Asp Leu Leu Lys Xaa Asn Val Glu Lys Pro Val Lys Met  
 50 55 60

Leu Ile Tyr Ser Ser Lys Thr Leu Glu Leu Arg Glu Thr Ser Val Thr  
 65 70 75 80

10 Pro Ser Asn Leu Trp Gly Gly Gln Gly Leu Leu Gly Val Ser Ile Arg  
 85 90 95

Phe Cys Ser Phe Asp Gly Ala Asn Glu Asn Val Trp His  
 100 105

15

(2) INFORMATION FOR SEQ ID NO: 514:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

25 Glu Ser Asn Ser Pro Ala Ala Leu Ala Gly Leu Arg Pro His Ser Asp  
 1 5 10 15

30 Tyr Ile Ile Gly Ala Asp Thr Val Met Asn Glu Ser Glu Asp Leu Phe  
 20 25 30

Ser Leu Ile Glu Thr His Glu Ala Lys Pro Leu Lys Leu Tyr Val Tyr  
 35 40 45

35 Asn Thr Asp Thr Asp Asn Cys Arg Glu Val Ile Ile Thr Pro Asn Ser  
 50 55 60

Ala Trp Gly Gly Glu Gly Ser Leu Gly Cys Gly Ile Gly Tyr Gly Tyr  
 65 70 75 80

40 Leu His Arg Ile Pro Thr Arg Pro Phe Glu Glu Gly Lys Lys Ile Ser  
 85 90 95

45 Leu Pro Gly Gln Met Ala Gly Thr Pro Ile Thr Pro Leu Lys Asp Gly  
 100 105 110

Phe Thr Glu Val Gln Leu Ser Ser Val Asn Pro Pro Ser Leu Ser Pro  
 115 120 125

50 Pro Gly Thr Thr Gly Ile Glu Gln Ser Leu Thr Gly Leu Ser Ile Ser  
 130 135 140

Ser  
 145

55

(2) INFORMATION FOR SEQ ID NO: 515:

60 (i) SEQUENCE CHARACTERISTICS:



627

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

5  
 Glu Ser Asn Ser Pro Ala Ala Leu Ala Gly Leu Arg Pro His Ser Asp  
 1 5 10 15  
 Tyr Ile Ile Gly Ala Asp Thr Val Met Asn Glu Ser Glu Asp Leu Phe  
 10 20 25 30  
 Ser Leu Ile Glu Thr His Glu Ala Lys Pro Leu Lys Leu Tyr Val Tyr  
 35 40 45  
 15 Asn Thr Asp Thr Asp Asn Cys Arg Glu Val Ile Ile Thr Pro Asn Ser  
 50 55 60  
 Ala Trp Gly Gly Glu Gly Ser Leu Gly Cys Gly Ile Gly Tyr Gly Tyr  
 65 70 75 80  
 20 Leu His Arg Ile Pro Thr Arg Pro Phe Glu Glu Gly Lys Lys Ile Ser  
 85 90 95  
 Leu Pro Gly Gln Met Ala Gly Thr Pro Ile Thr Pro Leu Lys Asp Gly  
 25 100 105 110  
 Phe Thr Glu Val Gln Leu Ser Ser Val Asn Pro Pro Ser Leu Ser Pro  
 115 120 125  
 30 Pro Gly Thr Thr Gly Ile Glu Gln Ser Leu Thr Gly Leu Ser Ile Ser  
 130 135 140  
 Ser  
 145  
 35

(2) INFORMATION FOR SEQ ID NO: 516:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:  
 Arg Ile Pro Thr Arg Pro Phe Glu Glu Gly Lys Lys Ile Ser Leu Pro  
 1 5 10 15  
 Gly Gln Met Ala Gly Thr Pro Ile Thr Pro Leu Lys Asp Gly Phe Thr  
 50 20 25 30  
 Glu Val Gln Leu Ser Ser Val Asn Pro Pro Ser Leu Ser Pro Pro Gly  
 35 40 45  
 55 Thr Thr Gly Ile Glu Gln Ser Leu Thr Gly Leu Ser Ile Ser Ser Thr  
 50 55 60  
 Pro Pro Ala Val Ser Ser Val Leu Ser Thr Gly Val Pro Thr Val Pro  
 65 70 75 80  
 60

628

Leu Leu Pro Pro Gln Val Asn Gln Ser Leu Thr Ser Val Pro Pro Met  
                             85                            90                            95  
 Asn Pro Ala Thr Thr Leu Pro Gly Leu Met Pro Leu Pro Ala Gly Leu  
 5                            100                            105                            110  
 Pro Asn Leu Pro Asn Leu Asn Leu Asn Leu Pro Ala Pro His Ile Met  
                             115                            120                            125  
 10 Pro Gly Val Gly Leu Pro Glu Leu Val Asn Pro Gly Leu Pro Pro Leu  
                             130                            135                            140  
 Pro Ser Met Pro Pro Arg Asn  
 15                            145                            150

(2) INFORMATION FOR SEQ ID NO: 517:

20 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 109 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:  
 Pro Gly Leu Pro Pro Leu Pro Ser Met Pro Pro Arg Asn Leu Pro Gly  
   1                            5                            10                            15  
 30 Ile Ala Pro Leu Pro Leu Pro Ser Glu Phe Leu Pro Ser Phe Pro Leu  
                             20                            25                            30  
 Val Pro Glu Ser Ser Ser Ala Ala Ser Ser Gly Glu Leu Leu Ser Ser  
                             35                            40                            45  
 35 Leu Pro Pro Thr Ser Asn Ala Pro Ser Asp Pro Ala Thr Thr Thr Ala  
                             50                            55                            60  
 Lys Ala Asp Ala Ala Ser Ser Leu Thr Val Asp Val Thr Pro Pro Thr  
   65                            70                            75                            80  
 40 Ala Lys Ala Pro Thr Thr Val Glu Asp Arg Val Gly Asp Ser Thr Pro  
                             85                            90                            95  
 Val Ser Glu Lys Pro Val Ser Ala Ala Val Asp Ala Asn  
 45                            100                            105

(2) INFORMATION FOR SEQ ID NO: 518:

50 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 93 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:  
 Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
   1                            5                            10                            15  
 60 Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa

629

20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Trp Ile Phe Gly Val Leu His Val Val His  
35 40 45

5 Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
50 55 60

10 Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
65 70 75 80

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys  
85 90

15

(2) INFORMATION FOR SEQ ID NO: 519:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

25

Trp Ile Phe Gly Val Leu His Val Val His Ala Ser Val Val Thr Ala  
1 5 10 15

30

Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln Gly Met Phe Ile Phe Leu  
20 25 30

Phe Leu Cys Val Leu Ser Arg Lys Ile Gln Glu Glu Tyr Tyr Arg Leu  
35 40 45

35

Phe Lys Asn Val Pro Cys Cys  
50 55

40

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

Ala Leu Thr Arg Ile Pro Pro Gly Asp Trp Val Ile Asn Val Thr Ala  
1 5 10 15

50

Val Ser Phe Ala Gly Lys Thr Thr Ala Arg Phe Phe Xaa His Ser Ser  
20 25 30

55

Pro Pro Ser Leu Gly Asp Gln Ala Arg Thr Asp Pro Gly His Gln Arg  
35 40 45

Arg Asp  
50

60

## (2) INFORMATION FOR SEQ ID NO: 521:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Leu Gln Glu Val Asn Ile Thr Leu Pro Glu Asn Ser Val Trp Tyr Glu  
 1 5 10 15

Arg Tyr Lys Phe Asp Ile Pro Val Phe His Leu  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 522:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Gln Gly Ser Gly Ser Gln Phe Arg Ala Cys Leu Leu Cys Leu Cys  
 1 5 10 15

Phe Ser Cys Pro Cys Ser Pro Gly Gly Pro Arg Trp Asn Ser Arg Gln  
 20 25 30

Gly Gly Arg Arg Phe Pro Lys Thr Cys Arg Ala Ile Ser Gln Asn Leu  
 35 40 45

Val Phe Lys Tyr Lys Thr Phe Cys Pro Val Arg Tyr Met Gln Pro His  
 50 55 60

Arg Ser Ser Leu Cys Leu His Phe Thr Ser Tyr Val Phe Ile Leu Ser  
 65 70 75 80

Thr Trp Gly Ser Leu Arg Thr Tyr Ser Thr Asp Leu Lys Lys Lys Lys  
 85 90 95

Lys Asn Ser Arg Gly Gly Pro Val Pro Ile Arg Pro Lys Ser  
 100 105 110

## (2) INFORMATION FOR SEQ ID NO: 523:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

TAGCATGTAG CCACTCGAAT AACNTATAAG GACAAAGTGG AGTCCACGCG TCGGGCCGTC 60

TAGACTAGTG GATCCCCCGG CTGCAGGATT CGGCACGAG 99

## 5 (2) INFORMATION FOR SEQ ID NO: 524:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Met Gln Gly Ser Gly Ser Gln Phe Arg Ala Cys Leu Leu Cys Leu Cys  
 1 5 10 15

15 Phe Ser Cys Pro Cys Ser Pro Gly Gly Pro Arg Trp Asn Ser Arg Gln  
 20 25 30

20 Gly Gly Arg Arg Phe Pro Lys Thr Cys Arg Ala Ile Ser Gln Asn Leu  
 35 40 45

Val Phe Lys  
 50

25

## (2) INFORMATION FOR SEQ ID NO: 525:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

35 Pro Val Arg Tyr Met Gln Pro His Arg Ser Ser Leu Cys Leu His Phe  
 1 5 10 15

Thr Ser Tyr Val Phe Ile Leu Ser Thr Trp Gly Ser Leu Arg Thr Tyr  
 20 25 30

40 Ser Thr Asp Leu Lys Lys Lys Lys Lys Asn Ser Arg Gly Gly Pro Val  
 35 40 45

45 Pro Ile Arg Pro Lys Ser  
 50

## 50 (2) INFORMATION FOR SEQ ID NO: 526:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Gly Glu Glu Gln Arg Asp Cys Ser Leu Gly Trp Arg Gly Val Gly Met  
 1 5 10 15

60 Arg Ala Thr His Cys Gln Ala Ala Arg Met Phe Val Leu Phe Ser Leu

632

20 25 30

Pro Lys Tyr Ala Gly Leu  
35

5

(2) INFORMATION FOR SEQ ID NO: 527:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 161 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

Met Pro Arg Lys Thr Ser Lys Cys Arg Gln Leu Leu Cys Ser Gly Ala  
1 5 10 15

Ser Arg Asn Ala Asp Thr Ala Ala Arg Gln Ser Thr Cys Ser Ser His  
20 25 30

Arg Pro Pro Gly Lys Ile Pro Ser Leu Gly Pro Arg Arg Xaa Pro Gly  
35 40 45

25 Cys Xaa Ser Val Pro Ser Ser Arg Gly Glu Gln Ser Thr Gly Ser Pro  
50 55 60

Ala Ala Pro Arg Cys Gly Arg Arg Asp Ala His Arg Gly Leu Pro Gly  
65 70 75 80

30 Gly Ala Ala Met Thr Pro Gly Asp Thr Trp Ala Ser Phe Asn Pro Arg  
85 90 95

Ala Gly His Ser Lys Ser Gln Gly Glu Gly Gln Glu Ser Ser Gly Ala  
35 100 105 110

Ser Arg Gln Asp Arg His Pro Val Ser His Trp Val Glu Arg Gln Arg  
115 120 125

40 Glu Ala Trp Gly Ala Pro Arg Ser Ser Ser Ala Gly Gly Val Lys Val  
130 135 140

Ala Ala Thr Thr Glu Arg Glu Pro Glu Phe Lys Ile Lys Thr Gly Lys  
145 150 155 160

45 Ala

50

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Cys Ser Gly Ala Ser Arg Asn Ala Asp Thr Ala Ala Arg Gln Ser Thr  
60 1 5 10 15

633

Cys Ser Ser His Arg Pro Pro Gly Lys Ile Pro Ser Leu Gly Pro Arg  
                   20                  25                  30  
 5 Arg Xaa Pro Gly Cys Xaa Ser Val Pro Ser Ser Arg Gly Glu Gln Ser  
                   35                  40                  45  
 Thr Gly Ser Pro Ala Ala Pro Arg Cys Gly Arg Arg Asp Ala His Arg  
                   50                  55                  60  
 10 Gly Leu Pro Gly Gly Ala Ala Met Thr Pro Gly Asp Thr Trp Ala Ser  
                   65                  70                  75                  80  
 Phe Asn Pro Arg Ala Gly His Ser  
 15                  85

(2) INFORMATION FOR SEQ ID NO: 529:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Gln Gly Glu Gly Gln Glu Ser Ser Gly Ala Ser Arg Gln Asp Arg His  
   1                  5                  10                  15  
 30 Pro Val Ser His Trp Val Glu Arg Gln Arg Glu Ala Trp Gly Ala Pro  
                   20                  25                  30  
 Arg Ser Ser Ser Ala Gly Gly Val Lys Val Ala Ala Thr Thr Glu Arg  
                   35                  40                  45  
 35 Glu Pro Glu Phe Lys Ile Lys Thr Gly Lys Ala  
                   50                  55

40

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

45

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Ser Pro Arg Tyr Pro Gly Gly Pro Arg Pro Pro Leu Arg Ile Pro  
   1                  5                  10                  15  
 Asn Gln Ala Leu Gly Gly Val Pro Gly Ser Gln Pro Leu Leu Pro Ser  
                   20                  25                  30  
 55 Gly Met Asp Pro Thr Arg Gln Gln Gly His Pro Asn Met Gly Gly Pro  
                   35                  40                  45  
 Met Gln Arg Met Thr Pro Pro Arg Gly Met Val Pro Leu Gly Pro Gln  
                   50                  55                  60

60

634

Asn Tyr Gly Gly Ala Met Arg Pro Pro Leu Asn Ala Leu Gly Gly Pro  
 65 70 75 80  
 5 Gly Met Pro Gly Met Asn Met Gly Pro Gly Gly Gly Arg Pro Trp Pro  
 85 90 95  
 Asn Pro Thr Asn Ala Asn Ser Ile Pro Tyr Ser Ser Ala Ser Pro Gly  
 100 105 110  
 10 Asn Tyr Val Gly Pro Pro Gly Gly Gly Gly Pro Pro Gly Thr Pro Ile  
 115 120 125  
 Met Pro Ser Pro Ala Asp Ser Thr Asn Ser Gly Asp Asn Met Tyr Thr  
 130 135 140  
 15 Leu Met Asn Ala Val Pro Pro Gly Pro Asn Arg Pro Asn Phe Pro Met  
 145 150 155 160  
 Gly Pro Gly Ser Asp Gly Pro Met Gly Gly Leu Gly Gly Met Glu Ser  
 165 170 175  
 20 His His Met Asn Gly Ser Leu Gly Ser Gly Asp Met Asp Ser Ile Ser  
 180 185 190  
 25 Lys Asn Ser Pro Asn Asn Met Ser Leu Ser Asn Gln Pro Gly Thr Pro  
 195 200 205  
 Arg Asp Asp Gly Glu Met Gly Gly Asn Phe Leu Asn Pro Phe Gln Ser  
 210 215 220  
 30 Glu Ser Tyr Ser Pro Ser Met Thr Met Ser Val  
 225 230 235  
 35 (2) INFORMATION FOR SEQ ID NO: 531:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:  
 40 Met Ser Pro Arg Tyr Pro Gly Gly Pro Arg Pro Pro Leu Arg Ile Pro  
 1 5 10 15  
 Asn Gln Ala Leu Gly Gly Val Pro Gly Ser Gln Pro Leu Leu Pro Ser  
 20 25 30  
 50 Gly Met Asp Pro Thr Arg Gln Gln Gly His Pro Asn Met Gly Gly Pro  
 35 40 45  
 Met Gln Arg Met Thr Pro Pro Arg Gly Met Val Pro Leu Gly Pro Gln  
 50 55 60  
 55 Asn Tyr Gly Gly Ala Met Arg Pro Pro Leu Asn Ala Leu Gly Gly Pro  
 65 70 75 80  
 Gly Met Pro Gly Met Asn Met Gly Pro Gly Gly Gly Arg Pro Trp Pro  
 85 90 95  
 60



635

Asn Pro Thr Asn Ala Asn Ser Ile Pro Tyr Ser Ser Ala Ser Pro Gly  
 100 105 110

5 Asn Tyr

10 (2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

Leu Asn Ala Leu Gly Gly Pro Gly Met Pro Gly Met Asn Met Gly Pro  
 1 5 10 15  
 20 Gly Gly Gly Arg Pro Trp Pro Asn Pro Thr Asn Ala Asn Ser Ile Pro  
 20 25 30  
 25 Tyr Ser Ser Ala Ser Pro Gly Asn Tyr Val Gly Pro Pro Gly Gly Gly  
 35 40 45  
 Gly Pro Pro Gly Thr Pro Ile Met Pro Ser Pro Ala Asp Ser Thr Asn  
 50 55 60  
 30 Ser Gly Asp Asn Met Tyr Thr Leu Met Asn Ala Val Pro Pro Gly Pro  
 65 70 75 80  
 Asn

35

(2) INFORMATION FOR SEQ ID NO: 533:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Gly Pro Met Gly Gly Leu Gly Gly Met Glu Ser His His Met Asn Gly  
 1 5 10 15  
 50 Ser Leu Gly Ser Gly Asp Met Asp Ser Ile Ser Lys Asn Ser Pro Asn  
 20 25 30  
 Asn Met Ser Leu Ser Asn Gln Pro Gly Thr Pro Arg Asp Asp Gly Glu  
 35 40 45  
 55 Met Gly Gly Asn Phe Leu Asn Pro Phe Gln Ser Glu Ser Tyr Ser Pro  
 50 55 60  
 Ser Met Thr Met Ser Val  
 65 70

60

## (2) INFORMATION FOR SEQ ID NO: 534:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

10

Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe His Asp Tyr  
 1 5 10

15

## (2) INFORMATION FOR SEQ ID NO: 535:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

20

Gln Ala Phe Val Leu Leu Ser Asp Leu Leu Leu Ile Phe Ser Pro Gln  
 1 5 10 15

25

Met Ile Val Gly Gly Arg Asp Phe Leu Arg Pro Leu Val Phe Phe Pro  
 20 25 30

30

Glu Ala Thr Leu Gln Ser Glu Leu Ala Ser Phe Leu Met Asp His Val  
 35 40 45

Phe Ile Gln Pro Gly Asp Leu Ser Gly Ala  
 50 55

35

## (2) INFORMATION FOR SEQ ID NO: 536:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

45

Ala Cys Ser Tyr Leu Leu Cys Asn Pro Glu Phe Thr Phe Phe Ser Arg  
 1 5 10 15

50

Ala Asp Phe Ala Arg Ser Gln Leu Val Asp Leu Leu Thr Asp Arg Phe  
 20 25 30

Gln Gln Glu Leu Glu Glu Leu Leu Gln Val Gly  
 35 40

55

## (2) INFORMATION FOR SEQ ID NO: 537:

60

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

637

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

5 Gln Lys Gln Leu Ser Ser Leu Arg Asp Arg Met Val Ala Phe Cys Glu  
 1 5 10 15  
 Leu Cys Gln Ser Cys Leu Ser Asp Val Asp Thr Glu Ile Gln Glu Gln  
 20 25 30  
 10 Val Ser Thr  
 35

15

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

20 Gln Val Ile Leu Pro Ala Leu Thr Leu Val Tyr Phe Ser Ile Leu Trp  
 25 1 5 10 15  
 Thr Leu Thr His Ile Ser Lys Ser Asp Ala Ser  
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

35 Ser Thr His Asp Leu Thr Arg Trp Glu Leu Tyr Glu Pro Cys Cys Gln  
 40 1 5 10 15  
 Leu Leu Gln Lys Ala Val Asp Thr Gly Xaa Val Pro His Gln Val  
 20 25 30

45

(2) INFORMATION FOR SEQ ID NO: 540:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

55

Leu Ala Val Ser Thr Ser Phe Ile Cys Cys Ala Asp Ile Ser Thr Ala  
 1 5 10 15  
 Leu Pro Leu Gly Ser Ser Arg Pro Ala Pro Ala Pro Arg His Arg Glu  
 20 25 30

60

638

His Glu His Gly His Gln Ala Arg Pro Pro Arg Leu Leu Xaa Thr Ser  
           35                    40                    45  
 5 Leu Met Pro Leu Ser Thr Pro Ala Ala Ala Gln Leu Trp Thr Gln  
       50                    55                    60  
 Leu Thr Pro Met Gly Gly Arg Pro Gly Gly Arg His Ser Pro Pro Thr  
   65                    70                    75                    80  
 10 Leu His Thr Gly Pro Arg Ala Leu Pro Pro Gly Pro Pro His Pro Ser  
                     85                    90                    95  
 Leu His Val Ala Ala Leu Ser Leu Leu Arg  
 15                    100                    105

20 (2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Glu Gln Val Leu Ala Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu  
   1                    5                    10                    15  
 30 Met Asn Val Gln Ser Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly  
                     20                    25                    30  
 Leu Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser  
   35                    40                    45  
 35 Ser Ala Leu Val Ser Ile Asn Gln Thr Ile Pro Asn Glu Arg Thr Met  
   50                    55                    60  
 Gln Leu Leu Gly Gln Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg  
 40  65                    70                    75                    80  
 Val Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile  
                     85                    90                    95  
 45 Asn Asn Tyr Asp Met Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp  
                     100                    105                    110  
 Asp Ser Lys Glu Val Glu Ser Phe Gln Gln Leu Leu Asn Ala Arg Thr  
   115                    120                    125  
 50 Gln Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro Phe Gly Gly Leu Val  
   130                    135                    140  
 Ala Phe Val Lys Glu Ala Glu Ala Leu Ile Glu Arg Gly Gln Ala Glu  
 55  145                    150                    155                    160  
 Arg Leu Arg Gly Glu Ala Arg Val Thr Gln Leu Ile Arg Gly Phe  
                     165                    170                    175  
 60 Gly Ser Ser Trp Lys Ser Ser Val Glu Ser Leu Ser Gln Asp Val Met

180 185 190  
 Arg Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser Ile Ile Gln Gly  
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO: 542:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

15

Ala Leu Leu Lys Tyr Arg Phe Phe Tyr Gln Phe Leu Leu Gly Asn Glu  
 1 5 10 15

20

Arg Ala Thr Ala Lys Glu Ile Arg Asp Glu Tyr Val Glu Thr Leu Ser  
 20 25 30

Lys Ile Tyr Leu Ser Tyr Tyr Arg Ser Tyr Leu Gly Arg Leu Met Lys  
 35 40 45

25

Val Gln Tyr Glu Glu Val Ala Glu Lys Asp Asp Leu Met Gly Val Glu  
 50 55 60

Asp Thr Ala Lys Lys Gly Phe Xaa Ser Lys Pro Ser Leu Arg Ser Arg  
 65 70 75 80

30

Asn Thr Ile Phe Thr Leu Gly Thr Arg Gly Ser Val Ile Ser Pro Thr  
 85 90 95

35

Glu Leu Glu Ala Pro Ile Leu Val Pro His Thr Ala Gln Arg  
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 543:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Glu Gln Arg Tyr Pro Phe Glu Ala Leu Phe Arg Ser Gln His Tyr Xaa  
 1 5 10 15

50

Leu Leu Asp Asn Ser Cys Arg Glu Tyr Leu Phe Ile Cys Glu Phe Phe  
 20 25 30

Val Val Ser Gly Pro Xaa Ala His Asp Leu Phe His Ala Val Met Gly  
 35 40 45

55

Arg Thr Leu Ser Met Thr Leu Lys His Leu Asp Ser Tyr Leu Ala Asp  
 50 55 60

60

Cys Tyr Asp Ala Ile Ala Val Phe Leu Cys Ile His Ile Val Leu Arg  
 65 70 75 80

640

Phe Arg Asn Ile Ala Ala Lys Arg Asp Val Pro Ala Leu Asp Arg Tyr  
                     85                    90                    95

5 Trp

10 (2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Gly Gly Leu Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu  
       1                    5                    10                    15

20 Phe Ser Ser Ala Leu Val Ser Ile Asn Gln  
                     20                    25

25

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

30 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

35 Ser Arg Lys Glu Gln Leu Val Phe Leu Ile Asn Asn Tyr Asp Met Met  
       1                    5                    10                    15

Leu Gly Val Leu  
                     20

40

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

50 Ala Leu Leu Lys Tyr Arg Phe Phe Tyr Gln Phe Leu Leu Gly Asn Glu  
       1                    5                    10                    15

Arg Ala Thr Ala Lys Glu Ile Arg Asp Glu Tyr Val Glu Thr Leu Ser  
                     20                    25                    30

55

Lys Ile Tyr Leu Ser Tyr Tyr Arg Ser Tyr Leu Gly Arg Leu Met Lys  
                     35                    40                    45

60 Val Gln Tyr Glu Glu Val Ala Glu Lys Asp Asp Leu Met Gly Val Glu  
                     50                    55                    60

Asp Thr Ala Lys Lys Gly Phe Xaa Ser Lys Pro Ser Leu Arg Ser Arg  
 65 70 75 80

5 Asn Thr Ile Phe Thr Leu Gly Thr Arg Gly Ser Val Ile Ser Pro Thr  
 85 90 95

Glu Leu Glu Ala Pro Ile Leu Val Pro His Thr Ala Gln Arg Xaa Glu  
 100 105 110

10 Gln Arg Tyr Pro Phe Glu Ala Leu Phe Arg Ser Gln His Tyr Xaa Leu  
 115 120 125

15 Leu Asp Asn Ser Cys Arg Glu Tyr Leu Phe Ile Cys Glu Phe Phe Val  
 130 135 140

Val Ser Gly Pro Xaa Ala His Asp Leu Phe His Ala Val Met Gly Arg  
 145 150 155 160

20 Thr Leu Ser Met Thr Leu Lys His Leu Asp Ser Tyr Leu Ala Asp Cys  
 165 170 175

Tyr Asp Ala Ile Ala Val Phe Leu Cys Ile His Ile Val Leu Arg Phe  
 180 185 190

25 Arg Asn Ile Ala Ala Lys Arg Asp Val Pro Ala Leu Asp Arg Tyr Trp  
 195 200 205

30 Glu Gln Val Leu Ala Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu  
 210 215 220

Met Asn Val Gln Ser Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly  
 225 230 235 240

35 Leu Asp Thr Arg Pro His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser  
 245 250 255

Ser Ala Leu Val Ser Ile Asn Gln Thr Ile Pro Asn Glu Arg Thr Met  
 260 265 270

40 Gln Leu Leu Gly Gln Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg  
 275 280 285

Val Ala Ala Glu Phe Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile  
 290 295 300

45 Asn Asn Tyr Asp Met Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp  
 305 310 315 320

50 Asp Ser Lys Glu Val Glu Ser Phe Gln Gln Leu Leu Asn Ala Arg Thr  
 325 330 335

Gln Glu Phe Ile Glu Glu Leu Leu Ser Pro Pro Phe Gly Gly Leu Val  
 340 345 350

55 Ala Phe Val Lys Glu Ala Glu Ala Leu Ile Glu Arg Gly Gln Ala Glu  
 355 360 365

60 Arg Leu Arg Gly Glu Glu Ala Arg Val Thr Gln Leu Ile Arg Gly Phe  
 370 375 380

642

Gly Ser Ser Trp Lys Ser Ser Val Glu Ser Leu Ser Gln Asp Val Met  
385 390 395 400

5 Arg Ser Phe Thr Asn Phe Arg Asn Gly Thr Ser  
405 410

10 (2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Tyr Glu Gly Lys Glu Phe Asp Tyr Val Phe Ser Ile Asp Val Asn Glu  
1 5 10 15

20 Gly Gly Pro Ser Tyr Lys Leu Pro Tyr Asn Thr Ser Asp Asp Pro Trp  
20 25 30

25 Leu Thr Ala Tyr Asn Phe Leu Gln Lys Asn Asp Leu Asn Pro Met Phe  
35 40 45

Leu Asp Gln Val Ala Lys Phe Ile Ile Asp Asn Thr Lys Gly Gln Met  
50 55 60

30 Leu Gly Leu Gly Asn Pro Ser Phe Ser Asp Pro Phe Thr Gly Gly Gly  
65 70 75 80

Arg Tyr Val Pro Gly Ser Ser Gly Ser Ser Asn Thr Leu Pro Thr Ala  
85 90 95

35 Asp Pro Phe Thr Gly Ala Gly Arg Tyr Val Pro Gly Ser Ala Ser Met  
100 105 110

40 Gly Thr Thr Met Ala Gly Val Asp Pro Phe Thr Gly Asn Ser Ala Tyr  
115 120 125

Arg Ser Ala Ala Ser Lys Thr Met Asn Ile Tyr Phe Pro Lys Lys Glu  
130 135 140

45 Ala Val Thr Phe Asp Gln Ala Asn Pro Thr Gln Ile Leu Gly Lys Leu  
145 150 155 160

Lys Glu Leu Asn Gly Thr Ala Pro Glu Glu Lys Lys Leu Thr Glu Asp  
165 170 175

50 Asp Leu Ile Leu Leu Glu Lys Ile Leu Ser Leu Ile Cys Asn Ser Ser  
180 185 190

Ser Glu Lys Pro Thr Val Gln Gln Leu Gln Ile Leu Trp Lys Ala Ile  
195 200 205

Asn Cys Pro Glu Asp Ile Val Phe Pro Ala Leu Asp Ile Leu Arg Leu  
210 215 220

60 Ser Ile Lys His Pro Ser Val Asn Glu Asn Phe Cys Asn Glu Lys Glu



643

225                      230                      235                      240  
 Gly Ala Gln Phe Ser Ser His Leu Ile Asn Leu Leu Asn Pro Lys Gly  
                          245                      250                      255  
 5 Lys Pro Ala Asn Gln Leu Leu Ala Leu Arg Thr Phe Cys Asn Cys Phe  
                          260                      265                      270  
 10 Val Gly Gln Ala Gly Gln Lys Leu Met Met Ser Gln Arg Glu Ser Leu  
                          275                      280                      285  
 Met Ser His Ala Ile Glu Leu Lys Ser Gly Ser Asn Lys Asn Ile  
                          290                      295                      300

15

(2) INFORMATION FOR SEQ ID NO: 548:

20 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 18 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

25 His Ile Ala Leu Ala Thr Leu Ala Leu Asn Tyr Ser Val Cys Phe His  
       1                      5                      10                      15

Lys Asp

30

(2) INFORMATION FOR SEQ ID NO: 549:

35 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 49 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

40 His Asn Ile Glu Gly Lys Ala Gln Cys Leu Ser Leu Ile Ser Thr Ile  
       1                      5                      10                      15

45 Leu Glu Val Val Gln Asp Leu Glu Ala Thr Phe Arg Leu Leu Val Ala  
                          20                      25                      30

Leu Gly Thr Leu Ile Ser Asp Asp Ser Asn Ala Val Gln Leu Ala Lys  
                          35                      40                      45

50 Ser

55 (2) INFORMATION FOR SEQ ID NO: 550:

60 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 30 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear

644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Leu Gly Val Asp Ser Gln Ile Lys Lys Tyr Ser Ser Val Ser Glu Pro  
 1 5 10 15

Ala Lys Val Ser Glu Cys Cys Arg Phe Ile Leu Asn Leu Leu  
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

20

Tyr Glu Gly Lys Glu Phe Asp Tyr Val Phe Ser Ile Asp Val Asn Glu  
 1 5 10 15

Gly Gly Pro Ser Tyr Lys Leu Pro Tyr Asn Thr Ser Asp Asp Pro Trp  
 20 25 30

25

Leu Thr Ala Tyr Asn Phe Leu Gln Lys Asn Asp Leu Asn Pro Met Phe  
 35 40 45

Leu Asp Gln Val Ala Lys Phe Ile Ile Asp Asn Thr Lys Gly Gln Met  
 50 55 60

30

Leu Gly Leu Gly Asn Pro Ser Phe Ser Asp Pro Phe Thr Gly Gly Gly  
 65 70 75 80

35

Arg Tyr Val Pro Gly Ser Ser Gly Ser Ser Asn Thr Leu Pro Thr Ala  
 85 90 95

Asp Pro Phe Thr Gly Ala Gly Arg Tyr Val Pro Gly Ser Ala Ser Met  
 100 105 110

40

Gly Thr Thr Met Ala Gly Val Asp Pro Phe Thr Gly Asn Ser Ala Tyr  
 115 120 125

Arg Ser Ala Ala Ser Lys Thr Met Asn Ile Tyr Phe Pro Lys Lys Glu  
 130 135 140

45

Ala Val Thr Phe Asp Gln Ala Asn Pro Thr Gln Ile Leu Gly Lys Leu  
 145 150 155 160

50

Lys Glu Leu Asn Gly Thr Ala Pro Glu Glu Lys Lys Leu Thr Glu Asp  
 165 170 175

Asp Leu Ile Leu Leu Glu Lys Ile Leu Ser Leu Ile Cys Asn Ser Ser  
 180 185 190

55

Ser Glu Lys Pro Thr Val Gln Gln Leu Gln Ile Leu Trp Lys Ala Ile  
 195 200 205

Asn Cys Pro Glu Asp Ile Val Phe Pro Ala Leu Asp Ile Leu Arg Leu  
 210 215 220

60

645

Ser Ile Lys His Pro Ser Val Asn Glu Asn Phe Cys Asn Glu Lys Glu  
 225 230 235 240  
 Gly Ala Gln Phe Ser Ser His Leu Ile Asn Leu Leu Asn Pro Lys Gly  
 5 245 250 255  
 Lys Pro Ala Asn Gln Leu Leu Ala Leu Arg Thr Phe Cys Asn Cys Phe  
 260 265 270  
 Val Gly Gln Ala Gly Gln Lys Leu Met Met Ser Gln Arg Glu Ser Leu  
 10 275 280 285  
 Met Ser His Ala Ile Glu Leu Lys Ser Gly Ser Asn Lys Asn Ile His  
 290 295 300  
 15 Ile Ala Leu Ala Thr Leu Ala Leu Asn Tyr Ser Val Cys Phe His Lys  
 305 310 315 320  
 Asp His Asn Ile Glu Gly Lys Ala Gln Cys Leu Ser Leu Ile Ser Thr  
 20 325 330 335  
 Ile Leu Glu Val Val Gln Asp Leu Glu Ala Thr Phe Arg Leu Leu Val  
 340 345 350  
 Ala Leu Gly Thr Leu Ile Ser Asp Asp Ser Asn Ala Val Gln Leu Ala  
 25 355 360 365  
 Lys Ser Leu Gly Val Asp Ser Gln Ile Lys Lys Tyr Ser Ser Val Ser  
 370 375 380  
 30 Glu Pro Ala Lys Val Ser Glu Cys Cys Arg Phe Ile Leu Asn Leu Leu  
 385 390 395 400

35

40 (2) INFORMATION FOR SEQ ID NO: 552:  
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Tyr Pro Asn Gln Asp Gly Asp Ile Leu Arg Asp Gln Val Leu His Glu  
 1 5 10 15  
 His Ile Gln Arg Leu Ser Lys Val Val Thr Ala Asn His Arg Ala Leu  
 20 25 30  
 Gln Ile Pro Glu Val Tyr Leu Arg Glu Ala Pro Trp Pro Ser Ala Gln  
 35 40 45  
 55 Ser Glu Ile Arg Thr Ile Ser Ala Tyr Lys Thr Pro Arg Asp Lys Val  
 50 55 60  
 Gln Cys Ile Leu Arg Met Cys Ser Thr Ile Met Asn Leu Leu Ser Leu  
 65 70 75 80

	Ala	Asn	Glu	Asp	Ser	Val	Pro	Gly	Ala	Asp	Asp	Phe	Val	Pro	Val	Leu
							85									95
5	Val	Phe	Val	Leu	Ile	Lys	Ala	Asn	Pro	Pro	Cys	Leu	Leu	Ser	Thr	Val
				100					105					110		
	Gln	Tyr	Ile	Ser	Ser	Phe	Tyr	Ala	Ser	Cys	Leu	Ser	Gly	Glu	Glu	Ser
				115					120					125		
10	Tyr	Trp	Trp	Met	Gln	Phe	Thr	Ala	Ala	Val	Glu					
				130				135								

15

(2) INFORMATION FOR SEQ ID NO: 553:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 144 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

25	Tyr	Pro	Asn	Gln	Asp	Gly	Asp	Ile	Leu	Arg	Asp	Gln	Val	Leu	His	Glu
	1															15
	His	Ile	Gln	Arg	Leu	Ser	Lys	Val	Val	Thr	Ala	Asn	His	Arg	Ala	Leu
					20					25					30	
30	Gln	Ile	Pro	Glu	Val	Tyr	Leu	Arg	Glu	Ala	Pro	Trp	Pro	Ser	Ala	Gln
					35				40					45		
	Ser	Glu	Ile	Arg	Thr	Ile	Ser	Ala	Tyr	Lys	Thr	Pro	Arg	Asp	Lys	Val
		50						55					60			
35	Gln	Cys	Ile	Leu	Arg	Met	Cys	Ser	Thr	Ile	Met	Asn	Leu	Leu	Ser	Leu
	65					70					75					80
	Ala	Asn	Glu	Asp	Ser	Val	Pro	Gly	Ala	Asp	Asp	Phe	Val	Pro	Val	Leu
40						85					90				95	
	Val	Phe	Val	Leu	Ile	Lys	Ala	Asn	Pro	Pro	Cys	Leu	Leu	Ser	Thr	Val
				100						105					110	
45	Gln	Tyr	Ile	Ser	Ser	Phe	Tyr	Ala	Ser	Cys	Leu	Ser	Gly	Glu	Glu	Ser
				115					120				125			
	Tyr	Trp	Trp	Met	Gln	Phe	Thr	Ala	Ala	Val	Glu	Phe	Ile	Lys	Thr	Ile
	130						135					140				

50

55

(2) INFORMATION FOR SEQ ID NO: 554:

60 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid

647

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

5 Tyr Pro Asn Gln Asp Gly Asp Ile Leu Arg Asp Gln Val Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 555:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Glu Ala Pro Trp Pro Ser Ala Gln Ser Glu Ile  
1 5 10

20

(2) INFORMATION FOR SEQ ID NO: 556:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

30 Ser Gly Glu Glu Ser Tyr Trp Trp Met Gln Phe Thr Ala Ala Val Glu  
1 5 10 15

Phe Ile Lys Thr Ile  
20

35

(2) INFORMATION FOR SEQ ID NO: 557:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

45

Ala Asp Asp Phe Val Pro Val Leu Val Phe Val Leu Ile Lys Ala Asn  
1 5 10 15

Pro Pro

50

(2) INFORMATION FOR SEQ ID NO: 558:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

648

Tyr Lys Thr Pro Arg Asp Lys Val Gln Cys Ile Leu  
 1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 559:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

15

Gly Ala Asp Asp Phe Val Pro Val Leu Val Phe Val Leu Ile Lys  
 1 5 10 15

20

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

Pro Val Leu Val Phe Val Leu Ile Lys Ala Asn Pro  
 1 5 10

30

(2) INFORMATION FOR SEQ ID NO: 561:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

40

Ser Ala Arg Ala Ser Thr Gln Pro Pro Ala Gly Gln His Pro Gly Pro  
 1 5 10 15

45

Cys

50

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Pro Gly Arg Trp Arg Trp Gln Arg Asp Met His Pro Ala Arg Lys  
 1 5 10 15

60

Leu Leu Ser Leu Leu Phe Leu Ile Leu Met Gly Thr Glu Leu Thr Gln

649

20

25

30

Asp

5

(2) INFORMATION FOR SEQ ID NO: 563:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

15

Ser Ala Ala Pro Asp Ser Leu Leu Arg Ser Ser Lys Gly Ser Thr Arg  
1 5 10 15

Gly Ser Leu

20

(2) INFORMATION FOR SEQ ID NO: 564:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Ala Ala Ile Val Ile Trp Arg Gly Lys Ser Glu Ser Arg Ile Ala Lys  
1 5 10 15

35

Thr Pro Gly Ile  
20

40

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Pro Leu Gly Ile Thr Leu Pro Leu Gly Ala Pro Glu Thr Gly Gly Gly  
1 5 10 15

50

Asp

55

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

60

(B) TYPE: amino acid

650

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

5 Cys Ala Ala Glu Thr Trp Lys Gly Ser Gln Arg Ala Gly Gln Leu Cys  
1 5 10 15  
Ala Leu Leu Ala  
20

10

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

20 Phe Arg Gly Gly Gly Thr Leu Val Leu Pro Pro Thr His Thr Pro Glu  
1 5 10 15  
Trp Leu Ile Leu  
20

25

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

35

Met Arg Ser Ala Arg Pro Ser Leu Gly Cys Leu Pro Ser Trp Ala Phe  
1 5 10 15  
Ser Gln Ala Leu Asn Ile  
20

40

(2) INFORMATION FOR SEQ ID NO: 569:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys  
1 5 10 15

55

Glu Lys Gly Asn Phe Asn  
20

60

(2) INFORMATION FOR SEQ ID NO: 570:



651

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Val Ala His Gly Leu Ala Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu  
1 5 10 15  
Ile Leu Pro Glu Leu Gln Ala Arg Ile Arg  
20 25

## (2) INFORMATION FOR SEQ ID NO: 571:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val Ser Gln  
1 5 10 15  
Arg Cys

## (2) INFORMATION FOR SEQ ID NO: 572:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp Asn Leu Ser Met Ala  
1 5 10 15  
Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro Gln Gln Thr Gly Asp  
20 25 30  
Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn  
35 40

## (2) INFORMATION FOR SEQ ID NO: 573:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr Cys Val  
1 5 10 15

Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser Gln Tyr  
 20 25 30

5 Ser Gln Ala Gly Phe Ser Gly Glu Asp Arg Leu Glu Gln  
 35 40 45

10 (2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

Ala Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro  
 1 5 10 15

20 Glu Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp  
 20 25 30

25 Asp Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln  
 35 40 45

Glu Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val  
 50 55 60

30 Pro Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ile Ser Gly  
 65 70 75 80

Met Glu Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser  
 85 90

35

(2) INFORMATION FOR SEQ ID NO: 575:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala Val Cys  
 1 5 10 15

50 Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser Tyr Tyr  
 20 25 30

Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu  
 35 40

55

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 22 amino acids

653

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

5 Thr Met Lys Leu Leu Lys Leu Arg Arg Asn Ile Val Lys Leu Ser Leu  
 1 5 10 15  
 Tyr Arg His Phe Thr Asn  
 20

10

(2) INFORMATION FOR SEQ ID NO: 577:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

20 Thr Leu Ile Leu Ala Val Ala Ala Ser Ile Val Phe Ile Ile Trp Thr  
 1 5 10 15  
 Thr Met Lys Phe Arg Ile  
 25

25

(2) INFORMATION FOR SEQ ID NO: 578:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

35

Val Thr Cys Gln Ser Asp Trp Arg Glu Leu Trp Val Asp Asp Ala Ile  
 1 5 10 15  
 Trp Arg Leu Leu Phe Ser Met Ile Leu Phe Val Ile  
 20 25

40

45 (2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

50

Met Val Leu Trp Arg Pro Ser Ala Asn Asn Gln Arg Phe Ala Phe Ser  
 1 5 10 15  
 Pro Leu Ser Glu Glu Glu Glu Asp Glu Gln  
 20 25

55

60

654

## (2) INFORMATION FOR SEQ ID NO: 580:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

Met Val Leu Trp Arg Pro Ser Ala Asn Asn Gln Arg Phe Ala Phe Ser  
1 5 10 15

Pro Leu Ser Glu Glu Glu Glu Asp Glu Gln  
20 25

15

## (2) INFORMATION FOR SEQ ID NO: 581:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

Lys Glu Pro Met Leu Lys Glu Ser Phe Glu Gly Met Lys Met Arg Ser  
1 5 10 15

Thr Lys Gln Glu Pro Asn Gly Asn Ser Lys Val Asn Lys Ala Gln Glu  
20 25 30

30

Asp Asp Leu  
35

35

## (2) INFORMATION FOR SEQ ID NO: 582:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

Lys Trp Val Glu Glu Asn Val Pro Ser Ser Val Thr Asp Val Ala Leu  
1 5 10 15

Pro Ala Leu Leu Asp Ser Asp Glu Glu Arg Met Ile Thr His Phe Glu  
20 25 30

Arg Ser Lys Met Glu  
35

50

## (2) INFORMATION FOR SEQ ID NO: 583:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883:

Asp Pro Arg Val Arg Leu Asn Ser Leu Thr Cys Lys His Ile Phe Ile  
 1 5 11 15  
 Ser Leu Thr Gln  
 20

(2) INFORMATION FOR SEQ ID NO: 884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884:

Tyr Glu Pro Met Asp Phe Xaa Met Ala Leu Ile Tyr Asp  
 1 5 11

(2) INFORMATION FOR SEQ ID NO: 885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885:

Ile Arg His Gly Leu Thr Val Leu Arg Asp Thr Arg Pro Ala Lys Ala  
 1 5 11 15

(2) INFORMATION FOR SEQ ID NO: 886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886:

Met Asp Phe Xaa Met Ala Leu Ile Tyr Asp  
 1 5 11

(2) INFORMATION FOR SEQ ID NO: 887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887:

656

Met Gln Glu Met Met Arg Asn Gln Asp Arg Ala Leu Ser Asn Leu Glu  
 1 5 10 15

Ser Ile Pro Gly Gly Tyr Asn Ala  
 20

10 (2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

Leu Arg Arg Met Tyr Thr Asp Ile Gln Glu Pro Met Leu Ser Ala Ala  
 1 5 10 15

20 Gln Glu Gln Phe Gly Gly Asn Pro Phe  
 20 25

25 (2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

Ala Ser Leu Val Ser Asn Thr Ser Ser Gly Glu Gly Ser Gln Pro Ser  
 1 5 10 15

35 Arg Thr Glu Asn Arg Asp Pro Leu Pro Asn Pro Trp Ala Pro Gln Thr  
 20 25 30

40

45 (2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

Ser Gln Ser Ser Ser Ala Ser Ser Gly Thr Ala Ser Thr Val Gly Gly  
 1 5 10 15

55 Thr Thr Gly Ser Thr Ala Ser Gly Thr Ser Gly Gln Ser Thr Thr Ala  
 20 25 30

Pro Asn Leu Val Pro Gly Val Gly Ala Ser Met Phe Asn Thr Pro Gly  
 35 40 45

60

657

Met Gln Ser Leu Leu Gln Gln Ile Thr Glu Asn Pro Gln Leu Met Gln  
 50 55 60

5 Asn Met Leu Ser Ala Pro Tyr  
 65 70

10 (2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

Met Arg Ser Met Met Gln Ser Leu Ser Gln Asn Pro Asp Leu Ala Ala  
 1 5 10 15

20 Gln Met Met Leu Asn Asn Pro Leu Phe Ala Gly Asn Pro Gln Leu Gln  
 20 25 30

Glu Gln Met Arg Gln Gln Leu Pro Thr Phe Leu Gln Gln  
 35 40 45  
 25

(2) INFORMATION FOR SEQ ID NO: 592:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

Met Gln Asn Pro Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala Met  
 1 5 10 15

40 Gln Ala Leu Leu Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr Glu  
 20 25 30

Ala Pro Gly Leu Ile Pro Gly Phe Thr Pro Gly Leu Gly Ala Leu Gly  
 35 40 45

45 Ser Thr Gly Gly Ser Ser Gly Thr Asn Gly Ser Asn Ala Thr Pro Ser  
 50 55 60

Glu Asn Thr Ser Pro Thr Ala Gly Thr  
 65 70  
 50

(2) INFORMATION FOR SEQ ID NO: 593:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

658

Thr Gln Pro Gly His Gln Gln Phe Ile Gln Gln Met Leu Gln Ala Leu  
 1 5 10 15  
 Ala Gly Val Asn Pro Gln Leu Gln Asn Pro Glu Val Arg Phe Gln Gln  
 5 20 25 30  
 Gln Leu Gln Gln Leu Ser Ala Met Gly Phe Leu Asn Arg Glu Ala Asn  
 35 40 45  
 Leu Gln Ala Leu Ile Ala Thr Gly Gly Asp Ile Asn Ala Ala Ile Glu  
 10 50 55 60  
 Arg Leu Leu Gly Ser Gln Pro Ser  
 15 65 70

## (2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 45 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:  
 Arg Asn Pro Ala Met Met Gln Glu Met Met Arg Asn Gln Asp Arg Ala  
 1 5 10 15  
 Leu Ser Asn Leu Glu Ser Ile Pro Gly Gly Tyr Asn Ala Leu Arg Arg  
 20 25 30  
 Met Tyr Thr Asp Ile Gln Glu Pro Met Leu Ser Ala Ala  
 35 40 45

35

## (2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:  
 Gly Asn Pro Phe Ala Ser Leu Val Ser Asn Thr Ser Ser  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

Glu Asn Arg Asp Pro Leu Pro Asn Pro Trp Ala  
 1 5 10  
 60



## (2) INFORMATION FOR SEQ ID NO: 597:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

10

Gly Lys Ile Leu Lys Asp Gln Asp Thr Leu Ser Gln His Gly Ile His  
1 5 10 15

Asp

15

## (2) INFORMATION FOR SEQ ID NO: 598:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

Gly Leu Thr Val His Leu Val Ile Lys Thr Gln Asn Arg Pro  
1 5 10

30

## (2) INFORMATION FOR SEQ ID NO: 599:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

40

Ser Glu Leu Gln Ser Gln Met Gln Arg Gln Leu Leu Ser Asn Pro Glu  
1 5 10 15

Met Met

45

## (2) INFORMATION FOR SEQ ID NO: 600:

50

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

55

Pro Glu Ile Ser His Met Leu Asn Asn Pro Asp Ile Met Arg  
1 5 10

60

660

## (2) INFORMATION FOR SEQ ID NO: 501:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Arg Gln Leu Ile Met Ala Asn Pro Gln Met Gln Gln Leu Ile Gln Arg  
 1 5 10 15

Asn Pro

## (2) INFORMATION FOR SEQ ID NO: 502:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn Leu Leu  
 1 5 10 15

Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 503:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser Asp Trp Leu Cys Leu Ala  
 1 5 10 15

Phe Val Glu Ser Lys Phe Asn  
 20

## (2) INFORMATION FOR SEQ ID NO: 504:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe Gln Ile Asn  
 1 5 10 15

Ser His Tyr Trp Cys Asn

661

20

## 5 (2) INFORMATION FOR SEQ ID NO: 605:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn Leu Leu  
1 5 10 15

15 Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser  
20 25

20

## (2) INFORMATION FOR SEQ ID NO: 606:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

30 Ile Arg Glu Val Asn Glu Val Ile Gln Asn Pro Ala Thr  
1 5 10

## 35 (2) INFORMATION FOR SEQ ID NO: 607:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

Ile Thr Arg Ile Leu Leu Ser His Phe Asn Trp Asp Lys Glu Lys Leu  
1 5 10 15

45 Met Glu Arg Tyr Phe Asp Gly Asn Leu Glu Lys Leu Phe Ala  
20 25 30

## 50 (2) INFORMATION FOR SEQ ID NO: 608:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

Asn Thr Arg Ser Ser Ala Gln Asp Met Pro Cys Gln Ile Cys Tyr Leu  
1 5 10 15

60

662

Asn Tyr Pro Asn Ser Tyr Phe  
20

5

(2) INFORMATION FOR SEQ ID NO: 609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

15 Cys Asp Ile Leu Val Asp Asp Asn Thr Val Met Arg Leu Ile Thr Asp  
1 5 10 15

Ser Lys Val Lys Leu Lys Tyr Gln His Leu Ile Thr Asn Ser Phe Val  
20 25 30

20 Glu Cys Asn Arg Leu Leu Lys Trp Cys Pro Ala Pro Asp Cys His His  
35 40 45

Val Val Lys Val Gln Tyr Pro Asp Ala Lys Pro Val  
50 55 60

25

(2) INFORMATION FOR SEQ ID NO: 610:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

35

Cys Asp Ile Leu Val Asp Asp Asn Thr Val Met Arg Leu Ile Thr Asp  
1 5 10 15

40 Ser Lys Val Lys Leu Lys Tyr Gln His Leu Ile Thr Asn Ser Phe Val  
20 25 30

Glu Cys Asn Arg Leu Leu Lys Trp Cys Pro Ala Pro Asp Cys His His  
35 40 45

45 Val Val Lys Val  
50

50

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

60

Gly Cys Asn His Met Val Cys Arg Asn Gln Asn Cys Lys Ala Glu Phe  
1 5 10 15

663

Cys Trp Val Cys Leu Gly Pro Trp Glu Pro His Gly Ser Ala Trp Tyr  
                   20                  25                  30  
 5 Asn Cys Asn Arg Tyr Asn Glu Asp Asp Ala Lys Ala Ala Arg Asp Ala  
                   35                  40                  45  
 Gln Glu Arg Ser Arg Ala Ala Leu Gln Arg Tyr Leu  
           50                  55                  60

10

(2) INFORMATION FOR SEQ ID NO: 612:

- 15 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 60 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

20 Phe Tyr Cys Asn Arg Tyr Met Asn His Met Gln Ser Leu Arg Phe Glu  
       1                  5                  10                  15  
 His Lys Leu Tyr Ala Gln Val Lys Gln Lys Met Glu Glu Met Gln Gln  
                   20                  25                  30  
 25 His Asn Met Ser Trp Ile Glu Val Gln Phe Leu Lys Lys Ala Val Asp  
                   35                  40                  45  
 Val Leu Cys Gln Cys Arg Ala Thr Leu Met Tyr Thr  
 30          50                  55                  60

(2) INFORMATION FOR SEQ ID NO: 613:

- 35 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 60 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

Tyr Val Phe Ala Phe Tyr Leu Lys Lys Asn Asn Gln Ser Ile Ile Phe  
       1                  5                  10                  15  
 45 Glu Asn Asn Gln Ala Asp Leu Glu Asn Ala Thr Glu Val Leu Ser Gly  
                   20                  25                  30  
 Tyr Leu Glu Arg Asp Ile Ser Gln Asp Ser Leu Gln Asp Ile Lys Gln  
                   35                  40                  45  
 50 Lys Val Gln Asp Lys Tyr Arg Tyr Cys Glu Ser Arg  
           50                  55                  60

55

(2) INFORMATION FOR SEQ ID NO: 614:

- 60 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 37 amino acids  
       (B) TYPE: amino acid

664

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

5 Thr Gly Leu Glu Cys Gly His Lys Phe Cys Met Gln Cys Trp Ser Glu  
 1 5 10 15  
 Tyr Leu Thr Thr Lys Ile Met Glu Glu Gly Met Gly Gln Thr Ile Ser  
 20 25 30  
 10 Cys Pro Ala His Gly  
 35

15 (2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

Met Trp Gly Tyr Leu Phe Val Asp Ala Ala Trp Asn Phe Leu Gly Cys  
 1 5 10 15  
 25 Leu Ile Cys Gly Trp  
 20

30

(2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

40 Met His Phe Ile Ser Ser Gly Asn Val Ser Ala Ile Arg Ser Ser Ile  
 1 5 10 15  
 Leu Leu Leu Arg Xaa Ser Leu Ser Tyr Leu Gly Asn Cys Leu Arg Val  
 20 25 30  
 45 Ser Ala Ile Phe Val Tyr Phe Leu Leu Phe Leu Leu Ser  
 35 40 45

50 (2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

Met Asp Gln Ala Leu Arg Gly Ser Pro Ser Glu Gly Phe Ser Thr Asp  
 1 5 10 15  
 60

665

Pro Ser Pro Pro Gln Val Gly Arg Gln Ile Pro Ser Phe Pro Pro Trp  
                   20                  25                  30

5 Arg Arg Leu Val Leu Pro Lys Ala Ser Gly Cys Phe Leu Glu Arg Glu  
                   35                  40                  45

Trp Trp Leu Cys Val Phe Lys Leu Arg Thr Arg Pro Gly Ala Glu Ala  
                   50                  55                  60

10 His Ala Tyr Asn Ser Ser Ile Leu Gly Gly Arg Gly Lys Gly Ile Thr  
                   65                  70                  75                  80

15

(2) INFORMATION FOR SEQ ID NO: 618:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

25

Met Leu Pro Ala Leu Ala Ser Cys Cys His Phe Ser Pro Pro Glu Gln  
           1                  5                  10                  15

30

Ala Ala Arg Leu Lys Lys Leu Gln Glu Gln Glu Lys Gln Gln Lys Val  
                   20                  25                  30

Glu Phe Arg Lys Arg Met Glu Lys Glu Val Ser Asp Phe Ile Gln Asp  
                   35                  40                  45

35

Ser Gly Gln Ile Lys Lys Lys Phe Gln Pro Met Asn Lys Ile Glu Arg  
                   50                  55                  60

Ser Ile Leu His Asp Val Val Glu Val Ala Gly Leu Thr Ser Phe Ser  
                   65                  70                  75                  80

40

Phe Gly Glu Asp Asp Asp Cys Arg Tyr Val Met Ile Phe Lys Lys Glu  
                   85                  90                  95

45

Phe Ala Pro Ser Asp Glu Glu Leu Asp Ser Tyr Arg Arg Gly Glu Glu  
                   100                  105                  110

Trp Asp Pro Gln Lys Ala Glu Glu Lys Arg Asn Xaa Lys Glu Leu Ala  
                   115                  120                  125

50

Gln Arg Gln  
                   130

55

(2) INFORMATION FOR SEQ ID NO: 619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

5      Glu Glu Glu Ala Ala Gln Gln Gly Pro Val Val Val Ser Pro Ala Ser  
       1                      5                      10                      15  
     Asp Tyr Lys Asp Lys Tyr Ser His Leu Ile Gly Lys Gly Ala Ala Lys  
           20                      25                      30  
 10     Asp Ala Ala His Met Leu Gln Ala Asn Lys Thr Tyr Gly Cys Xaa Pro  
           35                      40                      45  
     Val Ala Asn Lys Arg Asp Thr Arg Ser Ile Glu Glu Ala Met Asn Glu  
           50                      55                      60  
 15     Ile Arg Ala Lys Lys Arg Leu Arg Gln Ser Gly Glu  
           65                      70                      75

20      (2) INFORMATION FOR SEQ ID NO: 620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

30     Pro Pro Arg Arg Pro Ala Gln Leu Pro Leu Thr Pro Gly Ala Gly Gln  
           1                      5                      10                      15  
     Gly Ala Gly Arg Asp Lys Ala Ala Ala Ile Arg Ala His Pro Gly Ala  
           20                      25                      30  
 35     Pro Pro Leu Asn His Leu Leu Pro  
           35                      40

40      (2) INFORMATION FOR SEQ ID NO: 621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

50     Ala Val Pro Gln Ala Gly Gly Lys Gln Val Phe Asp Leu Ser Pro Leu  
           1                      5                      10                      15  
     Glu Leu Gly Tyr Val Arg Gly Met Cys Val Cys Val  
           20                      25

55      (2) INFORMATION FOR SEQ ID NO: 622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

60      (D) TOPOLOGY: linear



667

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

5 Met Leu Pro Ala Leu Ala Ser Cys Cys His Phe Ser Pro Pro Glu Gln  
 1 5 10 15  
 Ala Ala Arg Leu Lys Lys Leu Gln Glu Gln Glu Lys Gln Gln Lys Val  
 20 25 30  
 10 Glu Phe Arg Lys Arg Met Glu Lys Glu Val Ser Asp Phe Ile Gln Asp  
 35 40 45  
 Ser Gly Gln Ile Lys Lys Lys Phe Gln Pro Met Asn Lys Ile Glu Arg  
 50 55 60  
 15 Ser Ile Leu His Asp Val Val Glu Val Ala Gly Leu Thr Ser Phe Ser  
 65 70 75 80  
 Phe Gly Glu Asp Asp Asp Cys Arg Tyr Val Met Ile Phe Lys Lys Glu  
 85 90 95  
 20 Phe Ala Pro Ser Asp Glu Glu Leu Asp Ser Tyr Arg Arg Gly Glu Glu  
 100 105 110  
 Trp Asp Pro Gln Lys Ala Glu Glu Lys Arg Asn Xaa Lys Glu Leu Ala  
 115 120 125  
 25 Gln Arg Gln Glu Glu Glu Ala Ala Gln Gln Gly Pro Val Val Val Ser  
 130 135 140  
 30 Pro Ala Ser Asp Tyr Lys Asp Lys Tyr Ser His Leu Ile Gly Lys Gly  
 145 150 155 160  
 Ala Ala Lys Asp Ala Ala His Met Leu Gln Ala Asn Lys Thr Tyr Gly  
 165 170 175  
 35 Cys Xaa Pro Val Ala Asn Lys Arg Asp Thr Arg Ser Ile Glu Glu Ala  
 180 185 190  
 40 Met Asn Glu Ile Arg Ala Lys Lys Arg Leu Arg Gln Ser Gly Glu  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO: 623:

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

55 Leu Leu Cys Pro Val Leu Asn Ser Gly Xaa Ser Trp Asn Phe Pro His  
 1 5 10 15  
 Pro Ser Gln Pro Glu Tyr Ser Phe His Gly Phe His Ser Thr Arg Leu  
 20 25 30  
 Trp Ile

60

## (2) INFORMATION FOR SEQ ID NO: 624:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

10 Pro Ser Thr Pro Trp Phe Leu Phe Leu Leu Gly Leu Thr Cys Pro Phe  
 1 5 10 15  
 15 Ser Thr Ser His Pro Arg Trp Asp Ser Ile Pro Pro  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 625:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 227 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

Glu Leu Ser Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu  
 1 5 10 15  
 30 Tyr Thr Cys Ser Ile Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu  
 20 25 30  
 Val Thr Val Leu Gly Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys  
 35 35 40 45  
 Ser Ser Leu Arg Glu Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser  
 50 55 60  
 40 Gly Ser Lys Pro Ala Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu  
 65 70 75 80  
 Leu His Gly Glu Pro Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr  
 85 90 95  
 45 Phe Thr Val Ser Ser Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp  
 100 105 110  
 Gly Ala Ser Ile Val Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala  
 115 120 125  
 50 Asp Arg Ser Thr Ser Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala  
 130 135 140  
 Met Ile Arg Pro Asp Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu  
 55 145 150 155 160  
 Leu His Cys Glu Gly Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp  
 165 170 175  
 60 Glu Lys Glu Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala

669

180 185 190

Leu Ile Phe Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys  
195 200 205

5 Thr Ala Thr Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn  
210 215 220

Val Asn Asp  
10 225

(2) INFORMATION FOR SEQ ID NO: 626:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

Glu Leu Ser Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu  
1 5 10 15

25 Tyr Thr Cys Ser Ile Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu  
20 25 30

Val Thr Val Leu Gly Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys  
35 40 45

30 Ser Ser Leu Arg Glu Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser  
50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 627:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

Cys Gln Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr Trp Arg Lys  
1 5 10 15

50 Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln Glu Asp Pro  
20 25 30

Asn Gly Lys Thr Phe Thr Val Ser Ser Ser Val Thr Phe Gln Val Thr  
35 40 45

55 Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser Val Asn His Glu Ser  
50 55 60

Leu  
60 65

## (2) INFORMATION FOR SEQ ID NO: 628:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser Gln Arg Ile Glu  
 1 5 10 15

Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp Pro Pro His Pro  
 20 25 30

Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly Arg Gly Asn Pro  
 35 40 45

Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu  
 50 55

25

## (2) INFORMATION FOR SEQ ID NO: 629:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

Trp Glu Lys Glu Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser  
 1 5 10 15

Ala Leu Ile Phe Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly  
 20 25 30

Cys Thr Ala Thr Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu  
 35 40 45

Asn Val Asn Asp  
 50

45

## (2) INFORMATION FOR SEQ ID NO: 630:

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

Val Pro Glu Leu Pro Asp Arg Val His Gln Leu His Gln Ala Val Gln  
 1 5 10 15

Gly Cys Ala Leu Gly Arg Pro Gly Phe Pro Gly Gly Pro Thr His Ser  
 20 25 30

60

671

Gly His His Lys Ser His Pro Gly Pro Ala Gly Gly Asp Tyr Asn Arg  
           35                          40                          45  
 5 Cys Asp Arg Pro Gly Gln Val His Leu His Asn Pro Arg Gly Thr Gly  
       50                          55                          60  
 Arg Arg Gly Gln Leu His Pro Thr Ala Gly Pro Gly Val His Arg Arg  
       65                          70                          75                          80  
 10 Ala Cys Pro Ser Gln Gln Leu Pro His Arg Leu Gly Pro Gly Val Pro  
                           85                          90                          95  
 Cys Pro Ser Pro Ser Leu Thr Pro Val Leu Pro Ser Trp Thr Gln Ser  
 15                          100                          105                          110  
 Trp Cys Gly Leu Pro Gly Tyr Thr Ser Ser Ser  
           115                          120

20

(2) INFORMATION FOR SEQ ID NO: 631:

25 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 22 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

30 Val His Gln Leu His Gln Ala Val Gln Gly Cys Ala Leu Gly Arg Pro  
       1                          5                          10                          15  
 Gly Phe Pro Gly Gly Pro  
                           20

35

(2) INFORMATION FOR SEQ ID NO: 632:

40 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 42 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

45

Pro Thr His Ser Gly His His Lys Ser His Pro Gly Pro Ala Gly Gly  
       1                          5                          10                          15  
 Asp Tyr Asn Arg Cys Asp Arg Pro Gly Gln Val His Leu His Asn Pro  
 50                          20                          25                          30  
 Arg Gly Thr Gly Arg Arg Gly Gln Leu His  
           35                          40

55

(2) INFORMATION FOR SEQ ID NO: 633:

60 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 55 amino acids

672

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

5 Leu His Pro Thr Ala Gly Pro Gly Val His Arg Arg Ala Cys Pro Ser  
 1 5 10 15  
 Gln Gln Leu Pro His Arg Leu Gly Pro Gly Val Pro Cys Pro Ser Pro  
 20 25 30  
 10 Ser Leu Thr Pro Val Leu Pro Ser Trp Thr Gln Ser Trp Cys Gly Leu  
 35 40 45  
 Pro Gly Tyr Thr Ser Ser Ser  
 15 50 55

(2) INFORMATION FOR SEQ ID NO: 634:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

Ser Leu Arg Arg Pro Arg Ser Ala Ala Xaa Gln Thr Leu Thr Thr Phe  
 1 5 10 15  
 30 Leu Ser Ser Val Ser Ser Ala Ser Ser Ser Ala Leu Pro Gly Ser Arg  
 20 25 30  
 Glu Pro Cys Asp Pro Arg Ala Pro Pro Pro Pro Arg Ser Gly Ser Ala  
 35 40 45  
 35 Ala Ser Cys Cys Ser Cys Cys Cys Ser Cys Pro Arg Arg Arg Ala Pro  
 50 55 60  
 Leu Arg Ser Pro Arg Gly Ser Lys Arg Arg Ile Arg Gln Arg Glu Val  
 40 65 70 75 80  
 Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro  
 85 90 95  
 45 Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly  
 100 105 110  
 Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg  
 115 120 125  
 50 Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp  
 130 135 140  
 Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr  
 55 145 150 155 160  
 Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly  
 165 170 175  
 60 Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe

673

180 185 190

Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile  
195 200 205

5 Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile  
210 215 220

10 His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly  
225 230 235 240

Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys  
245 250 255

15 Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu  
260 265 270

Glu Leu Pro Lys  
275

20

(2) INFORMATION FOR SEQ ID NO: 635:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

30 Ser Leu Arg Arg Pro Arg Ser Ala Ala Xaa Gln Thr Leu Thr Thr Phe  
1 5 10 15

35 Leu Ser Ser Val Ser Ser Ala Ser Ser Ser Ala Leu Pro Gly Ser Arg  
20 25 30

Glu Pro Cys Asp Pro Arg Ala Pro Pro Pro Pro Arg Ser Gly Ser Ala  
35 40 45

40 Ala Ser Cys Cys Ser Cys Cys Ser Cys Pro Arg Arg  
50 55 60

(2) INFORMATION FOR SEQ ID NO: 636:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

Arg Ala Pro Leu Arg Ser Pro Arg Gly Ser Lys Arg Arg Ile Arg Gln  
1 5 10 15

55 Arg Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
20 25 30

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly  
35 40 45

60

Thr Pro Gly Ile  
50

5

(2) INFORMATION FOR SEQ ID NO: 637:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

15 Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu  
1 5 10 15

Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln  
20 25 30

20 Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala  
35 40 45

25 Glu Cys Thr Phe  
50

(2) INFORMATION FOR SEQ ID NO: 638:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly  
1 5 10 15

40 Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe  
20 25 30

Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile  
35 40 45

45 Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile  
50 55 60

50 His Arg  
65

(2) INFORMATION FOR SEQ ID NO: 639:

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:



675

Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu  
 1 5 10 15  
 5 Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly  
 20 25 30  
 Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
 35 40 45  
 10 Leu Pro Lys  
 50

15

(2) INFORMATION FOR SEQ ID NO: 640:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

25 Thr Lys Lys Glu Asn Cys Arg Pro Ala Ser Leu Met Asn Ile Asp Thr  
 1 5 10 15  
 Lys Ile Leu Asn Lys Ile Leu Met Asn Gln  
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 641:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 214 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

40 Met Cys Asn Leu Pro Ile Lys Val Val Cys Arg Ala Asn Ala Glu Tyr  
 1 5 10 15  
 Met Ser Pro Ser Gly Lys Val Pro Xaa Xaa His Val Gly Asn Gln Val  
 20 25 30  
 45 Val Ser Glu Leu Gly Pro Ile Val Gln Phe Val Lys Ala Lys Gly His  
 35 40 45  
 Ser Leu Ser Asp Gly Leu Glu Glu Val Gln Lys Ala Glu Met Lys Ala  
 50 50 55 60  
 Tyr Met Glu Leu Val Asn Asn Met Leu Leu Thr Ala Glu Leu Tyr Leu  
 65 70 75 80  
 55 Gln Trp Cys Asp Glu Ala Thr Val Gly Xaa Ile Thr His Xaa Arg Tyr  
 85 90 95  
 Gly Ser Pro Tyr Pro Trp Pro Leu Xaa His Ile Leu Ala Tyr Gln Lys  
 100 105 110

60

676

Gln Trp Glu Val Lys Arg Lys Xaa Lys Ala Ile Gly Trp Gly Lys Lys  
 115 120 125  
 5 Thr Leu Asp Gln Val Leu Glu Asp Val Asp Gln Cys Cys Gln Ala Leu  
 130 135 140  
 Ser Gln Arg Leu Gly Thr Gln Pro Tyr Phe Phe Asn Lys Gln Pro Thr  
 145 150 155 160  
 10 Glu Leu Asp Ala Leu Val Phe Gly His Leu Tyr Thr Ile Leu Thr Thr  
 165 170 175  
 Gln Leu Thr Asn Asp Glu Leu Ser Glu Lys Val Lys Asn Tyr Ser Asn  
 180 185 190  
 15 Leu Leu Ala Phe Cys Arg Arg Ile Glu Gln His Tyr Phe Glu Asp Arg  
 195 200 205  
 20 Gly Lys Gly Arg Leu Ser  
 210

25 (2) INFORMATION FOR SEQ ID NO: 642:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

Met Cys Asn Leu Pro Ile Lys Val Val Cys Arg Ala Asn Ala Glu Tyr  
 1 5 10 15  
 35 Met Ser Pro Ser Gly Lys Val Pro Xaa Xaa His Val Gly Asn Gln Val  
 20 25 30  
 Val Ser Glu Leu Gly Pro Ile Val Gln Phe Val Lys  
 35 40  
 40

45 (2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

50 Phe Val Lys Ala Lys Gly His Ser Leu Ser Asp Gly Leu Glu Glu Val  
 1 5 10 15  
 55 Gln Lys Ala Glu Met Lys Ala Tyr Met Glu Leu Val Asn Asn Met Leu  
 20 25 30  
 Leu Thr Ala Glu Leu Tyr Leu Gln Trp Cys Asp Glu  
 35 40  
 60

## (2) INFORMATION FOR SEQ ID NO: 644:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

5  
 10 Leu Gln Trp Cys Asp Glu Ala Thr Val Gly Xaa Ile Thr His Xaa Arg  
     1                    5                    10                    15  
     Tyr Gly Ser Pro Tyr Pro Trp Pro Leu Xaa His Ile Leu Ala Tyr Gln  
                     20                    25                    30  
 15 Lys Gln Trp Glu Val Lys Arg Lys Xaa Lys Ala Ile Gly Trp Gly Lys  
                     35                    40                    45  
     Lys Thr Leu  
 20                    50

## (2) INFORMATION FOR SEQ ID NO: 645:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

25  
 30 Asp Gln Val Leu Glu Asp Val Asp Gln Cys Cys Gln Ala Leu Ser Gln  
     1                    5                    10                    15  
 35 Arg Leu Gly Thr Gln Pro Tyr Phe Phe Asn Lys Gln Pro Thr Glu Leu  
                     20                    25                    30  
     Asp Ala Leu Val Phe Gly His Leu Tyr Thr Ile  
                     35                    40  
 40

## (2) INFORMATION FOR SEQ ID NO: 646:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

45  
 50 Leu Thr Thr Gln Leu Thr Asn Asp Glu Leu Ser Glu Lys Val Lys Asn  
     1                    5                    10                    15  
     Tyr Ser Asn Leu Leu Ala Phe Cys Arg Arg Ile Glu Gln His Tyr Phe  
 55                    20                    25                    30  
     Glu Asp Arg Gly Lys Gly Arg Leu Ser  
                     35                    40

678

## (2) INFORMATION FOR SEQ ID NO: 647:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

10 Met Xaa Xaa Xaa Asn Ser His Ile Thr Ile Phe Thr Leu Asn Val Asn  
     1                    5                    10                    15  
     Gly Leu Asn Ala Pro Asn Glu Arg His Arg Leu Ala Asn Trp Ile Gln  
                     20                    25                    30  
 15 Ser Gln Asp Gln Val Cys Cys Ile Gln Glu Thr His Leu Thr Gly Arg  
                     35                    40                    45  
     Asp Thr His Arg Leu Lys Ile Lys Gly Trp Arg Lys Ile Tyr Gln Ala  
 20                    50                    55                    60  
     Asn Gly Lys Gln Lys Lys  
     65                    70

25

## (2) INFORMATION FOR SEQ ID NO: 648:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

35 Phe Thr Leu Asn Val Asn Gly Leu Asn Ala Pro Asn Glu Arg His Arg  
     1                    5                    10                    15  
     Leu Ala Asn Trp Ile Gln Ser Gln Asp Gln Val Cys  
                     20                    25

40

## (2) INFORMATION FOR SEQ ID NO: 649:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

50 Thr His Leu Thr Gly Arg Asp Thr His Arg Leu Lys Ile Lys Gly Trp  
     1                    5                    10                    15  
     Arg

55

## (2) INFORMATION FOR SEQ ID NO: 650:

60

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

Gly Trp Arg Lys Ile Tyr Gln Ala Asn Gly Lys Gln Lys Lys  
 1 5 10

10

## (2) INFORMATION FOR SEQ ID NO: 651:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

20 Ile Tyr His Leu His Ser Trp Ile Phe Phe His Phe Lys Arg Ala Phe  
 1 5 10 15

Cys Met Cys Phe Ile Thr Met Lys Val Ile His Ala His Cys Ser Lys  
 20 25 30

25

Leu Arg Lys Cys Xaa Asn Ala Gln Ile Ser Val Phe Cys Thr Thr Leu  
 35 40 45

30

Thr Ala Ser Tyr Pro Thr  
 50

## (2) INFORMATION FOR SEQ ID NO: 652:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

Ile Tyr His Leu His Ser Trp Ile Phe Phe His Phe Lys Arg Ala Phe  
 1 5 10 15

45

Cys Met Cys Phe Ile Thr Met  
 20

50

## (2) INFORMATION FOR SEQ ID NO: 653:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

Lys Val Ile His Ala His Cys Ser Lys Leu Arg Lys Cys Xaa Asn Ala  
 1 5 10 15

60

680

Gln Ile Ser Val Phe Cys Thr Thr Leu Thr Ala Ser Tyr Pro Thr  
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

15

Trp Asn Leu Leu Trp Tyr Phe Gln Arg Leu Arg Leu Pro Ser Ile Leu  
 1 5 10 15

Pro Gly Leu Val Leu Ala Ser Cys Asp Gly Pro Ser Xaa Ser Gln Ala  
 20 25 30

20

Pro Ser Pro Trp Leu Thr Pro Asp Pro Ala Ser Val Gln Val Arg Leu  
 35 40 45

Leu Trp Asp Val Leu Thr Pro Asp Pro Asn  
 50 55

25

(2) INFORMATION FOR SEQ ID NO: 655:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

Gln Arg Gly Ile Tyr Arg Glu Ile Leu Phe Leu Thr Met Ala Ala Leu  
 1 5 10 15

40

Gly Lys Asp His Val Asp Ile Val Ala Phe Asp Lys Lys Tyr Lys Ser  
 20 25 30

Ala Phe Asn Lys Leu Ala Ser Ser Met Gly Lys Glu Glu Leu Arg His  
 35 40 45

45

Arg Arg Ala Gln Met Pro  
 50

50

(2) INFORMATION FOR SEQ ID NO: 656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

Trp Asn Leu Leu Trp Tyr Phe Gln Arg Leu Arg Leu Pro Ser Ile Leu  
 1 5 10 15

60

681

Pro Gly Leu Val Leu Ala Ser  
20

5

(2) INFORMATION FOR SEQ ID NO: 657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

10

15

Glu Asp Asp Gly Phe Asn Arg Ser Ile His Glu Val Ile Leu Lys Asn  
1 5 10 15

Ile Thr Trp Tyr Ser Glu Arg Val Leu Thr Glu Ile Ser Leu Gly Ser  
20 25 30

20

Leu Leu Ile Leu Val Val Ile Arg Thr Ile Gln Tyr Asn Met Thr Arg  
35 40 45

25

Thr Arg Asp Lys Tyr Leu His Thr Asn Cys Leu Ala Ala Leu Ala Asn  
50 55 60

Met Ser Ala Gln Phe Arg Ser Leu His Gln Tyr Ala Ala Gln Arg Ile  
65 70 75 80

30

Ile Ser Leu Phe Ser Leu Leu Ser Lys Lys His Asn Lys Val Leu Glu  
85 90 95

Gln Ala Thr Gln Ser Leu Arg Gly Ser Leu Ser Ser Asn Asp Val Pro  
100 105 110

35

Leu Pro Asp Tyr Ala Gln Asp Leu Asn Val Ile Glu Glu Val Ile Arg  
115 120 125

40

Met Met Leu Glu Ile Ile Asn Ser Cys Leu Thr Asn Ser Leu His His  
130 135 140

Asn Pro Asn Leu Val Tyr Ala Leu Leu Tyr Lys Arg Asp Leu Phe Glu  
145 150 155 160

45

Gln Phe Arg Thr His Pro Ser Phe Gln Asp Ile Met Gln Asn Ile Asp  
165 170 175

Leu Val Ile Ser Phe Phe Ser Ser Arg Leu Leu Gln Ala Gly Ser  
180 185 190

50

(2) INFORMATION FOR SEQ ID NO: 658:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

55

60

Glu Asp Asp Gly Phe Asn Arg Ser Ile His Glu Val Ile Leu Lys Asn

682

1                      5                      10                      15  
 Ile Thr Trp Tyr Ser Glu Arg Val Leu Thr Glu Ile Ser Leu Gly Ser  
                     20                      25                      30  
 5 Leu Leu Ile Leu Val Val  
                     35

10

(2) INFORMATION FOR SEQ ID NO: 659:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 53 amino acids  
 15       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

20 Arg Thr Ile Gln Tyr Asn Met Thr Arg Thr Arg Asp Lys Tyr Leu His  
     1                      5                      10                      15  
 Thr Asn Cys Leu Ala Ala Leu Ala Asn Met Ser Ala Gln Phe Arg Ser  
                     20                      25                      30  
 25 Leu His Gln Tyr Ala Ala Gln Arg Ile Ile Ser Leu Phe Ser Leu Leu  
                     35                      40                      45  
 Ser Lys Lys His Asn  
                     50

30

(2) INFORMATION FOR SEQ ID NO: 660:

35 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 56 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660:

40

Ser Cys Leu Thr Asn Ser Leu His His Asn Pro Asn Leu Val Tyr Ala  
     1                      5                      10                      15  
 45 Leu Leu Tyr Lys Arg Asp Leu Phe Glu Gln Phe Arg Thr His Pro Ser  
                     20                      25                      30  
 Phe Gln Asp Ile Met Gln Asn Ile Asp Leu Val Ile Ser Phe Phe Ser  
                     35                      40                      45  
 50 Ser Arg Leu Leu Gln Ala Gly Ser  
                     50                      55

55

(2) INFORMATION FOR SEQ ID NO: 661:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 31 amino acids  
 60       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661:

Lys Lys His Asn Lys Val Leu Glu Gln Ala Thr Gln Ser Leu Arg Gly  
 1 5 10 15  
 Ser Leu Ser Ser Asn Asp Val Pro Leu Pro Asp Tyr Ala Gln Asp  
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662:

Met Ala Asp Ile Gln Thr Glu Arg Ala Tyr Gln Lys Gln Pro Thr Ile  
 1 5 10 15  
 Phe Gln Asn Lys Lys Arg Val Leu Leu Gly Glu Thr Gly Lys Glu Lys  
 20 25 30  
 Leu Pro Arg Val Thr Asn Lys Asn Ile Gly Leu Gly Phe Lys Asp Thr  
 35 40 45  
 Pro Arg Arg Leu Leu Arg Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe  
 50 55 60  
 Thr Gly Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val Thr  
 65 70 75 80  
 Gln Asp Glu Asp Ala Glu Asp His Cys His Pro Pro Arg Leu Ser Ala  
 85 90 95  
 Leu His Pro Gln Val Gln Pro Leu Arg Glu Ala Pro Gln Glu His Val  
 100 105 110  
 Cys Thr Pro Val Pro Leu Leu Gln Gly Arg Pro Asp Arg  
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663:

Met Lys Met Gln Arg Thr Ile Val Ile Arg Arg Asp Tyr Leu His Tyr  
 1 5 10 15  
 Ile Arg Lys Tyr Asn Arg Phe Glu Lys Arg His Lys Asn Met Ser Val  
 20 25 30  
 His Leu Ser Pro Cys Phe Arg Asp Val Gln Ile Gly Asp Ile Val Thr  
 35 40 45

684

Val Gly Glu Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu  
50 55 60

5 Lys Val Thr Lys Ala Ala Gly Thr Lys Lys Gln Phe Gln Lys Phe  
65 70 75

10 (2) INFORMATION FOR SEQ ID NO: 664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

15 (C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664:

Met Ala Asp Ile Gln Thr Glu Arg Ala Tyr Gln Lys Gln Pro Thr Ile  
1 5 10 15

20 Phe Gln Asn Lys Lys Arg Val Leu Leu Gly Glu Thr Gly Lys  
20 25 30

25 (2) INFORMATION FOR SEQ ID NO: 665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

30 (B) TYPE: amino acid

(C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665:

Lys Leu Pro Arg Val Thr Asn Lys Asn Ile Gly Leu Gly Phe Lys Asp  
1 5 10 15

Thr Pro Arg Arg Leu Leu Arg Gly Thr Tyr Ile Asp Lys Lys Cys Pro  
20 25 30

40 Phe Thr Gly Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val  
35 40 45

Thr Gln Asp Glu Asp Ala Glu Asp His Cys  
50 55

45 (2) INFORMATION FOR SEQ ID NO: 666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666:

His Cys His Pro Pro Arg Leu Ser Ala Leu His Pro Gln Val Gln Pro  
1 5 10 15

60 Leu Arg Glu Ala Pro Gln Glu His Val Cys Thr Pro Val Pro Leu Leu  
20 25 30

Gln Gly Arg Pro Asp Arg  
35

5

(2) INFORMATION FOR SEQ ID NO: 667:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667:

15

Met Lys Met Gln Arg Thr Ile Val Ile Arg Arg Asp Tyr Leu His Tyr  
1 5 10 15

Ile Arg Lys Tyr Asn Arg Phe Glu Lys Arg His Lys Asn Met Ser Val  
20 25 30

20

His Leu Ser Pro  
35

25

(2) INFORMATION FOR SEQ ID NO: 668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668:

30

35

Cys Phe Arg Asp Val Gln Ile Gly Asp Ile Val Thr Val Gly Glu Cys  
1 5 10 15

Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val Thr Lys  
20 25 30

40

Ala Ala Gly Thr Lys Lys Gln Phe Gln Lys Phe  
35 40

45

(2) INFORMATION FOR SEQ ID NO: 669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669:

50

Pro Arg Arg Leu Leu Arg Gly Thr Tyr Ile Asp Lys Lys Cys Pro Phe  
1 5 10 15

55

Thr Gly Asn Val Ser Ile Arg Gly Arg Ile Leu Ser Gly Val Val Thr  
20 25 30

Gln

60

## (2) INFORMATION FOR SEQ ID NO: 670:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670:

```

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met
 1             5             10             15
Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg
          20             25             30
Leu Ile Cys Lys Gly Thr Ile Glu Glu Arg Ile Leu Gln Arg Ala Lys
          35             40             45
Glu Lys Ser Glu Ile Gln Arg Met Val Ile Ser Gly
          50             55             60

```

## (2) INFORMATION FOR SEQ ID NO: 671:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671:

```

Thr Arg Met Ile Asp Leu Leu Glu Glu Tyr Met Val Tyr Arg Lys His
 1             5             10             15
Thr Tyr Xaa Arg Leu Asp Gly Ser Ser Lys Ile Ser Glu Arg Arg Asp
          20             25             30
Met Val Ala Asp Phe Gln Asn Arg Asn Asp Ile Phe Val Phe Leu Leu
          35             40             45
Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala Xaa Asp Thr
          50             55             60
Val His Phe
          65

```

## (2) INFORMATION FOR SEQ ID NO: 672:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672:

```

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met
 1             5             10             15

```

687

Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg  
 20 25 30

5

10 (2) INFORMATION FOR SEQ ID NO: 673:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673:

Val Tyr Arg Leu Ile Cys Lys Gly Thr Ile Glu Glu Arg Ile Leu Gln  
 1 5 10 15

20

Arg Ala Lys Glu Lys Ser Glu Ile Gln Arg Met Val Ile Ser Gly  
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674:

Thr Arg Met Ile Asp Leu Leu Glu Glu Tyr Met Val Tyr Arg Lys His  
 1 5 10 15

35

Thr Tyr Xaa Arg Leu Asp Gly Ser Ser Lys Ile Ser Glu Arg Arg Asp  
 20 25 30

40 Met

45 (2) INFORMATION FOR SEQ ID NO: 675:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675:

Arg Arg Asp Met Val Ala Asp Phe Gln Asn Arg Asn Asp Ile Phe Val  
 1 5 10 15

55

Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Thr Ala  
 20 25 30

60

Xaa Asp Thr Val His Phe  
 35

## (2) INFORMATION FOR SEQ ID NO: 676:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676:

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met  
1 5 10 15  
Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg  
20 25 30  
Leu Ile Cys Lys Gly  
35

## (2) INFORMATION FOR SEQ ID NO: 677:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677:

Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Val Asp Gln Gln Ala Met  
1 5 10 15  
Asp Arg Ala His Arg Leu Gly Gln Thr Lys Gln Val Thr Val Tyr Arg  
20 25 30  
Leu Ile Cys Lys Gly  
35

## (2) INFORMATION FOR SEQ ID NO: 678:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678:

Arg Leu Ile Cys Lys Gly Thr Ile Glu Glu Arg Ile Leu Gln Arg Ala  
1 5 10 15  
Lys Glu Lys Ser Glu Ile Gln Arg Met Val Ile Ser Gly  
20 25

## (2) INFORMATION FOR SEQ ID NO: 679:

## (i) SEQUENCE CHARACTERISTICS:

689

(A) LENGTH: 364 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679:

5 Met Ser Leu His Gly Lys Arg Lys Glu Ile Tyr Lys Tyr Glu Ala Pro  
 1 5 10 15  
 10 Trp Thr Val Tyr Ala Met Asn Trp Ser Val Arg Pro Asp Lys Arg Phe  
 20 25 30  
 Arg Leu Ala Leu Gly Ser Phe Val Glu Glu Tyr Asn Asn Lys Val Gln  
 35 40 45  
 15 Leu Val Gly Leu Asp Glu Glu Ser Ser Glu Phe Ile Cys Arg Asn Thr  
 50 55 60  
 Phe Asp His Pro Tyr Pro Thr Thr Lys Leu Met Trp Ile Pro Asp Thr  
 65 70 75 80  
 20 Lys Gly Val Tyr Pro Asp Leu Leu Ala Thr Ser Gly Asp Tyr Leu Arg  
 85 90 95  
 25 Val Trp Arg Val Gly Glu Thr Glu Thr Arg Leu Glu Cys Leu Leu Asn  
 100 105 110  
 Asn Asn Lys Asn Ser Asp Phe Cys Ala Pro Leu Thr Ser Phe Asp Trp  
 115 120 125  
 30 Asn Glu Val Asp Pro Tyr Leu Leu Gly Thr Ser Ser Ile Asp Thr Thr  
 130 135 140  
 Cys Thr Ile Trp Gly Leu Glu Thr Gly Gln Val Leu Gly Arg Val Asn  
 145 150 155 160  
 35 Leu Val Ser Gly His Val Lys Thr Gln Leu Ile Ala His Asp Lys Glu  
 165 170 175  
 40 Val Tyr Asp Ile Ala Phe Ser Arg Ala Gly Gly Gly Arg Asp Met Phe  
 180 185 190  
 Ala Ser Val Gly Ala Asp Gly Ser Val Arg Met Phe Asp Leu Arg His  
 195 200 205  
 45 Leu Glu His Ser Thr Ile Ile Tyr Glu Asp Pro Gln His His Pro Leu  
 210 215 220  
 Leu Arg Leu Cys Trp Asn Lys Gln Asp Pro Asn Tyr Leu Ala Thr Met  
 225 230 235 240  
 50 Ala Met Asp Gly Met Glu Val Val Ile Leu Asp Val Arg Val Pro Ala  
 245 250 255  
 His Leu Xaa Pro Gly Thr Thr Ile Glu His Val Ser Met Ala Leu Leu  
 260 265 270  
 55 Gly Pro His Ile His Pro Ala Thr Ser Ala Leu Gln Arg Met Thr Thr  
 275 280 285  
 60 Arg Leu Ser Ser Gly Thr Ser Ser Lys Cys Pro Glu Pro Leu Arg Thr

690

290                      295                      300

Leu Ser Trp Pro Thr Gln Leu Xaa Gly Glu Ile Asn Asn Val Gln Trp  
 305                      310                      315                      320

5                      Ala Ser Thr Gln Pro Glu Leu Ser Pro Ser Ala Thr Thr Thr Ala Trp  
                                  325                      330                      335

10                      Arg Tyr Ser Glu Cys Ser Val Gly Gly Ala Val Pro Thr Arg Gln Gly  
                                  340                      345                      350

Leu Leu Tyr Phe Leu Pro Leu Pro His Pro Gln Ser  
                                  355                      360

15

(2) INFORMATION FOR SEQ ID NO: 680:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680:

25

Met Ser Leu His Gly Lys Arg Lys Glu Ile Tyr Lys Tyr Glu Ala Pro  
 1                      5                      10                      15

30

Trp Thr Val Tyr Ala Met Asn Trp Ser Val Arg Pro Asp Lys Arg Phe  
                                  20                      25                      30

Arg Leu Ala Leu Gly Ser Phe Val Glu Glu Tyr Asn Asn Lys Val Gln  
                                  35                      40                      45

35

Leu Val Gly Leu Asp Glu Glu Ser Ser Glu Phe Ile Cys Arg Asn Thr  
                                  50                      55                      60

Phe Asp His Pro Tyr Pro Thr Thr Lys Leu Met Trp Ile Pro Asp Thr  
                                  65                      70                      75                      80

40

Lys Gly Val Tyr Pro Asp Leu Leu Ala Thr Ser Gly Asp Tyr Leu Arg  
                                  85                      90                      95

45

Val Trp Arg Val Gly Glu Thr Glu Thr Arg Leu Glu Cys Leu Leu Asn  
                                  100                      105                      110

Asn Asn Lys Asn Ser Asp Phe Cys Ala Pro Leu Thr Ser Phe Asp Trp  
                                  115                      120                      125

50

Asn Glu Val Asp Pro Tyr Leu Leu  
                                  130                      135

55

(2) INFORMATION FOR SEQ ID NO: 681:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681:



691

Ser Phe Asp Trp Asn Glu Val Asp Pro Tyr Leu Leu Gly Thr Ser Ser  
 1 5 10 15  
 5 Ile Asp Thr Thr Cys Thr Ile Trp Gly Leu Glu Thr Gly Gln Val Leu  
 20 25 30  
 Gly Arg Val Asn Leu Val Ser Gly His Val Lys Thr Gln Leu Ile Ala  
 35 40 45  
 10 His Asp Lys Glu Val Tyr Asp Ile Ala Phe Ser Arg Ala Gly Gly Gly  
 50 55 60  
 15 Arg Asp Met Phe Ala Ser Val Gly Ala Asp Gly Ser Val Arg Met Phe  
 65 70 75 80  
 Asp Leu Arg His Leu Glu His Ser Thr Ile Ile Tyr Glu Asp Pro Gln  
 85 90 95  
 20 His His Pro Leu Leu Arg Leu Cys Trp Asn Lys Gln Asp Pro Asn Tyr  
 100 105 110  
 Leu Ala Thr Met Ala Met Asp Gly Met Glu Val Val Ile Leu Asp Val  
 115 120 125  
 25 Arg Val Pro Ala His Leu Xaa Pro Gly Thr Thr Ile  
 130 135 140

30

(2) INFORMATION FOR SEQ ID NO: 682:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682:

Val Gly Ala Asp Gly Ser Val Arg Met Phe Asp Leu Arg His Leu Glu  
 1 5 10 15  
 His Ser Thr Ile Ile Tyr Glu Asp Pro Gln His His Pro Leu Leu Arg  
 20 25 30  
 45 Leu Cys Trp Asn Lys Gln Asp Pro Asn Tyr Leu Ala Thr Met Ala Met  
 35 40 45  
 Asp Gly Met Glu Val Val Ile Leu Asp Val Arg Val Pro Ala His Leu  
 50 55 60  
 Xaa Pro Gly Thr Thr Ile Glu His Val Ser Met Ala Leu Leu Gly Pro  
 65 70 75 80  
 55 His Ile His Pro Ala Thr Ser Ala Leu Gln Arg Met Thr Thr Arg Leu  
 85 90 95  
 Ser Ser Gly Thr Ser Ser Lys Cys Pro Glu Pro Leu Arg Thr Leu Ser  
 100 105 110  
 60 Trp Pro Thr Gln Leu Xaa Gly Glu Ile Asn Asn Val Gln Trp Ala Ser

692

115 120 125

Thr Gln Pro Glu Leu Ser Pro Ser Ala Thr Thr Thr Ala Trp Arg Tyr  
130 135 140

5 Ser Glu Cys Ser Val Gly Gly Ala Val Pro Thr Arg Gln Gly Leu Leu  
145 150 155 160

10 Tyr Phe Leu Pro Leu Pro His Pro Gln Ser  
165 170

15 (2) INFORMATION FOR SEQ ID NO: 683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683:

Leu Tyr Ala Thr Ala Thr Val Ile Ser Ser Pro Ser Thr Glu Xaa Leu  
1 5 10 15

25 Ser Gln Asp Gln Gly Asp Arg Ala Ser Leu Asp Ala Ala Asp Ser Gly  
20 25 30

Arg Gly Ser Trp Thr Ser Cys Ser Ser Gly Ser His Asp Asn Ile Gln  
35 40 45

30 Thr Ile Gln His Gln Arg Ser Trp Glu Thr Leu Pro Phe Gly His Thr  
50 55 60

His Phe Asp Tyr Ser Gly Asp Pro Ala Gly Leu Trp Ala Ser Ser Ser  
35 65 70 75 80

His Met Asp Gln Ile Met Phe Ser Asp His Ser Thr Lys Tyr Asn Arg  
85 90 95

40 Gln Asn Gln Ser Arg Glu Ser Leu Glu Gln Ala Gln Ser Arg Ala Ser  
100 105 110

Trp Ala Ser Ser Thr Gly Tyr Trp Gly Glu Asp Ser Glu Gly Asp Thr  
115 120 125

45 Gly Thr Ile Lys Arg Arg Gly Gly Lys Asp Val Ser Ile Glu Ala Glu  
130 135 140

Ser Ser Ser Leu Thr Ser Val Thr Thr Glu Glu Thr Lys Pro Val Pro  
50 145 150 155 160

Met Pro Ala His Ile Ala Val Ala Ser Ser Thr Thr Lys Gly Leu Ile  
165 170 175

55 Ala Arg Lys Glu Gly Arg Tyr Arg Glu Pro Pro Pro Thr Pro Pro Gly  
180 185 190

Tyr Ile Gly Ile Pro Ile Thr Asp Phe Pro Glu Gly His Ser His Pro  
195 200 205

60

693

Ala Arg Lys Pro Pro Asp Tyr Asn Val Ala Leu Gln Arg Ser Arg Met  
 210 215 220

5 Val Ala Arg Ser Ser Asp Thr Ala Gly Pro Ser Ser Val Gln Gln Pro  
 225 230 235 240

His Gly His Pro Thr Ser Ser Arg Pro Val Asn Lys Pro Gln Trp His  
 245 250 255

10 Lys Xaa Asn Glu Ser Asp Pro Arg Leu Ala Pro Tyr Gln Ser Gln Gly  
 260 265 270

Phe Ser Thr Glu Glu Asp Glu Asp Glu Gln Val Ser Ala Val  
 275 280 285

15

(2) INFORMATION FOR SEQ ID NO: 684:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684:

25 His Met Asp Gln Ile Met Phe Ser Asp His Ser Thr Lys Tyr Asn Arg  
 1 5 10 15

30 Gln Asn Gln Ser Arg Glu Ser Leu Glu Gln Ala Gln Ser Arg Ala Ser  
 20 25 30

Trp Ala Ser Ser Thr Gly Tyr Trp Gly Glu  
 35 40

35

(2) INFORMATION FOR SEQ ID NO: 685:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685:

45 Ser Val Thr Thr Glu Glu Thr Lys Pro Val Pro Met Pro Ala His Ile  
 1 5 10 15

Ala Val Ala Ser Ser Thr Thr Lys Gly Leu Ile Ala Arg Lys Glu Gly  
 20 25 30

50 Arg Tyr Arg Glu Pro Pro Pro Thr Pro Pro Gly Tyr Ile Gly Ile Pro  
 35 40 45

Ile Thr Asp  
 55 50

60

(2) INFORMATION FOR SEQ ID NO: 686:

694

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686:

Val Ala Leu Gln Arg Ser Arg Met Val Ala Arg Ser Ser Asp Thr Ala  
 1 5 10 15

10 Gly Pro Ser Ser Val Gln Gln Pro His Gly His Pro Thr Ser Ser Arg  
 20 25 30

Pro Val Asn Lys Pro Gln Trp His Lys Xaa Asn Glu Ser Asp Pro Arg  
 35 40 45

15 Leu Ala Pro Tyr Gln Ser Gln Gly Phe  
 50 55

20

(2) INFORMATION FOR SEQ ID NO: 687:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687:

30 Cys Leu Leu Phe Val Phe Val Ser Leu Gly Met Arg Cys Leu Phe Trp  
 1 5 10 15

Thr Ile Val Tyr Asn Val Leu Tyr Leu Lys His Lys Cys Asn Thr Val  
 20 25 30

35 Leu Leu Cys Tyr His Leu Cys Ser Ile  
 35 40

40

(2) INFORMATION FOR SEQ ID NO: 688:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688:

Ala Cys Ser Lys Leu Ile Pro Ala Phe Glu Met Val Met Arg Ala Lys  
 1 5 10 15

50 Asp Asn Val Tyr His Leu Asp Cys Phe Ala Cys Gln Leu Cys Asn Gln  
 20 25 30

55 Arg Xaa Cys Val Gly Asp Lys Phe Phe Leu Lys Asn Asn Xaa Xaa Leu  
 35 40 45

Cys Gln Thr Asp Tyr Glu Glu Gly Leu Met Lys Glu Gly Tyr Ala Pro  
 50 55 60

60 Xaa Val Arg

695

65

## 5 (2) INFORMATION FOR SEQ ID NO: 689:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689:

Ser Ala Leu Ser Glu Pro Gly Ala Pro Asp Arg Arg Arg Pro Cys Pro  
 1 5 10 15  
 Glu Ser Val Pro Arg Arg Pro Asp Asp Glu Gln Trp Pro Pro Pro Thr  
 20 25 30  
 Ala Leu Cys Leu Asp Val Ala Pro Leu Pro Pro Ser Ser  
 35 40 45

## 25 (2) INFORMATION FOR SEQ ID NO: 690:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690:

Pro Val Gly Tyr Leu Asp Lys Gln Val Pro Asp Thr Ser Val Gln Glu  
 1 5 10 15  
 Thr Asp Arg Ile Leu Val Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly  
 20 25 30  
 Pro Leu Lys Gln Ile Pro Met Asn Leu Phe Ile  
 35 40

40

## (2) INFORMATION FOR SEQ ID NO: 691:

## 45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691:

Ala His Ala Ser Glu Ser Gly Glu Arg Trp Trp Ala Cys Cys Gly Val  
 1 5 10 15  
 Arg Phe Gly Leu Arg Ser Ile Glu Ala Ile Gly Arg Ser Cys Cys His  
 20 25 30  
 Asp Gly Pro Gly Gly Leu Val Ala Asn Arg Gly Arg Arg Phe Lys Trp  
 35 40 45  
 Ala Ile Glu Leu Ser Gly Pro Gly Gly Gly Ser Arg Gly Arg Ser Asp  
 60

696

50                      55                      60

Arg Gly Ser Gly Gln Gly Asp Ser Leu Tyr Pro Val Gly Tyr Leu Asp  
 65                      70                      75                      80

5 Lys Gln Val Pro Asp Thr Ser Val Gln Glu Thr Asp Arg Ile Leu Val  
                     85                      90                      95

10 Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly Pro Leu Lys Gln Ile Pro  
                     100                      105                      110

Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile Phe  
                     115                      120                      125

15 Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala Leu  
                     130                      135                      140

Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys  
                     145                      150                      155                      160

20 Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala  
                     165                      170                      175

25 Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala  
                     180                      185                      190

Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Phe Ser  
                     195                      200                      205

30 Gly Gly Gly Leu Leu Leu  
                     210

35 (2) INFORMATION FOR SEQ ID NO: 692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692:

Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln Lys Phe Leu Gln Gly  
 1                      5                      10                      15

45 Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu Ala Leu Ala Val Tyr  
                     20                      25                      30

Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His Ala Ser Asp  
 50                      35                      40                      45

55 (2) INFORMATION FOR SEQ ID NO: 693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693:

697

Pro Val Gly Tyr Leu Asp Lys Gln Val Pro Asp Thr Ser Val Gln Glu  
1 5 10 15

5 Thr Asp Arg Ile Leu Val Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly  
20 25 30

Pro Leu Lys Gln Ile Pro Met Asn Leu Phe Ile  
35 40

10

(2) INFORMATION FOR SEQ ID NO: 694:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694:

20

Pro Thr Thr Lys Leu Asp Ile Met Glu Lys Lys Lys His Ile Gln Ile  
1 5 10 15

25

Arg Phe Pro Ser Phe Tyr His Lys Leu Val Asp Ser Gly Arg Met Arg  
20 25 30

Ser Lys Arg Glu Thr Arg Arg Glu Asp Ser Asp Thr Lys His Asn Leu  
35 40 45

30

35

(2) INFORMATION FOR SEQ ID NO: 695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695:

40

Thr Glu His Ile Ile Ala Val Met Ile Thr Glu Leu Arg Gly Lys Asp  
1 5 10 15

45

Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val Gln Met Thr Ile Ala  
20 25 30

50

Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser Arg Gly Ser Leu Val  
35 40 45

Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Ser Ala Trp  
50 55 60

55

Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr Thr Asn Ala Arg Asp  
65 70 75 80

Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys Ala Ile Ser Lys  
85 90 95

60

698

Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys Glu Thr Asp Pro Asp  
 100 105 110  
 5 Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr Lys Gln Asn Asp Val  
 115 120 125  
 Val Arg Ile Leu Pro Cys Lys His Val Phe His Lys Ser Cys Val Asp  
 130 135 140  
 10 Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met Cys Lys Leu Asn Ile  
 145 150 155 160  
 Leu Lys Ala Leu Gly Ile Val  
 165  
 15

(2) INFORMATION FOR SEQ ID NO: 696:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696:

Met Thr His Pro Gly Thr Glu His Ile Ile Ala Val Met Ile Thr Glu  
 1 5 10 15  
 30 Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val  
 20 25 30  
 Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser  
 35 40 45  
 35 Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile  
 50 55 60  
 Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr  
 65 70 75 80  
 40 Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys  
 85 90 95  
 45 Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys  
 100 105 110  
 Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr  
 115 120 125  
 50 Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe His  
 130 135 140  
 Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met  
 145 150 155 160  
 55 Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu Pro  
 165 170 175  
 60 Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr Gln  
 180 185 190



699

Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn Ser  
 195 200 205

5 Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro Gln  
 210 215 220

Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val Thr  
 225 230 235 240

10 Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu Thr  
 245 250 255

15 Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn Glu  
 260 265 270

Val Glu Trp Phe  
 275

20

(2) INFORMATION FOR SEQ ID NO: 697:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697:

30 Thr Glu His Ile Ile Ala Val Met Ile Thr Glu Leu Arg Gly Lys Asp  
 1 5 10 15

Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val Gln Met Thr Ile Ala  
 20 25 30

35 Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser Arg Gly Ser Leu Val  
 35 40 45

40 Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Ser Ala Trp  
 50 55 60

Leu Ile Phe Tyr Phe  
 65

45

(2) INFORMATION FOR SEQ ID NO: 698:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698:

55 Ser Ile Ser Phe Ile Val Leu Met Ile Ile Ser Ser Ala Trp Leu Ile  
 1 5 10 15

Phe Tyr Phe Ile Gln Lys Ile Arg Tyr Thr Asn Ala Arg Asp Arg Asn  
 20 25 30

60

700

Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys Ala Ile Ser Lys Leu Thr  
                   35                                  40                                  45

5 Thr Arg Thr Val Lys Lys Gly Asp Lys Glu  
                   50                                  55

10 (2) INFORMATION FOR SEQ ID NO: 699:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 66 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699:

Val Lys Lys Gly Asp Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala  
   1                                  5                                  10                                  15

20 Val Cys Ile Glu Ser Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro  
                   20                                  25                                  30

Cys Lys His Val Phe His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu  
                   35                                  40                                  45

25 His Cys Thr Cys Pro Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly  
                   50                                  55                                  60

30 Ile Val  
       65

35 (2) INFORMATION FOR SEQ ID NO: 700:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 106 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700:

Met Thr His Pro Gly Thr Glu His Ile Ile Ala Val Met Ile Thr Glu  
   1                                  5                                  10                                  15

45 Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val  
                   20                                  25                                  30

Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser  
                   35                                  40                                  45

50 Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile  
                   50                                  55                                  60

55 Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr  
                   65                                  70                                  75                                  80

Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys  
                   85                                  90                                  95

60 Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr

701

100

105

5 (2) INFORMATION FOR SEQ ID NO: 701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701:

Ala Ala Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys  
1 5 10 15

15 Gly Asp Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile  
20 25 30

20 Glu Ser Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His  
35 40 45

Val Phe His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr  
50 55 60

25 Cys Pro Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro  
65 70 75 80

Asn Leu Pro Cys

30

(2) INFORMATION FOR SEQ ID NO: 702:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702:

40 Thr Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp  
1 5 10 15

45 Asn Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu  
20 25 30

Pro Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala  
35 40 45

50 Val Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala  
50 55 60

Leu Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala  
65 70 75 80

55

Asn Glu Val Glu Trp Phe  
85

60

702

## 2) INFORMATION FOR SEQ ID NO: 703:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

## (ii) SEQUENCE DESCRIPTION: SEQ ID NO: 703:

5  
 10 Pro Leu His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg  
 1 5 10 15  
 Phe Phe Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg  
 20 25 30  
 15 Gly Asn Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn  
 35 40 45  
 Ala Val Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val  
 50 55 60  
 20 Thr Met Thr His Pro Gly Thr Glu His Ile Ile Ala Val Met Ile Thr  
 65 70 75 80  
 25 Glu Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Gln Lys Asn Ile Ser  
 85 90 95  
 Val Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe  
 100 105 110  
 30 Ser Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met  
 115 120 125  
 35 Ile Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg  
 130 135 140  
 Tyr Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala  
 145 150 155 160  
 40 Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp  
 165 170 175  
 Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser  
 180 185 190  
 45 Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe  
 195 200 205  
 50 His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro  
 210 215 220  
 Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu  
 225 230 235 240  
 55 Pro Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr  
 245 250 255  
 Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn  
 260 265 270  
 60 Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro

703

275                      280                      285

Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val  
 290                      295                      300

5 Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu  
 305                      310                      315                      320

10 Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn  
 325                      330                      335

Glu Val Glu Trp Phe  
 340

15

(2) INFORMATION FOR SEQ ID NO: 704:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704:

25 His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg Phe Phe  
 1                      5                      10                      15

Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg Gly Asn  
 20                      25                      30

30 Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn Ala Val  
 35                      40                      45

Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu  
 35 50                      55                      60

40 (2) INFORMATION FOR SEQ ID NO: 705:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705:

Met Ser Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile  
 1                      5                      10                      15

50 Cys Ala Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr  
 20                      25                      30

Phe Ile Thr Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu  
 35                      40                      45

55 Gly Leu Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu  
 50                      55                      60

Glu Gly Pro Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly  
 60 65                      70                      75                      80

704

Glu Glu Pro Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn  
                             85                            90                            95  
 5 Ser Gln Pro Thr Asn Glu Ser His Ser Ile Lys Ala Ile Leu Lys Asn  
                             100                            105                            110  
 Ile Ser Val Leu Ala Phe Ser Val Cys Phe Ile Phe Thr Ile Thr Ile  
                             115                            120                            125  
 10 Gly Met Phe Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile Ala Gly  
                             130                            135                            140  
 15 Ser Ser Thr Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe Leu Thr  
                             145                            150                            155                            160  
 Phe Asn Ile Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val Phe Met  
                             165                            170                            175  
 20 Trp Pro Gly Lys Asp Ser Arg Trp Leu Pro Ser Trp Xaa Leu Ala Arg  
                             180                            185                            190  
 Leu Val Phe Val Pro Leu Leu Leu Leu Cys Asn Ile Lys Pro Arg Arg  
                             195                            200                            205  
 25 Tyr Leu Thr Val Val Phe Glu His Asp Ala Trp Phe Ile Phe Phe Met  
                             210                            215                            220  
 30 Ala Ala Phe Ala Phe Ser Asn Gly Tyr Leu Ala Ser Leu Cys Met Cys  
                             225                            230                            235                            240  
 Phe Gly Pro Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Glu Pro  
                             245                            250                            255  
 35 Ser Trp Pro Ser Ser Cys Val Trp Val Trp His Trp Gly Leu Phe Ser  
                             260                            265                            270  
 Pro Ser Cys Ser Gly Gln Leu Cys Asp Lys Gly Trp Thr Glu Gly Leu  
                             275                            280                            285  
 40 Pro Ala Ser Leu Pro Val Cys Leu Leu Pro Leu Pro Ser Ala Arg Gly  
                             290                            295                            300  
 45 Asp Pro Glu Trp Ser Gly Gly Phe Phe Phe  
                             305                            310

- 50 (2) INFORMATION FOR SEQ ID NO: 706:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 106 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706:

Met Ser Gly Gln Gly Leu Ala Gly Phe Phe Ala Ser Val Ala Met Ile  
   1                            5                            10                            15  
 60 Cys Ala Ile Ala Ser Gly Ser Glu Leu Ser Glu Ser Ala Phe Gly Tyr

705

20                      25                      30  
 Phe Ile Thr Ala Cys Ala Val Ile Ile Leu Thr Ile Ile Cys Tyr Leu  
                     35                      40                      45  
 5 Gly Leu Pro Arg Leu Glu Phe Tyr Arg Tyr Tyr Gln Gln Leu Lys Leu  
                     50                      55                      60  
 10 Glu Gly Pro Gly Glu Gln Glu Thr Lys Leu Asp Leu Ile Ser Lys Gly  
                     65                      70                      75                      80  
 Glu Glu Pro Arg Ala Gly Lys Glu Glu Ser Gly Val Ser Val Ser Asn  
                     85                      90                      95  
 15 Ser Gln Pro Thr Asn Glu Ser His Ser Ile  
                     100                      105

20 (2) INFORMATION FOR SEQ ID NO: 707:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 81 amino acids  
       (B) TYPE: amino acid  
 25 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707:

Ser Gly Val Ser Val Ser Asn Ser Gln Pro Thr Asn Glu Ser His Ser  
 1                      5                      10                      15  
 30 Ile Lys Ala Ile Leu Lys Asn Ile Ser Val Leu Ala Phe Ser Val Cys  
                     20                      25                      30  
 35 Phe Ile Phe Thr Ile Thr Ile Gly Met Phe Pro Ala Val Thr Val Glu  
                     35                      40                      45  
 Val Lys Ser Ser Ile Ala Gly Ser Ser Thr Trp Glu Arg Tyr Phe Ile  
                     50                      55                      60  
 40 Pro Val Ser Cys Phe Leu Thr Phe Asn Ile Phe Asp Trp Leu Gly Arg  
                     65                      70                      75                      80  
 Ser

45

(2) INFORMATION FOR SEQ ID NO: 708:

50 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 92 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708:

Thr Ile Gly Met Phe Pro Ala Val Thr Val Glu Val Lys Ser Ser Ile  
 1                      5                      10                      15  
 60 Ala Gly Ser Ser Thr Trp Glu Arg Tyr Phe Ile Pro Val Ser Cys Phe  
                     20                      25                      30

706

Leu Thr Phe Asn Ile Phe Asp Trp Leu Gly Arg Ser Leu Thr Ala Val  
           35                    40                    45

5 Phe Met Trp Pro Gly Lys Asp Ser Arg Trp Leu Pro Ser Trp Xaa Leu  
       50                    55                    60

Ala Arg Leu Val Phe Val Pro Leu Leu Leu Cys Asn Ile Lys Pro  
   65                    70                    75                    80

10 Arg Arg Tyr Leu Thr Val Val Phe Glu His Asp Ala  
                     85                    90

15

(2) INFORMATION FOR SEQ ID NO: 709:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709:

20 (i) SEQUENCE CHARACTERISTICS:

25 Phe Gly Pro Lys Lys Val Lys Pro Ala Glu Ala Glu Thr Ala Glu Pro  
       1                    5                    10                    15

Ser Trp Pro Ser Ser Cys Val Trp Val Trp His Trp Gly Leu Phe Ser  
                     20                    25                    30

30 Pro Ser Cys Ser Gly Gln Leu Cys Asp Lys Gly Trp Thr Glu Gly Leu  
                     35                    40                    45

Pro Ala Ser Leu Pro Val Cys Leu Leu Pro Leu Pro Ser Ala Arg Gly  
   50                    55                    60

35 Asp Pro Glu Trp Ser Gly Gly Phe Phe Phe  
   65                    70

40

(2) INFORMATION FOR SEQ ID NO: 710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710:

45 (i) SEQUENCE CHARACTERISTICS:

50 Asp Asp Asp Gly Phe Glu Ile Val Pro Ile Glu Asp Pro Ala Lys His  
       1                    5                    10                    15

Arg Ile Leu Asp Pro Glu Gly Leu Ala Leu Gly Ala Val Ile Ala Ser  
                     20                    25                    30

55 Ser Lys Lys Ala Lys Arg Asp Leu Ile Asp Asn Ser Phe Asn Arg Tyr  
                     35                    40                    45

Thr Phe Asn Glu Asp Glu Gly Glu Leu Pro Glu Trp Phe Val Gln Glu  
   50                    55                    60

60



707

Glu Lys Gln His Arg Ile Arg Gln Leu Pro Val Gly Lys Lys Glu Val  
 65 70 75 80  
 5 Glu His Tyr Arg Lys Arg Trp Arg Glu Ile Asn Ala Arg Pro Ile Xaa  
 85 90 95  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 100 105 110  
 10 Leu Glu Gln Thr Arg Lys Lys Ala Glu Ala Val Val Asn Thr Val Asp  
 115 120 125  
 Ile Xaa Arg Thr Arg Glu Ser  
 130 135  
 15

(2) INFORMATION FOR SEQ ID NO: 711:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711:  
 25 Asp Asp Asp Gly Phe Glu Ile Val Pro Ile Glu Asp Pro Ala Lys His  
 1 5 10 15  
 Arg Ile Leu Asp Pro Glu Gly Leu Ala Leu Gly Ala Val Ile Ala Ser  
 30 20 25 30  
 Ser Lys Lys Ala Lys Arg Asp Leu Ile Asp Asn Ser Phe Asn Arg Tyr  
 35 40 45  
 35 Thr Phe  
 50

40 (2) INFORMATION FOR SEQ ID NO: 712:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712:  
 Lys Arg Trp Arg Glu Ile Asn Ala Arg Pro Ile Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15  
 50 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30  
 Arg Lys Lys Ala Glu Ala Val Val Asn Thr Val Asp Ile Xaa Arg Thr  
 55 35 40 45  
 Arg Glu Ser  
 50  
 60

## (2) INFORMATION FOR SEQ ID NO: 713:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 216 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713:  
 10 Met Ile Lys Asp Lys Gly Arg Ala Arg Thr Ala Leu Thr Ser Ser Gln  
 1 5 10 15  
 Pro Ala His Leu Cys Pro Glu Asn Pro Leu Leu His Leu Lys Ala Ala  
 20 25 30  
 15 Val Lys Glu Lys Lys Arg Asn Lys Lys Lys Thr Ile Gly Ser Pro  
 35 40 45  
 20 Lys Arg Ile Gln Ser Pro Leu Asn Asn Lys Leu Leu Asn Ser Pro Ala  
 50 55 60  
 Lys Thr Leu Pro Gly Ala Cys Gly Ser Pro Gln Lys Leu Ile Asp Gly  
 65 70 75 80  
 25 Phe Leu Lys His Glu Gly Pro Pro Ala Glu Lys Pro Leu Glu Glu Leu  
 85 90 95  
 Ser Ala Ser Thr Ser Gly Val Pro Gly Leu Ser Ser Leu Gln Ser Asp  
 100 105 110  
 30 Pro Ala Gly Cys Val Arg Pro Pro Ala Pro Asn Leu Ala Gly Ala Val  
 115 120 125  
 35 Glu Phe Asn Asp Val Lys Thr Leu Leu Arg Glu Trp Ile Thr Thr Ile  
 130 135 140  
 Ser Asp Pro Met Glu Glu Asp Ile Leu Gln Val Val Lys Tyr Cys Thr  
 145 150 155 160  
 40 Asp Leu Ile Glu Glu Lys Asp Leu Glu Lys Leu Asp Leu Val Ile Lys  
 165 170 175  
 Tyr Met Lys Arg Leu Met Gln Gln Ser Val Glu Ser Val Trp Asn Met  
 180 185 190  
 45 Ala Phe Asp Phe Ile Leu Asp Asn Val Gln Val Val Leu Gln Gln Thr  
 195 200 205  
 50 Tyr Gly Ser Thr Leu Lys Val Thr  
 210 215

## (2) INFORMATION FOR SEQ ID NO: 714:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714:

Met Ile Lys Asp Lys Gly Arg Ala Arg Thr Ala Leu Thr Ser Ser Gln  
 1 5 10 15  
 5 Pro Ala His Leu Cys Pro Glu Asn Pro Leu Leu His Leu Lys Ala Ala  
 20 25 30  
 Val Lys Glu Lys Lys Arg Asn Lys Lys Lys Lys Thr Ile Gly Ser Pro  
 35 40 45  
 10 Lys Arg Ile Gln  
 50

15

(2) INFORMATION FOR SEQ ID NO: 715:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715:

25 Lys Arg Ile Gln Ser Pro Leu Asn Asn Lys Leu Leu Asn Ser Pro Ala  
 1 5 10 15  
 Lys Thr Leu Pro Gly Ala Cys Gly Ser Pro Gln Lys Leu Ile Asp Gly  
 20 25 30  
 30 Phe Leu Lys His Glu Gly Pro Pro Ala Glu Lys Pro Leu Glu Glu Leu  
 35 40 45  
 Ser Ala Ser Thr Ser Gly Val Pro Gly Leu Ser Ser Leu Gln Ser Asp  
 50 55 60  
 35 Pro Ala Gly Cys Val Arg Pro Pro Ala Pro Asn Leu Ala Gly Ala Val  
 65 70 75 80  
 40 Glu Phe Asn Asp Val Lys Thr Leu Leu Arg Glu Trp Ile Thr Thr Ile  
 85 90 95  
 Ser Asp Pro Met  
 100

45

(2) INFORMATION FOR SEQ ID NO: 716:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 74 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716:

55 Thr Ile Ser Asp Pro Met Glu Glu Asp Ile Leu Gln Val Val Lys Tyr  
 1 5 10 15  
 Cys Thr Asp Leu Ile Glu Glu Lys Asp Leu Glu Lys Leu Asp Leu Val  
 20 25 30

60

710

Ile Lys Tyr Met Lys Arg Leu Met Gln Gln Ser Val Glu Ser Val Trp  
 35 40 45

5 Asn Met Ala Phe Asp Phe Ile Leu Asp Asn Val Gln Val Val Leu Gln  
 50 55 60

Gln Thr Tyr Gly Ser Thr Leu Lys Val Thr  
 65 70

10

(2) INFORMATION FOR SEQ ID NO: 717:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717:

20 Phe Cys His Asp Cys Lys Phe Pro Glu Ala Ser Pro Ala Met Asn Cys  
 1 5 10 15

Glu Pro

25

(2) INFORMATION FOR SEQ ID NO: 718:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718:

35 Phe Cys His Asp Cys Lys Phe Pro Glu Ala Ser Pro Ala Met Asn Cys  
 1 5 10 15

Glu Pro

40

(2) INFORMATION FOR SEQ ID NO: 719:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719:

Pro Gln Pro Ser Asn Phe Pro Thr Thr Val Arg Asn Leu Pro Tyr Ser  
 1 5 10 15

55 Gly Ala Gly Ala Gln Pro Pro Pro Ser Asn Cys  
 20 25

60 (2) INFORMATION FOR SEQ ID NO: 720:

711

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720:

5 Met Ala Ser Ser Val Pro Ala Gly Gly His Thr Arg Ala Gly Gly Ile  
1 5 10 15

10 Phe Leu Ile Gly Lys Leu Asp Leu Glu Ala Ser Leu Phe Lys Ser Phe  
20 25 30

15 Gln Trp Leu Pro Phe Val Leu Arg Lys Lys Cys Asn Phe Phe Cys Trp  
35 40 45

Asp Ser Ser Ala His Ser Leu Pro Leu His Pro Leu Ser Ala Ser Cys  
50 55 60

20 Ser Ala Pro Ala Cys His Ala Ser Asp Thr His Leu Leu Tyr Pro Ser  
65 70 75 80

Thr Arg Ala Leu Cys Pro Ser Ile Phe Ala Trp Leu Val Ala Pro His  
85 90 95

25 Ser Val Phe Arg Thr Asn Ala Pro Gly Pro Thr Pro Ser Ser Gln Ser  
100 105 110

30 Ser Pro Val Phe Pro Val Phe Pro Val Ser Phe Met Ala Leu Ile Val  
115 120 125

Cys Xaa Leu Val Cys Cys  
130

35

## (2) INFORMATION FOR SEQ ID NO: 721:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721:

45 Met Ala Ser Ser Val Pro Ala Gly Gly His Thr Arg Ala Gly Gly Ile  
1 5 10 15

Phe Leu Ile Gly Lys Leu Asp Leu Glu Ala Ser Leu Phe Lys Ser Phe  
20 25 30

50 Gln Trp Leu Pro Phe Val Leu Arg Lys Lys Cys Asn Phe Phe Cys Trp  
35 40 45

55 Asp Ser Ser Ala His Ser Leu Pro Leu His Pro Leu Ser Ala Ser Cys  
50 55 60

Ser Ala Pro Ala Cys His Ala  
65 70

60

712

## (2) INFORMATION FOR SEQ ID NO: 722:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722:

5  
 10 Phe Ala Trp Leu Val Ala Pro His Ser Val Phe Arg Thr Asn Ala Pro  
     1                    5                    10                    15  
     Gly Pro Thr Pro Ser Ser Gln Ser Ser Pro Val Phe Pro Val Phe Pro  
                     20                    25                    30  
 15 Val Ser Phe Met Ala Leu Ile Val Cys Xaa Leu Val Cys Cys  
             35                    40                    45

20

## (2) INFORMATION FOR SEQ ID NO: 723:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723:

25  
 30 Met Ala Ser Ser Val Pro Ala Gly Gly His Thr Arg Ala Gly Gly Ile  
     1                    5                    10                    15  
     Phe Leu Ile Gly Lys Leu Asp Leu Glu Ala Ser Leu Phe Lys Ser Phe  
                     20                    25                    30  
 35 Gln Trp Leu Pro Phe Val Leu Arg Lys Lys Cys Asn Phe Phe Cys Trp  
             35                    40                    45  
     Asp Ser Ser Ala His Ser Leu Pro Leu His Pro Leu Ser Ala Ser Cys  
             50                    55                    60  
 40 Ser Ala Pro Ala Cys His Ala Ser Asp Thr His Leu Leu Tyr Pro Ser  
     65                    70                    75                    80  
     Thr Arg Ala Leu Cys Pro Ser Ile Phe Ala Trp Leu Val Ala Pro His  
                     85                    90                    95  
     Ser Val Phe Arg Thr Asn Ala Pro Gly Pro Thr Pro Ser Ser Gln Ser  
             100                    105                    110  
 50 Ser Pro Val Phe Pro Val Phe Pro Val Ser Phe Met Ala Leu Ile Val  
             115                    120                    125  
     Cys Xaa Leu Val Cys Cys  
             130

55

## (2) INFORMATION FOR SEQ ID NO: 724:

60

## (i) SEQUENCE CHARACTERISTICS:

713

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:

5 Met Ala Met Glu Gly Tyr Trp Arg Phe Leu Ala Leu Leu Gly Ser Ala  
1 5 10 15

10 Leu Leu Val Gly Phe Leu Ser Val Ile Phe Ala Leu Val Trp Val Leu  
20 25 30

His Tyr Arg Glu Gly Leu Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn  
35 40 45

15 Trp His Pro Val Leu Met Val Thr Gly Phe Val Phe Ile Gln Gly Ile  
50 55 60

Ala Ile Ile Val Tyr Arg Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu  
65 70 75 80

20 Leu Met Lys Ser Ile His Ala Gly Leu Asn Ala Val Ala Ala Ile Leu  
85 90 95

Ala Ile Ile Ser Val Val Ala Val Phe Glu Asn His Asn Val Asn Asn  
100 105 110

25 Ile Ala Asn Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala Val  
115 120 125

30 Ile Cys Tyr Leu Leu Gln Leu Leu Ser Gly Phe Ser Val Phe Leu Leu  
130 135 140

Pro Trp Ala Pro Leu Ser Leu Arg Ala Phe Leu Met Pro Ile His Val  
145 150 155 160

35 Tyr Ser Gly Ile Val Ile Phe Gly Thr Val Ile Ala Thr Ala Leu Met  
165 170 175

Gly Leu Thr Glu Lys Leu Ile Phe Ser Leu Arg Asp Pro Ala Tyr Ser  
180 185 190

40 Thr Phe Pro Pro Glu Gly Val Phe Val Asn Thr Leu Gly Leu Leu Ile  
195 200 205

45 Leu Val Phe Gly Ala Leu Ile Phe Trp Ile Val Thr Arg Pro Gln Trp  
210 215 220

Lys Arg Pro Lys Glu Pro Asn Ser Thr Ile Leu His Pro Asn Gly Gly  
225 230 235 240

50 Thr Glu Gln Gly Ala Arg Gly Ser Met Pro Ala Tyr Ser Gly Asn Asn  
245 250 255

Met Asp Lys Ser Asp Ser Glu Leu Asn Ser Glu Val Ala Ala Arg Lys  
260 265 270

55 Arg Asn Leu Ala Leu Asp Glu Ala Gly Gln Arg Ser Thr Met  
275 280 285

60

## (2) INFORMATION FOR SEQ ID NO: 725:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725:

5  
10 Pro Gly Arg Ala Gly Pro Ser Pro Gly Leu Ser Leu Gln Leu Pro Ala  
1 5 10 15  
Glu Pro Gly His Pro Ala Gly Asn Leu Ala Pro Leu Thr Ser Arg Pro  
20 25 30  
15 Gln Pro Leu Cys Arg Ile Pro Ala Val Pro Gly  
35 40

20

## (2) INFORMATION FOR SEQ ID NO: 726:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726:

30 Met Lys Leu Leu Gly Glu Cys Ser Ser Ser Ile Asp Ser Val Lys Arg  
1 5 10 15  
Leu Glu His Lys Leu Lys Glu Glu Glu Glu Ser Leu Pro Gly Phe Val  
20 25 30  
35 Asn Leu His Ser Thr Glu Thr Gln Thr Ala Gly Val Ile Asp Arg Trp  
35 40 45  
Glu Leu Leu Gln Ala Gln Ala Leu Ser Lys Glu Leu Arg Met Lys Gln  
50 55 60  
40 Asn Leu Gln Lys Trp Gln Phe Asn Ser Asp Leu Asn Ser Ile Trp  
65 70 75 80  
45 Ala Trp Leu Gly Asp Thr Glu Glu Glu Leu Glu Gln Leu Gln Arg Leu  
85 90 95  
Glu Leu Ser Thr Asp Ile Gln Thr Ile Glu Leu Gln Ile Lys Lys Leu  
100 105 110  
50 Lys Glu Leu Gln Lys Ala Val Asp His Arg Lys Ala Ile Ile Leu Ser  
115 120 125  
Ile Asn Leu Cys Ser Pro Glu Phe Thr Gln Ala Asp Ser Lys Glu Ser  
130 135 140  
55 Arg Asp Leu Gln Asp Arg Leu Xaa Gln Met Asn Gly Arg Trp Asp Arg  
145 150 155 160  
60 Val Cys Ser Leu Leu Glu Glu Trp Arg Gly Leu Leu Gln Asp Ala Leu  
165 170 175



715

Met Gln Cys Gln Gly Phe His Glu Met Ser His Gly Leu Leu Leu Met  
180 185 190

5 Leu Glu Asn Ile Asp Arg Arg Lys Asn Glu Ile Val Pro Ile Asp Ser  
195 200 205

Asn Leu Asp Ala Glu Ile Leu Gln Asp His His Lys Gln Leu Met Gln  
210 215 220

10 Ile Lys His Glu Leu Leu Glu Ser Gln Leu Arg Val Ala Ser Leu Gln  
225 230 235 240

Asp Met Ser Cys Gln Leu Leu Val Asn Ala Glu Gly Thr Asp Cys Leu  
15 245 250 255

Glu Ala Lys Glu Lys Val His Val Ile Gly Asn Arg Leu Lys Leu Leu  
260 265 270

20 Leu Lys Glu Val Ser Arg His Ile Lys Glu Leu Glu Lys Leu Leu Asp  
275 280 285

Val Ser Ser Ser Gln Gln Asp Leu Ser Ser Trp Ser Ser Ala Asp Glu  
290 295 300

25 Leu Asp Thr Ser Gly Ser Val Ser Pro Xaa Ser Gly Arg Ser Thr Pro  
305 310 315 320

Asn Arg Gln Lys Thr Pro Arg Gly Lys Cys Ser Leu Ser Gln Pro Gly  
30 325 330 335

Pro Ser Val Ser Ser Pro His Ser Arg Ser Thr Lys Gly Gly Ser Asp  
340 345 350

35 Ser Ser Leu Ser Glu Pro Xaa Pro Gly Arg Ser Gly Arg Gly Phe Leu  
355 360 365

Phe Arg Val Leu Arg Ala Ala Leu Pro Leu Gln Leu Leu Leu Leu  
40 370 375 380

Leu Ile Gly Leu Ala Cys Leu Val Pro Met Ser Glu Glu Asp Tyr Ser  
385 390 395 400

45 Cys Ala Leu Ser Asn Asn Phe Ala Arg Ser Phe His Pro Met Leu Arg  
405 410 415

Tyr Thr Asn Gly Pro Pro Pro Leu  
420

50

(2) INFORMATION FOR SEQ ID NO: 727:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727:

60

Met Lys Leu Leu Gly Glu Cys Ser Ser Ser Ile Asp Ser Val Lys Arg

716

1                    5                    10                    15  
 Leu Glu His Lys Leu Lys Glu Glu Glu Glu Ser Leu Pro Gly Phe Val  
                          20                    25                    30  
 5    Asn Leu His Ser Thr Glu Thr Gln Thr Ala Gly Val Ile Asp Arg Trp  
                          35                    40                    45  
 10    Glu Leu Leu Gln Ala Gln Ala Leu Ser Lys Glu Leu Arg Met Lys Gln  
                          50                    55                    60  
 Asn Leu Gln Lys Trp Gln Gln Phe Asn Ser Asp Leu Asn Ser Ile Trp  
                          65                    70                    75                    80  
 15    Ala Trp Leu Gly Asp Thr Glu Glu Glu Leu Glu Gln Leu Gln Arg Leu  
                                  85                    90                    95  
 Glu Leu Ser Thr Asp Ile Gln Thr Ile Glu Leu Gln Ile Lys  
                                  100                    105                    110  
 20

(2) INFORMATION FOR SEQ ID NO: 728:

25                    (i) SEQUENCE CHARACTERISTICS:  
                          (A) LENGTH: 136 amino acids  
                          (B) TYPE: amino acid  
                          (D) TOPOLOGY: linear  
 30                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728:  
 Lys Leu Lys Glu Leu Gln Lys Ala Val Asp His Arg Lys Ala Ile Ile  
   1                                    5                    10                    15  
 35    Leu Ser Ile Asn Leu Cys Ser Pro Glu Phe Thr Gln Ala Asp Ser Lys  
                                  20                    25                    30  
 Glu Ser Arg Asp Leu Gln Asp Arg Leu Xaa Gln Met Asn Gly Arg Trp  
                                  35                    40                    45  
 40    Asp Arg Val Cys Ser Leu Leu Glu Glu Trp Arg Gly Leu Leu Gln Asp  
                                  50                    55                    60  
 Ala Leu Met Gln Cys Gln Gly Phe His Glu Met Ser His Gly Leu Leu  
   65                                    70                    75                    80  
 45    Leu Met Leu Glu Asn Ile Asp Arg Arg Lys Asn Glu Ile Val Pro Ile  
                                  85                    90                    95  
 Asp Ser Asn Leu Asp Ala Glu Ile Leu Gln Asp His His Lys Gln Leu  
 50                                    100                    105                    110  
 Met Gln Ile Lys His Glu Leu Leu Glu Ser Gln Leu Arg Val Ala Ser  
                                  115                    120                    125  
 55    Leu Gln Asp Met Ser Cys Gln Leu  
                                  130                    135

60 (2) INFORMATION FOR SEQ ID NO: 729:

717

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729:

5 Gln Asp Met Ser Cys Gln Leu Leu Val Asn Ala Glu Gly Thr Asp Cys  
 1 5 10 15  
 10 Leu Glu Ala Lys Glu Lys Val His Val Ile Gly Asn Arg Leu Lys Leu  
 20 25 30  
 15 Leu Leu Lys Glu Val Ser Arg His Ile Lys Glu Leu Glu Lys Leu Leu  
 35 40 45  
 Asp Val Ser Ser Ser Gln Gln Asp Leu Ser Ser Trp Ser Ser Ala Asp  
 50 55 60  
 20 Glu Leu Asp Thr Ser Gly Ser Val Ser Pro Xaa Ser Gly Arg Ser Thr  
 65 70 75 80  
 Pro Asn Arg Gln Lys Thr Pro Arg Gly Lys Cys Ser Leu Ser Gln Pro  
 85 90 95  
 25 Gly Pro Ser Val Ser Ser Pro His Ser  
 100 105

30

## (2) INFORMATION FOR SEQ ID NO: 730:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730:

35 Asp Ser Ser Leu Ser Glu Pro Xaa Pro Gly Arg Ser Gly Arg Gly Phe  
 1 5 10 15  
 Leu Phe Arg Val Leu Arg Ala Ala Leu Pro Leu Gln Leu Leu Leu  
 20 25 30  
 45 Leu Leu Ile Gly Leu Ala Cys Leu Val Pro Met Ser Glu Glu Asp Tyr  
 35 40 45  
 Ser Cys Ala Leu Ser Asn Asn Phe Ala Arg Ser Phe His Pro Met Leu  
 50 55 60  
 50 Arg Tyr Thr Asn Gly Pro Pro Pro Leu  
 65 70

55

## (2) INFORMATION FOR SEQ ID NO: 731:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731:

5 Met Lys Leu Leu Ile Cys Gly Asn Tyr Leu Ala Pro Ser His Ser Glu  
 1 5 10 15  
 Ser Ser Arg Arg Cys Cys Leu Leu Cys Phe Tyr Pro Leu Cys Leu Glu  
 20 25 30  
 10 Ile Asn Phe Gly Met Lys Val Phe Leu Ser Met Pro Phe Leu Val Leu  
 35 40 45  
 Phe Gln Ser Leu Ile Gln Glu Asp  
 50 55  
 15

(2) INFORMATION FOR SEQ ID NO: 732:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732:

25 Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn Lys Tyr Asp  
 1 5 10 15  
 30 Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu Val Lys Leu Val  
 20 25 30  
 Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys Lys Asp His Gln Ser  
 35 40 45  
 35 Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu Phe Ser Asp Phe Met Lys  
 50 55 60  
 Trp Ser Ile Pro Ala Phe Leu Tyr Phe Leu Asp Asn Leu Ile Val Phe  
 40 65 70 75 80  
 Tyr Val Leu Ser Tyr Leu Gln Pro Ala Met Ala Val Ile Phe Ser Asn  
 85 90 95  
 45 Phe Ser Ile Ile Thr Thr Ala Leu Leu Phe Arg Ile Val Leu Lys Xaa  
 100 105 110  
 Arg Leu Asn Trp Ile Gln Trp Ala Ser Leu Leu Thr Leu Phe Leu Ser  
 115 120 125  
 50 Ile Val Ala Leu Thr Ala Gly Thr Lys Thr Leu Gln His Asn Leu Ala  
 130 135 140  
 Gly Arg Gly Phe His His Asp Ala Phe Phe Ser Pro Ser Asn Ser Cys  
 55 145 150 155 160  
 Leu Leu Phe Arg Asn Glu Cys Pro Arg Lys Asp Asn Cys Thr Ala Lys  
 165 170 175  
 60 Glu Trp Thr Phe Pro Glu Ala Lys Trp Asn Thr Thr Ala Arg Val Phe  
 180 185 190

719

Ser His Ile Arg Leu Gly Met Gly His Val Leu Ile Ile Val Gln Cys  
 195 200 205

5 Phe Ile Ser Ser Met Ala Asn Ile Tyr Asn Glu Lys Ile Leu Lys Glu  
 210 215 220

Gly Asn Gln Leu Thr Glu Xaa Ile Phe Ile Gln Asn Ser Lys Leu Tyr  
 225 230 235 240

10 Phe Phe Gly Ile Leu Phe Asn Gly Leu Thr Leu Gly Leu Gln Arg Ser  
 245 250 255

15 Asn Arg Asp Gln Ile Lys Asn Cys Gly Phe Phe Tyr Gly His Ser  
 260 265 270

20 (2) INFORMATION FOR SEQ ID NO: 733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733:

Asn Ser Val Pro Asn Leu Gln Thr Leu Ala Val Leu Thr Glu Ala Ile  
 1 5 10 15

30 Gly Pro Glu Pro Ala Ile Pro Arg Xaa Pro Arg Glu Pro Pro Val Ala  
 20 25 30

Thr Ser Thr Pro Ala Thr Pro Ser Ala Gly Pro Gln Pro Leu Pro Thr  
 35 40 45

35 Gly Thr Val Leu Val Pro Gly Gly Pro Ala Pro Pro Cys Leu Gly Glu  
 50 55 60

40 Ala Trp Ala Leu Leu Leu Pro Pro Cys Arg Pro Ser Leu Thr Ser Cys  
 65 70 75 80

Phe Trp Ser Pro Arg Pro Ser Pro Trp Lys Glu Thr Gly Val  
 85 90

45

(2) INFORMATION FOR SEQ ID NO: 734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734:

55 Ala Leu Gln Leu Ala Phe Tyr Pro Asp Ala Val Glu Glu Trp Leu Glu  
 1 5 10 15

Glu Asn Val His Pro Ser Leu Gln Arg Leu Gln Xaa Leu Leu Gln Asp  
 20 25 30

60

720

Leu Ser Glu Val Ser Ala Pro Pro  
35 40

5

(2) INFORMATION FOR SEQ ID NO: 735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735:

10

15

Cys His Pro Pro Ala Leu Ala Gly Thr Leu Leu Arg Thr Pro Glu Gly  
1 5 10 15

Arg Ala His Ala Arg Gly Leu Leu Leu Glu Ala Gly Gly Ala  
20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736:

25

30

Gly Ser Ser Ser Thr Arg Ser Trp Phe Ser Thr Ser Ser Pro Gln Arg  
1 5 10 15

Ser Ala Ser Trp His Ser Gly Ala Pro Ser Cys Arg Ser Trp Arg Leu  
20 25 30

35

Pro Cys Ser Trp Leu Ser Thr Arg Met Pro Trp Arg Ser Gly Trp Arg  
35 40 45

40

Lys Thr Cys Thr Pro Ala Cys Ser Gly Cys Lys  
50 55

45

(2) INFORMATION FOR SEQ ID NO: 737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737:

50

Met Arg Pro Asp Trp Lys Ala Gly Ala Gly Pro Gly Gly Pro Pro Gln  
1 5 10 15

55

Lys Pro Ala Pro Ser Ser Gln Arg Lys Pro Pro Ala Arg Pro Ser Ala  
20 25 30

Ala Ala Ala Ala Ile Ala Val Ala Ala Glu Glu Glu Arg Arg Leu  
35 40 45

60

721

Arg Gln Arg Asn Arg Leu Arg Leu Glu Glu Asp Lys Pro Ala Val Glu  
 50 55 60  
 5 Arg Cys Leu Glu Glu Leu Val Phe Gly Asp Val Glu Asn Asp Glu Asp  
 65 70 75 80  
 Ala Leu Leu Arg Arg Leu Arg Gly Pro Arg Val Gln Glu His Glu Asp  
 85 90 95  
 10 Ser Gly Asp Ser Glu Val Glu Asn Glu Ala Lys Gly Asn Phe Pro Pro  
 100 105 110  
 Gln Lys Lys Pro Val Trp Val Asp Glu Glu Asp Glu Asp Glu Glu Met  
 115 120 125  
 15 Val Asp Met Met Asn Asn Arg Phe Arg Lys Asp Met Met Lys Asn Ala  
 130 135 140  
 Ser Glu Ser Lys Leu Ser Lys Asp Asn Leu Lys Lys Arg Leu Lys Glu  
 145 150 155 160  
 Glu Phe Gln His Ala Met Gly Gly Val Pro Ala Trp Ala Glu Thr Thr  
 165 170 175  
 25 Lys Arg Lys Thr Ser Ser Asp Asp Glu Ser Glu Glu Asp Glu Asp Asp  
 180 185 190  
 Leu Leu Gln Arg Thr Gly Asn Phe Ile Ser Thr Ser Thr Ser Leu Pro  
 195 200 205  
 30 Arg Gly Ile Leu Lys Met Lys Asn Cys Gln His Ala Asn Ala Glu Arg  
 210 215 220  
 Pro Thr Val Ala Arg Ile Ser Ile Cys Ala Val Pro Ser Arg Cys Thr  
 225 230 235 240  
 Asp Cys Asp Gly Cys Trp Asp  
 245

40

(2) INFORMATION FOR SEQ ID NO: 738:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738:

50 Cys Leu Glu Glu Leu Val Phe Gly Asp Val Glu Asn Asp Glu Asp Ala  
 1 5 10 15  
 Leu Leu Arg Arg Leu Arg Gly Pro Arg Val Gln Glu His Glu Asp Ser  
 20 25 30  
 55 Gly Asp Ser Glu Val Glu Asn Glu Ala Lys Gly Asn Phe Pro Pro Gln  
 35 40 45  
 60 Lys Lys Pro Val Trp Val Asp Glu Glu Asp Glu Asp Glu Glu Met Val  
 50 55 60

722

Asp Met Met Asn Asn Arg Phe Arg Lys Asp Met Met Lys Asn Ala Ser  
 65 70 75 80  
 5 Glu Ser Lys Leu Ser Lys Asp Asn Leu Lys Lys Arg Leu Lys Glu Glu  
 85 90 95  
 Phe Gln His Ala Met Gly Gly Val Pro Ala Trp Ala Glu Thr Thr Lys  
 100 105 110  
 10 Arg Lys Thr Ser Ser Asp Asp Glu Ser Glu Glu Asp Glu Asp Asp Leu  
 115 120 125  
 15 Leu Gln Arg Thr Gly Asn Phe Ile Ser Thr Ser Thr Ser Leu Pro Arg  
 130 135 140  
 Gly Ile Leu Lys Met Lys Asn Cys Gln His Ala Asn Ala Glu Arg Pro  
 145 150 155 160  
 20 Thr Val Ala Arg Ile Ser Ile Cys Ala Val Pro Ser Arg Cys Thr Asp  
 165 170 175  
 Cys Asp Gly Cys  
 180  
 25

(2) INFORMATION FOR SEQ ID NO: 739:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 218 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739:  
 35 Leu Lys Glu Lys Ile Val Arg Ser Phe Glu Val Ser Pro Asp Gly Ser  
 1 5 10 15  
 40 Phe Leu Leu Ile Asn Gly Ile Ala Gly Tyr Leu His Leu Leu Ala Met  
 20 25 30  
 Lys Thr Lys Glu Leu Ile Gly Ser Met Lys Ile Asn Gly Arg Val Ala  
 35 40 45  
 45 Ala Ser Thr Phe Ser Ser Asp Ser Lys Lys Val Tyr Ala Ser Ser Gly  
 50 55 60  
 Asp Gly Glu Val Tyr Val Trp Asp Val Asn Ser Arg Lys Cys Leu Asn  
 65 70 75 80  
 50 Arg Phe Val Asp Glu Gly Ser Leu Tyr Gly Leu Ser Ile Ala Thr Ser  
 85 90 95  
 55 Arg Asn Gly Gln Tyr Val Ala Cys Gly Ser Asn Cys Gly Val Val Asn  
 100 105 110  
 Ile Tyr Asn Gln Asp Ser Cys Leu Gln Glu Thr Asn Pro Lys Pro Ile  
 115 120 125  
 60 Lys Ala Ile Met Asn Leu Val Thr Gly Val Thr Ser Leu Thr Phe Asn



723

130                      135                      140

Pro Thr Thr Glu Ile Leu Ala Ile Ala Ser Glu Lys Met Lys Glu Ala  
 145                      150                      155                      160

5 Val Arg Leu Val His Leu Pro Ser Cys Thr Val Phe Ser Asn Phe Pro  
                     165                      170                      175

10 Val Ile Lys Asn Lys Asn Ile Ser His Val His Thr Met Asp Phe Ser  
                     180                      185                      190

Pro Arg Ser Gly Tyr Phe Ala Leu Gly Asn Glu Lys Gly Lys Ala Leu  
                     195                      200                      205

15 Met Tyr Arg Leu His His Tyr Ser Asp Phe  
                     210                      215

20 (2) INFORMATION FOR SEQ ID NO: 740:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740:

Lys Ile Asn Gly Arg Val Ala Ala Ser Thr Phe Ser Ser Asp Ser Lys  
 1                      5                      10                      15

30 Lys Val Tyr Ala Ser Ser Gly Asp Gly Glu Val Tyr Val Trp Asp Val  
                     20                      25                      30

35 Asn Ser Arg Lys Cys Leu Asn Arg Phe Val Asp Glu Gly Ser Leu Tyr  
                     35                      40                      45

Gly Leu Ser Ile Ala Thr Ser Arg Asn Gly Gln Tyr Val Ala Cys Gly  
 50                      55                      60

40 Ser Asn Cys Gly Val Val Asn Ile Tyr Asn Gln Asp Ser Cys Leu Gln  
 65                      70                      75                      80

Glu Thr Asn Pro Lys Pro Ile Lys Ala Ile Met Asn Leu Val Thr Gly  
 85                      90                      95

45 Val Thr Ser Leu Thr Phe Asn Pro Thr Thr Glu Ile Leu Ala Ile Ala  
                     100                      105                      110

50 Ser Glu Lys Met Lys Glu Ala Val Arg Leu Val His Leu Pro Ser Cys  
                     115                      120                      125

Thr Val Phe Ser Asn Phe Pro Val Ile Lys Asn Lys Asn Ile Ser His  
 130                      135                      140

55 Val His Thr Met Asp Phe Ser Pro Arg Ser Gly Tyr Phe Ala Leu Gly  
 145                      150                      155                      160

Asn Glu Lys Gly Lys Ala Leu  
 165

60

## (2) INFORMATION FOR SEQ ID NO: 741:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val  
 1 5 10 15  
 Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Leu His Ser  
 15 20 25 30  
 Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly  
 35 40 45  
 Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu  
 50 55 60  
 Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu  
 65 70 75 80  
 Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro  
 85 90 95  
 Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met  
 100 105 110  
 Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro  
 115 120 125  
 Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Ser Phe  
 130 135 140  
 Pro Ala Gly Ala Ala Arg Pro Asp Pro Ser Tyr Ala Cys Leu Thr Pro  
 145 150 155 160  
 Cys Asp Ala Pro Thr Ser Pro Ser Leu Ser Thr Arg Ser Val Arg Thr  
 165 170 175  
 Pro Thr Pro Ala Thr Ser Gln Thr Pro Trp Cys Val Pro Ala Cys Arg  
 180 185 190  
 Lys Gly Ala Arg Thr Pro Ala Arg Val Thr Pro Gly Ala Leu Trp Ser  
 195 200 205  
 Val Thr Ser Leu Phe Lys Ala Leu Ser Pro Gly Ala Arg Ile Arg Val  
 210 215 220  
 Arg Ser Pro Glu Ser Leu Val Ser Thr Arg Lys Ser Ala Asn Met Trp  
 225 230 235 240  
 Thr Gly Ser Arg Arg Arg  
 245

60

725

## (2) INFORMATION FOR SEQ ID NO: 742:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742:

5  
 10 Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Leu His Ser Gln Pro  
 1 5 10 15  
 Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr  
 20 25 30  
 15 Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro  
 35 40 45  
 Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu Glu Gly  
 50 55 60  
 20 Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe  
 65 70 75 80  
 25 Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val  
 85 90 95  
 Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro Leu Thr  
 100 105 110  
 30 Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Ser Phe Pro Ala  
 115 120 125  
 Gly Ala Ala Arg Pro Asp Pro Ser Tyr Ala Cys Leu Thr Pro Cys Asp  
 130 135 140  
 35 Ala Pro Thr Ser Pro Ser Leu Ser Thr Arg Ser Val Arg Thr Pro Thr  
 145 150 155 160  
 40 Pro Ala Thr Ser Gln Thr Pro Trp Cys Val Pro Ala Cys Arg Lys Gly  
 165 170 175  
 Ala Arg Thr Pro Ala Arg Val Thr Pro Gly Ala Leu Trp Ser Val Thr  
 180 185 190  
 45 Ser Leu Phe Lys Ala Leu Ser Pro Gly Ala Arg Ile Arg Val Arg Ser  
 195 200 205  
 Pro Glu Ser Leu Val Ser Thr Arg Lys Ser Ala Asn Met Trp Thr Gly  
 210 215 220  
 50 Ser Arg Arg Arg  
 225

55

## (2) INFORMATION FOR SEQ ID NO: 743:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

60

726

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

5 Cys Lys Leu His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr  
 1 5 10 15  
 Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr  
 20 25 30  
 10 Ala Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His  
 35 40 45  
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu  
 50 55 60  
 15 Ser Phe Pro His Pro Gly Phe Asn Asn Ser  
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 744:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744:

30 Val Leu Gln Gly Arg Tyr Phe Ser Pro Ile Leu Glu Met Arg Arg Leu  
 1 5 10 15  
 Arg Pro Glu Gly Xaa Xaa Asn Leu Pro Gly Gly Ser Arg Ala Gln Lys  
 20 25 30  
 35 Glu Pro Arg Gln Asp Leu Thr Leu Val Leu Trp Pro His Cys Pro His  
 35 40 45  
 Phe Ala Met Thr Arg Ser Tyr Val Pro Thr Lys Gln Cys Met Val Gln  
 50 55 60  
 40 Gly Ser Phe Tyr Cys Ile Phe Ile Phe Lys Gly Pro Val Gln Asn Trp  
 65 70 75 80

45

Cys

50

(2) INFORMATION FOR SEQ ID NO: 745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745:

Met Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His Asp Phe Met Gln  
 1 5 10 15  
 60 Ser Ala Glu Val Gly Thr Ile Phe Ala Leu Ser Trp Leu Ile Thr Trp

727

20 25 30  
 Phe Gly His Val Leu Ser Asp Phe Arg His Val Val Arg Leu Tyr Asp  
 35 40 45  
 5 Phe Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr Phe Ala Ala Val  
 50 55 60  
 10 Ile Val Leu Tyr Arg Glu Gln Glu Val Leu Asp Cys Asp Cys Asp Met  
 65 70 75 80  
 Ala Ser Val His His Leu Leu Ser Gln Ile Pro Gln Asp Leu Pro Tyr  
 85 90 95  
 15 Glu Thr Leu Ile Ser Arg Xaa Glu Thr Phe Leu Phe Ser Phe Pro His  
 100 105 110  
 Pro Asn Leu Leu Gly Arg Pro Leu Pro Asn Ser Lys Leu Arg Gly Arg  
 115 120 125  
 20 Gln Pro Leu Leu Ser Lys Thr Leu Ser Trp His Gln Pro Ser Arg Gly  
 130 135 140  
 Leu Ile Trp Cys Cys Gly Ser Gly Xaa Arg Gly Leu Leu Arg Pro Glu  
 145 150 155 160  
 Asp Arg Thr Lys Asp Val Leu Thr Lys Pro Arg Thr Asn Arg Phe Val  
 165 170 175  
 30 Lys Leu Ala Val Met Gly Leu Thr Val Ala Leu Gly Ala Ala Ala Leu  
 180 185 190  
 Ala Val Val Lys Ser Ala Leu Glu Trp Ala Pro Lys Phe Gln Leu Gln  
 195 200 205  
 35 Leu Phe Pro  
 210

(2) INFORMATION FOR SEQ ID NO: 746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746:

50 Cys Pro Glu Phe Phe Ile Pro Ala Thr Leu Pro Cys Pro Phe Val Phe  
 1 5 10 15  
 Ala Phe Thr Ser Glu Ala Ser Ser Arg Ala Tyr Leu Thr Gln Arg Gly  
 20 25 30  
 55 Pro Gly Gly Leu Ala Gln Asn Leu Met Pro Leu Pro Val Gly Phe Trp  
 35 40 45  
 60 Met Gly Ser Leu Pro Pro Pro Trp Cys Trp Arg Lys Trp Val Ser Glu  
 50 55 60

728

Ala Cys Ser Cys Phe Cys  
65 70

5

(2) INFORMATION FOR SEQ ID NO: 747:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747:

15

Gly Phe Gly Ser Val Ser Ala Ala Gly Arg Arg Ser Gly Gly Thr Trp  
1 5 10 15

Gln Pro Val Gln  
20

20

(2) INFORMATION FOR SEQ ID NO: 748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

25

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748:

30

Pro Gly Gly Leu Ala Val Gly Ser Arg Trp Trp Ser Arg Ser Leu Thr  
1 5 10 15

35

(2) INFORMATION FOR SEQ ID NO: 749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

40

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749:

45

Leu Glu Pro Ser Arg Gln Arg Arg Pro Arg Arg Arg Gly Gly Thr Ser  
1 5 10 15

50

Arg Pro Glu Thr Asp Gln Arg Ala Lys Cys Trp Arg Gln Leu  
20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750:

Val Cys Leu Arg Cys Gln Asn Arg Met Glu Asn  
 1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 751:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751:

15

Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
 1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
 20 25 30

20

Ala Xaa Ala Gly Ala Phe Ser Pro Ala Ser Thr Thr Thr Thr Arg Arg  
 35 40 45

25

His Leu Ser Ser Arg Asn Arg Pro Glu Gly Lys Val Leu Glu Thr Val  
 50 55 60

Gly Val Phe Glu Val Pro Lys Gln Asn Gly Lys Tyr Glu Thr Gly Gln  
 65 70 75 80

30

Leu Phe Leu His Ser Ile Phe Gly Tyr Arg Gly Val Val Leu Phe Pro  
 85 90 95

Trp Gln Ala Arg Leu Xaa Asp Arg Asp Val Ala Ser Ala Ala Pro Glu  
 100 105 110

35

Lys Ala Glu Asn Pro Ala Gly His Gly Ser Lys Glu Val Lys Gly Lys  
 115 120 125

40

Thr His Thr Tyr Tyr Gln Val Leu Ile Asp Ala Arg Asp Cys Pro His  
 130 135 140

Ile Ser Gln Arg Ser Gln Thr Glu Ala Val Thr Phe Leu Ala Asn His  
 145 150 155 160

45

Asp Asp Ser Arg Ala Leu Tyr Ala Ile Pro Gly Leu Asp Tyr Val Ser  
 165 170 175

His Glu Asp Ile Leu Pro Tyr Thr Ser Thr Asp Gln Val Pro Ile Gln  
 180 185 190

50

His Glu Leu Phe Glu Arg Phe Leu Leu Tyr Asp Gln Thr Lys Ala Pro  
 195 200 205

55

Pro Phe Val Ala Arg Glu Thr Leu Arg Ala Trp Gln Glu Lys Asn His  
 210 215 220

Pro Trp Leu Glu Leu Ser Asp Val His Arg Glu Thr Thr Glu Asn Ile  
 225 230 235 240

60

Arg Val Thr Val Ile Pro Phe Tyr Met Gly Met Arg Glu Ala Gln Asn

730

245 250 255

Ser His Val Tyr Trp Trp Arg Tyr Cys Ile Arg Leu Glu Asn Leu Asp  
260 265 270

5 Ser Asp Val Val Gln Leu Arg Glu Arg His Trp Arg Ile Phe Ser Leu  
275 280 285

10 Ser Gly Thr Leu Glu Thr Val Arg Gly Arg Gly Val Val Gly Arg Glu  
290 295 300

Pro Val Leu Ser Lys Glu Gln Pro Ala Phe Gln Tyr Ser Ser His Val  
305 310 315 320

15 Ser Leu Gln Ala Ser Ser Gly His Met Trp Gly Thr Phe Arg Phe Glu  
325 330 335

Arg Pro Asp Gly Ser His Phe Asp Val Arg Ile Pro Pro Phe Ser Leu  
340 345 350

20 Glu Ser Asn Lys Asp Glu Lys Thr Pro Pro Ser Gly Leu His Trp  
355 360 365

25

(2) INFORMATION FOR SEQ ID NO: 752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752:

35 Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
20 25 30

40 Ala

45

(2) INFORMATION FOR SEQ ID NO: 753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753:

55 Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
20 25 30

60 Ala



5 (2) INFORMATION FOR SEQ ID NO: 754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754:

Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
1 5 10 15

15 Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
20 25 30

Ala

20

(2) INFORMATION FOR SEQ ID NO: 755:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755:

Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
1 5 10 15

35 Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
20 25 30

Ala

40

(2) INFORMATION FOR SEQ ID NO: 756:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756:

50 Met Ala Ala Cys Thr Ala Arg Arg Pro Gly Arg Gly Gln Pro Leu Val  
1 5 10 15

Val Pro Val Ala Asp Xaa Gly Pro Val Ala Lys Ala Ala Leu Cys Ala  
20 25 30

55

Ala

60

732

## (2) INFORMATION FOR SEQ ID NO: 757:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757:

Val Leu Glu Thr Val Gly Val Phe Glu Val Pro Lys Gln Asn Gly Lys  
1 5 10 15  
Tyr Glu Thr Gly Gln Leu Phe Leu His Ser Ile Phe Gly Tyr Arg Gly  
20 25 30  
Val Val Leu  
35

## (2) INFORMATION FOR SEQ ID NO: 758:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758:

Gly Leu Asp Tyr Val Ser His Glu Asp Ile Leu Pro Tyr Thr Ser Thr  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO: 759:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759:

Asp Val His Arg Glu Thr Thr Glu Asn Ile Arg Val Thr Val Ile Pro  
1 5 10 15

Phe Tyr Met

## (2) INFORMATION FOR SEQ ID NO: 760:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760:

Trp Trp Arg Tyr Cys Ile Arg Leu Glu Asn Leu Asp Ser Asp Val Val

733

1                      5                      10                      15

Gln Leu Arg Glu Arg  
                    20

5

(2) INFORMATION FOR SEQ ID NO: 761:

10                      (i) SEQUENCE CHARACTERISTICS:  
                            (A) LENGTH: 26 amino acids  
                            (B) TYPE: amino acid  
                            (D) TOPOLOGY: linear  
                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761:

15

Pro Ala Phe Gln Tyr Ser Ser His Val Ser Leu Gln Ala Ser Ser Gly  
1                      5                      10                      15

20

His Met Trp Gly Thr Phe Arg Phe Glu Arg  
                    20                      25

(2) INFORMATION FOR SEQ ID NO: 762:

25                      (i) SEQUENCE CHARACTERISTICS:  
                            (A) LENGTH: 11 amino acids  
                            (B) TYPE: amino acid  
                            (D) TOPOLOGY: linear  
                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762:

30

Ser Leu Cys Cys Pro Glu Gly Ala Glu Gly Cys  
1                      5                      10

35

(2) INFORMATION FOR SEQ ID NO: 763:

40                      (i) SEQUENCE CHARACTERISTICS:  
                            (A) LENGTH: 12 amino acids  
                            (B) TYPE: amino acid  
                            (D) TOPOLOGY: linear  
                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763:

45

Gln Leu Lys Lys Thr His Tyr Asp Arg Pro Cys Pro  
1                      5                      10

50

(2) INFORMATION FOR SEQ ID NO: 764:

                    (i) SEQUENCE CHARACTERISTICS:  
                            (A) LENGTH: 12 amino acids  
                            (B) TYPE: amino acid  
                            (D) TOPOLOGY: linear  
                    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764:

55

Gln Leu Lys Lys Thr His Tyr Asp Arg Pro Cys Pro  
1                      5                      10

60

## (2) INFORMATION FOR SEQ ID NO: 765:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765:

Ala Gln Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu  
1 5 10 15

15

Met Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
20 25 30

Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val  
35 40 45

20

Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln  
50 55 60

25

Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser  
65 70 75 80

Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp Phe Asp Glu Gly  
85 90 95

30

Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser Ala Pro Thr Phe Ile  
100 105 110

Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg Gly Asp Thr Tyr Glu Leu  
115 120 125

35

Gln Val Arg Gly Phe Ser Ala Glu Gln Ile Ala Arg Trp Ile Ala Asp  
130 135 140

40

Arg Thr Asp Val Asn Ile Arg Val Ile Arg Pro Pro Asn Met Ala Ala  
145 150 155 160

Arg Trp Arg Phe Trp Cys Val Ser Val Thr  
165 170

45

## (2) INFORMATION FOR SEQ ID NO: 766:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766:

55

Met Val Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser  
1 5 10 15

60

## (2) INFORMATION FOR SEQ ID NO: 767:

735

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767:

Ala Gln Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu  
1 5 10 15

10

15 (2) INFORMATION FOR SEQ ID NO: 768:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768:

Met Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
1 5 10 15

25

Phe

30

(2) INFORMATION FOR SEQ ID NO: 769:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769:

40 Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val Met  
1 5 10 15

Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln Ala  
20 25 30

45 Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser Ala  
35 40 45

Phe Thr Asn Arg Ile Phe Phe Ala  
50 55

50

(2) INFORMATION FOR SEQ ID NO: 770:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770:

736

Met Val Asp Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met  
 1 5 10 15

5 Asn Ser Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro  
 20 25 30

10 (2) INFORMATION FOR SEQ ID NO: 771:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771:

Lys Arg Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu  
 1 5 10 15

20 Gln Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val  
 20 25 30

Ile Arg Pro Pro Asn  
 35

25

(2) INFORMATION FOR SEQ ID NO: 772:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772:

Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu Ala Val Ile Gly Gly  
 1 5 10 15

40 Leu Val Tyr Leu Arg Arg Val Ile Trp Asn Phe Ser Leu Ile Lys Leu  
 20 25 30

Asp Gly Leu Leu Gln Leu Cys Val Leu Cys Leu Leu  
 35 40

45

(2) INFORMATION FOR SEQ ID NO: 773:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773:

55 Asp Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp  
 1 5 10 15

Ser

60

## (2) INFORMATION FOR SEQ ID NO: 774:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774:

10

Cys Gln Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg Lys Glu Ser  
1 5 10 15

15

Lys Asn Leu Asn  
20

## (2) INFORMATION FOR SEQ ID NO: 775:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775:

Val Leu Leu Val Ser Leu Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe  
1 5 10 15

30

35

## (2) INFORMATION FOR SEQ ID NO: 776:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776:

Met Gly Leu Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val  
1 5 10 15

45

Gln Ile Ala Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp  
20 25 30

50

Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Ser  
35 40 45

55

## (2) INFORMATION FOR SEQ ID NO: 777:

60

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

738

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777:

5 Pro Ala Ala Trp Asp Asp Lys Thr Asn Ile Lys Thr Val Cys Thr Tyr  
 1 5 10 15  
 Trp Glu Asp Phe His Ser Cys Thr Val Thr Ala Leu Thr Asp Cys Gln  
 20 25 30  
 10 Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg Lys Glu Ser Lys Asn  
 35 40 45  
 Leu Asn Ile Gln Gly Ser Leu Phe Glu Leu Cys Gly Ser Gly Asn Gly  
 15 50 55 60  
 Ala Ala Gly Ser Leu Leu Pro Ala Phe Pro Val Leu Leu Val Ser Leu  
 65 70 75 80  
 20 Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe  
 85 90

25 (2) INFORMATION FOR SEQ ID NO: 778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778:

Met Gly Leu Lys Leu Asn Gly Arg Tyr Ile Ser Leu Ile Leu Ala Val  
 1 5 10 15  
 35 Gln Ile Ala Tyr Leu Val Gln Ala Val Arg Ala Ala Gly Lys Cys Asp  
 20 25 30  
 Ala Val Phe Lys Gly Phe Ser Asp Cys Leu Leu Lys Leu Gly Asp Ser  
 40 35 40 45  
 Xaa Xaa Xaa Xaa Xaa Pro Ala Ala Trp Asp Asp Lys Thr Asn Ile Lys  
 50 55 60  
 45 Thr Val Cys Thr Tyr Trp Glu Asp Phe His Ser Cys Thr Val Thr Ala  
 65 70 75 80  
 Leu Thr Asp Cys Gln Glu Gly Ala Lys Asp Met Trp Asp Lys Leu Arg  
 85 90 95  
 50 Lys Glu Ser Lys Asn Leu Asn Ile Gln Gly Ser Leu Phe Glu Leu Cys  
 100 105 110  
 Gly Ser Gly Asn Gly Ala Ala Gly Ser Leu Leu Pro Ala Phe Pro Val  
 55 115 120 125  
 Leu Leu Val Ser Leu Ser Ala Ala Leu Ala Thr Trp Leu Ser Phe  
 130 135 140

60



739

## (2) INFORMATION FOR SEQ ID NO: 779:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779:

5  
10 Met Asn Ser Ala Ala Gly Phe Ser His Leu Asp Arg Arg Glu Arg Val  
1 5 10 15  
Leu Lys Leu Gly Glu Ser Phe Glu Lys Gln Pro Arg Cys Ala Ser Thr  
20 25 30  
15 Leu Cys

20

## (2) INFORMATION FOR SEQ ID NO: 780:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780:

25  
30 Thr Ile Tyr Pro Thr Glu Glu Glu Leu Gln Ala Val Gln Lys Ile Val  
1 5 10 15  
Ser Ile Thr Glu Arg Ala Leu Lys Leu Val Ser Asp  
20 25

35

## (2) INFORMATION FOR SEQ ID NO: 781:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781:

40  
45 Arg Ala Leu Lys Gly Val Leu Arg Val Gly Val Leu Ala Lys Gly Leu  
1 5 10 15  
Leu Leu Arg Gly Asp Arg Asn Val Asn Leu Val Leu Leu Cys  
20 25 30

50

## (2) INFORMATION FOR SEQ ID NO: 782:

55

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782:

60

740

Ala Leu Ala Ala Leu Arg His Ala Lys Trp Phe Gln Ala Arg Ala Asn  
1 5 10 15

5 Gly Leu Gln Ser Cys Val Ile Ile Ile Arg Ile Leu Arg Asp Leu Cys  
20 25 30

Gln Arg Val Pro Thr Trp Ser  
35

10

(2) INFORMATION FOR SEQ ID NO: 783:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783:

20 Gly Asp Ala Leu Arg Arg Val Phe Glu Cys Ile Ser Ser Gly Ile Ile  
1 5 10 15

Leu

25

(2) INFORMATION FOR SEQ ID NO: 784:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784:

35 Leu Ala Phe Arg Gln Ile His Lys Val Leu Gly Met Asp Pro Leu Pro  
1 5 10 15

40

(2) INFORMATION FOR SEQ ID NO: 785:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785:

Thr Ile Tyr Pro Thr Glu Glu Glu Leu Gln Ala Val Gln Lys Ile Val  
1 5 10 15

55 Ser Ile Thr Glu Arg Ala Leu Lys Leu Val Ser Asp Ser Leu Ser Glu  
20 25 30

His Glu Lys Asn Lys Asn Lys Glu Gly Asp Asp Lys Lys Glu Gly Gly  
35 40 45

60

741

Lys Asp Arg Ala Leu Lys Gly Val Leu Arg Val Gly Val Leu Ala Lys  
 50 55 60  
 Gly Leu Leu Leu Arg Gly Asp Arg Asn Val Asn Leu Val Leu Leu Cys  
 5 65 70 75 80  
 Ser Glu Lys Pro Ser Lys Thr Leu Leu Ser Arg Ile Ala Glu Asn Leu  
 85 90 95  
 10 Pro Lys Gln Leu Ala Val Ile Ser Pro Glu Lys Tyr Asp Ile Lys Cys  
 100 105 110  
 Ala Val Ser Glu Ala Ala Ile Ile Leu Asn Ser Cys Val Glu Pro Lys  
 115 120 125  
 15 Met Gln Val Thr Ile Thr Leu Thr Ser Pro Ile Ile Arg Glu Glu Asn  
 130 135 140  
 Met Arg Glu Gly Asp Val Thr Ser Gly Met Val Lys Asp Pro Pro Asp  
 20 145 150 155 160  
 Val Leu Asp Arg Gln Lys Cys Leu Asp Ala Leu Ala Ala Leu Arg His  
 165 170 175  
 25 Ala Lys Trp Phe Gln Ala Arg Ala Asn Gly Leu Gln Ser Cys Val Ile  
 180 185 190  
 Ile Ile Arg Ile Leu Arg Asp Leu Cys Gln Arg Val Pro Thr Trp Ser  
 195 200 205  
 30 Asp Phe Pro Ser Trp Ala Met Glu Leu Leu Val Glu Lys Ala Ile Ser  
 210 215 220  
 Ser Ala Ser Ser Pro Gln Ser Pro Gly Asp Ala Leu Arg Arg Val Phe  
 35 225 230 235 240  
 Glu Cys Ile Ser Ser Gly Ile Ile Leu Lys Gly Ser Pro Gly Leu Leu  
 245 250 255  
 40 Asp Pro Cys Glu Lys Asp Pro Phe Asp Thr Leu Ala Thr Met Thr Asp  
 260 265 270  
 Gln Gln Arg Glu Asp Ile Thr Ser Ser Ala Gln Phe Ala Leu Arg Leu  
 275 280 285  
 45 Leu Ala Phe Arg Gln Ile His Lys Val Leu Gly Met Asp Pro Leu Pro  
 290 295 300  
 Gln Met Ser Gln Arg Phe Asn Ile His Asn Asn Arg Lys Arg Arg Arg  
 50 305 310 315 320  
 Asp Ser Asp Gly Val Asp Gly Phe Glu Ala Glu Gly Lys Lys Asp Lys  
 325 330 335  
 55 Lys Asp Tyr Asp Asn Phe  
 340

60 (2) INFORMATION FOR SEQ ID NO: 786:

742

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786:

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg  
1 5 10 15  
Lys Gln Glu Asp Asp Arg Asp Gly  
20

## (2) INFORMATION FOR SEQ ID NO: 787:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787:

Leu Leu Ala Glu Arg Glu Gln Glu Glu Ala Ile Ala Gln Phe Pro Tyr  
1 5 10 15  
Val Glu Phe Thr Gly Arg Asp Ser Ile Thr Cys Leu Thr Cys  
20 25 30

## (2) INFORMATION FOR SEQ ID NO: 788:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788:

Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln Val Asn Glu Leu Val Ala  
1 5 10 15  
Leu Ile Pro His Ser Asp Gln Arg Leu Arg Pro Gln Arg Thr Lys Gln  
20 25 30  
Tyr Val

## (2) INFORMATION FOR SEQ ID NO: 789:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789:

Ala Arg Leu Asn Val Gly Arg Glu Ser Leu Lys Arg Glu Met Leu Lys  
1 5 10 15

Ser Gln Gly Val Lys Val Ser Glu Ser Pro Met Gly Ala Arg His Ser  
 20 25 30

5 Ser Trp Pro Glu Gly Ala Ala Phe Cys Lys Lys Val Gln Gly Ala Gln  
 35 40 45

Met Gln Phe Pro Pro Arg Arg  
 50 55

10

(2) INFORMATION FOR SEQ ID NO: 790:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790:

20

Ala Arg Leu Asn Val Gly Arg Glu Ser Leu Lys Arg Glu Met Leu  
 1 5 10 15

25

(2) INFORMATION FOR SEQ ID NO: 791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

30

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791:

35

Leu Lys Ser Gln Gly Val Lys Val Ser Glu Ser Pro Met Gly Ala Arg  
 1 5 10 15

His Ser Ser Trp  
 20

40

(2) INFORMATION FOR SEQ ID NO: 792:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792:

50

Ala Phe Cys Lys Lys Val Gln Gly Ala Gln Met Gln Phe Pro Pro Arg  
 1 5 10 15

Arg

55

(2) INFORMATION FOR SEQ ID NO: 793:

60

(i) SEQUENCE CHARACTERISTICS:

744

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793:

5

Ala Phe Cys Lys Lys Val Gln Gly Ala Gln Met Gln Phe Pro Pro Arg  
 1 5 10 15

Arg

10

(2) INFORMATION FOR SEQ ID NO: 794:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794:

Val Gln Val Leu Glu Gln Leu Thr Asn Asn Ala Val Ala Glu Ser Arg  
 1 5 10 15

25

Phe Asn Asp Ala Ala Tyr Tyr Tyr Trp Met Leu Ser Met Gln Cys Leu  
 20 25 30

Asp Ile Ala Gln Asp  
 35

30

(2) INFORMATION FOR SEQ ID NO: 795:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795:

Pro Ala Gln Lys Asp Thr Met Leu Gly Lys Phe Tyr His Phe Gln Arg  
 1 5 10 15

45

Leu Ala Glu Leu Tyr His Gly Tyr His Ala Ile His Arg His Thr Glu  
 20 25 30

Asp Pro

50

(2) INFORMATION FOR SEQ ID NO: 796:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796:

60

Leu Ala Lys Gln Ser Lys Ala Leu Gly Ala Tyr Arg Leu Ala Arg His

745

1                    5                    10                    15  
 Ala Tyr Asp Lys Leu Arg Gly Leu Tyr Ile Pro  
                   20                    25  
 5

(2) INFORMATION FOR SEQ ID NO: 797:

10            (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 36 amino acids  
               (B) TYPE: amino acid  
               (D) TOPOLOGY: linear  
               (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797:

15            Ala Arg Phe Gln Lys Ser Ile Glu Leu Gly Thr Leu Thr Ile Arg Ala  
               1                    5                    10                    15  
               Lys Pro Phe His Asp Ser Glu Glu Leu Val Pro Leu Cys Tyr Arg Cys  
 20                    20                    25                    30  
               Ser Thr Asn Asn  
                   35

25

(2) INFORMATION FOR SEQ ID NO: 798:

30            (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 73 amino acids  
               (B) TYPE: amino acid  
               (D) TOPOLOGY: linear  
               (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798:

35            Pro Leu Leu Asn Asn Leu Gly Asn Val Cys Ile Asn Cys Arg Gln Pro  
               1                    5                    10                    15  
               Phe Ile Phe Ser Ala Ser Ser Tyr Asp Val Leu His Leu Val Glu Phe  
                   20                    25                    30  
 40            Tyr Leu Glu Glu Gly Ile Thr Asp Glu Glu Ala Ile Ser Leu Ile Asp  
                   35                    40                    45  
               Leu Glu Val Leu Arg Pro Lys Arg Asp Asp Arg Gln Leu Glu Ile Cys  
 45                    50                    55                    60  
               Lys Gln Gln Leu Pro Asp Ser Cys Gly  
                   65                    70

50

(2) INFORMATION FOR SEQ ID NO: 799:

55            (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 29 amino acids  
               (B) TYPE: amino acid  
               (D) TOPOLOGY: linear  
               (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799:

60            Met Pro Tyr Ala Gln Trp Leu Ala Glu Asn Asp Arg Phe Glu Glu Ala

746

1                    5                    10                    15  
Gln Lys Ala Phe His Lys Ala Gly Arg Gln Arg Glu Ala  
                  20                    25  
5

(2) INFORMATION FOR SEQ ID NO: 800:

10            (i) SEQUENCE CHARACTERISTICS:  
              (A) LENGTH: 36 amino acids  
              (B) TYPE: amino acid  
              (D) TOPOLOGY: linear

15            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800:

Phe Ser Val His Arg Pro Glu Thr Leu Phe Asn Ile Ser Arg Phe Leu  
1                    5                    10                    15  
Leu His Ser Leu Pro Lys Asp Thr Pro Ser Gly Ile Ser Lys Val Lys  
20                    25                    30  
Ile Leu Phe Thr  
                  35

25



## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>161</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>March 27, 1997</u>	Accession Number <u>97979</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")          	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>162</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>April 4, 1997</u>	Accession Number <u>97974</u>
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<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")          	
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Authorized officer	

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>162</u> . line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>May 29, 1997</u>	Accession Number <u>209080</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <u>---</u>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>164</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit December 3, 1997	Accession Number 209511
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")          	
<div style="display: flex; justify-content: space-between;"><div style="width: 45%;"><p><b>For receiving Office use only</b></p><div style="border: 1px solid black; padding: 5px;"><div><input checked="" type="checkbox"/> This sheet was received with the international application G. Anton Smith Paternal Specialist LEP. PCT. ORGANIS (703) 505-3747</div><div>Authorized officer</div><div style="text-align: center; font-weight: bold; font-size: 1.2em;">04 JUN 1998</div></div></div><div style="width: 45%;"><p><b>For International Bureau use only</b></p><div style="border: 1px solid black; padding: 5px;"><div><input type="checkbox"/> This sheet was received by the International Bureau on:</div><div>Authorized officer</div></div></div></div>	

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>167</u> . line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 4, 1997	Accession Number 97975
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div style="display: flex; justify-content: space-between;"><div style="width: 45%;"><b>For receiving Office use only</b> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer <p style="font-size: 1.2em; margin-top: 10px;">04 JUN 1998</p></div></div></div><div style="width: 45%;"><b>For International Bureau use only</b> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on: <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer</div></div></div></div>	

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>167</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>May 29, 1997</u>	Accession Number <u>209081</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")          	
<b>For receiving Office use only</b>	
<input checked="" type="checkbox"/> This sheet was received with the international application   Authorized officer <u>1001 005-07-7</u> <b>04 JUN 1998</b>	
<b>For International Bureau use only</b>	
<input type="checkbox"/> This sheet was received by the International Bureau on:   Authorized officer _____	

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>171</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>April 4, 1997</u>	Accession Number <u>97976</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (If the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")          	
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Authorized officer <u>04 JUN 1998</u>	
<b>For International Bureau use only</b>	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>172</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>	
Date of deposit <u>April 4, 1997</u>	Accession Number <u>97977</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (If the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")          	
<b>For receiving Office use only</b>	
<input checked="" type="checkbox"/> This sheet was received with the international application Patent Specialist PCT/US98/11422	
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<b>For International Bureau use only</b>	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>172</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 29, 1997	Accession Number 209082
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<b>For receiving Office use only</b>	<b>For International Bureau use only</b>
<input checked="" type="checkbox"/> This sheet was received with the international application Specialist Operations	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer 04 JUN 1998	Authorized officer

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>176</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit April 28, 1997	Accession Number 209007
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (If the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div style="display: flex; justify-content: space-between;"><div style="width: 45%;"><p>For receiving Office use only</p><div style="border: 1px solid black; padding: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application <p style="text-align: center;">Authorized officer</p><p>04 JUN 1998</p></div></div><div style="width: 45%;"><p>For International Bureau use only</p><div style="border: 1px solid black; padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on: <p style="text-align: center;">Authorized officer</p></div></div></div>	

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>176</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>May 29, 1997</u>	Accession Number <u>209083</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (If the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")     	
<b>For receiving Office use only</b>	
<input type="checkbox"/> This sheet was received with the international application by <u>Patent Specialist</u> <u>Operations</u>	
Authorized officer <u>180, 808-1747</u> <b>04 JUN 1998</b>	
<b>For International Bureau use only</b>	
<input type="checkbox"/> This sheet was received by the International Bureau on:	
Authorized officer	

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>179</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit    April 28, 1997	Accession Number    209008
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	
<div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;"><div style="text-align: center;">For receiving Office use only</div><div style="display: flex; justify-content: space-between; align-items: center;"><input type="checkbox"/> This sheet was received with the international application</div><div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer <div style="text-align: center;">396</div></div></div>	<div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;"><div style="text-align: center;">For International Bureau use only</div><div style="display: flex; justify-content: space-between; align-items: center;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div><div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer</div></div>

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 179, line N/A	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 29, 1997	Accession Number 209084
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	
<b>For receiving Office use only</b>	<b>For International Bureau use only</b>
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Authorized officer 04 JUN 1998	Authorized officer

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>180</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution ( <i>including postal code and country</i> ) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit    April 28, 1997	Accession Number    209010
<b>C. ADDITIONAL INDICATIONS</b> ( <i>leave blank if not applicable</i> )    This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> ( <i>if the indications are not for all designated States</i> )	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> ( <i>leave blank if not applicable</i> )	
The indications listed below will be submitted to the International Bureau later ( <i>specify the general nature of the indications, e.g., "Accession Number of Deposit"</i> )	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer <div style="text-align: center; margin-top: 10px;">APR 29 1998</div></div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>180</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <u>May 29, 1997</u>	Accession Number <u>209085</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")          	
<b>For receiving Office use only</b>	
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Authorized officer <p style="font-size: 1.2em;">04 JUN 1998</p>	
<b>For International Bureau use only</b>	
<input type="checkbox"/> This sheet was received by the International Bureau on:	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>182</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit    April 28, 1997	Accession Number    209009
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; height: 40px; margin-top: 5px;"></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; height: 40px; margin-top: 5px;"></div>
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>186</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</p>	
Date of deposit <u>April 28, 1997</u>	Accession Number <u>209011</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")          	
<div style="display: flex; justify-content: space-between;"><div style="width: 45%;"><p>For receiving Office use only</p><div style="border: 1px solid black; padding: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application by the Specialist WIPO-PCT Operations Authorized officer <u>(700) 303-8147</u>  <p style="font-size: 1.2em;">04 JUN 1998</p></div></div><div style="width: 45%;"><p>For International Bureau use only</p><div style="border: 1px solid black; padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:  Authorized officer</div></div></div>	

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>174</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution ( <i>including postal code and country</i> ) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit    April 7, 1998	Accession Number    209746
<b>C. ADDITIONAL INDICATIONS</b> ( <i>leave blank if not applicable</i> ) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> ( <i>if the indications are not for all designated States</i> )	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> ( <i>leave blank if not applicable</i> )	
The indications listed below will be submitted to the International Bureau later ( <i>specify the general nature of the indications, e.g., "Accession Number of Deposit"</i> )	

<div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="" type="checkbox"/> This sheet was received with the international application</div> <div style="padding: 5px;">Authorized officer <div style="font-size: 1.2em; margin-top: 10px;">64 JUN 1998</div></div>	<div style="text-align: center; border-top: 1px solid black; border-bottom: 1px solid black;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="padding: 5px;">Authorized officer</div>
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*What Is Claimed Is:*

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:
  - (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
  - (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
  - (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
  - (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
  - (e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;
  - (f) a polynucleotide which is a variant of SEQ ID NO:X;
  - (g) a polynucleotide which is an allelic variant of SEQ ID NO:X;
  - (h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;
  - (i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.
2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.
3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
  - (h) an allelic variant of SEQ ID NO:Y; or
  - (i) a species homologue of the SEQ ID NO:Y.
12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.
13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.
14. A recombinant host cell that expresses the isolated polypeptide of claim 11.
15. A method of making an isolated polypeptide comprising:
- (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
  - (b) recovering said polypeptide.
16. The polypeptide produced by claim 15.
17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.
18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
- (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
  - (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.
19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
- (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and
  - (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- (a) contacting the polypeptide of claim 11 with a binding partner; and
- (b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
- (b) isolating the supernatant;
- (c) detecting an activity in a biological assay; and
- (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.

# PATENT COOPERATION TREATY

## PCT

### DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a) and Rule 39)

Applicant's or agent's file reference <b>PZ007PCT</b>	<b>IMPORTANT DECLARATION</b>	Date of mailing (day/month/year) <b>14 OCT 1998</b>
International application No. <b>PCT/US98/11422</b>	International filing date (day/month/year) <b>04 JUNE 1998</b>	(Earliest) Priority Date (day/month/year) <b>06 JUNE 1997</b>
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.		
Applicant <b>HUMAN GENOME SCIENCES, INC.</b>		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
  - a. ☐ scientific theories.
  - b. ☐ mathematical theories.
  - c. ☐ plant varieties.
  - d. ☐ animal varieties.
  - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
  - f. ☐ schemes, rules or methods of doing business.
  - g. ☐ schemes, rules or methods of performing purely mental acts.
  - h. ☐ schemes, rules or methods of playing games.
  - i. ☐ methods for treatment of the human body by surgery or therapy.
  - j. ☐ methods for treatment of the animal body by surgery or therapy.
  - k. ☐ diagnostic methods practiced on the human or animal body.
  - l. ☐ mere presentations of information.
  - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
 

☐ the description
☐ the claims
☐ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the prescribed requirements prevents a meaningful search from being carried out:
 

☒ it does not comply with the prescribed standard  
☒ it is not in the prescribed machine readable form
4. Further comments:  
Please See Continuation Sheet.

Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer:  <b>BRIAN R. STANTON</b>
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

**DECLARATION OF NON-ESTABLISHMENT OF  
INTERNATIONAL SEARCH REPORT**

International application No.  
PCT/US98/11422

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

IPC(6): A01N 37/18, 43/04; C12Q 1/00, 1/02, 1/68; C12N 5/00, 5/06, 15/00, 15/06, 15/09, 15/10, 15/11; G01N 33/53

US CL.: 435, 4, 7.1, 69.1, 70.1, 71.1, 172.3, 243, 320.1, 325, 410; 514/2, 44; 530/350, 387.1

**4. Further Comments (Continued):**

Applicant has not responded to the invitation to pay additional fees mailed on 04 August 1998. Therefore, the search would be conducted on the first appearing invention which includes claims 1-10, 14, and 15 in so far as these claims are drawn to the first ten (10) appearing nucleotide sequences. However, no meaningful search could be carried out on these sequences because the CRF that was received for this case on 15 June 1998 was technically defective and could not be used to conduct a search of the prior art.